OM protein - protein search, using sw model

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            GenCore version 5.1.6
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```

Run on: October 5, 2004, 18:50:04 ; Search time 33.2533 Seconds
                                             (without alignments)
                                         1232.039 Million cell updates/sec

Title: US-09-830-321a-1
Perfect score: 852
Sequence: 1 MELALLCGLVVMAGVIPIQG.........YQKRLRFYWRPHCRGQTPGC 145

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   A_Geneseq_29jan04:*
               1: geneseqp1980s:*
               2: geneseqp1990s:*
               3: geneseqp2000s:*
               4: geneseqp2001s:*
               5: geneseqp2002s:*
               6: geneseqp2003as:*
               7: geneseqp2003bs:*
               8: geneseqp2004s:*

                         SUMMARIES

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

Result No.	Score	% Query Match	Length	DB	ID	Description
1	852	100.0	145	3	AAB03627	Aab03627 Human pho
2	852	100.0	145	4	AAB12537	Aab12537 Human sec
3	852	100.0	145	4	AAM24100	Aam24100 Human EST
4	852	100.0	145	4	AAE11924	Aae11924 Human CG9
5	852	100.0	150	4	AAM25827	Aam25827 Human pro
6	846	99.3	145	4	AAU09096	Aau09096 Novel hum
7	846	99.3	145	6	ABR44234	Abr44234 Human sec
8	846	99.3	145	6	ABR58706	Abr58706 Human can
9	846	99.3	145	6	ABU63124	Abu63124 Human gro
10	624.5	73.3	144	3	AAB12536	Aab12536 Mouse sec
11	624.5	73.3	144	3	AAB11994	Aab11994 Mouse sec
12	500.5	58.7	116	3	AAB24434	Aab24434 Human PRO
13	500.5	58.7	116	3	AAY99450	Aay99450 Human PRO
14	500.5	58.7	116	4	AAB66199	Aab66199 Protein o
15	500.5	58.7	116	4	AAU12438	Aau12438 Human PRO
16	500.5	58.7	116	6	ABO17882	Abo17882 Novel hum
17	500.5	58.7	116	6	ABU81136	Abu81136 Human PRO
18	500.5	58.7	116	6	ABU66836	Abu66836 Human PRO
19	500.5	58.7	116	6	ABU59917	Abu59917 Novel sec
20	500.5	58.7	116	6	ABO25107	Abo25107 Human sec
21	500.5	58.7	116	6	ABU67112	Abu67112 Human sec
22	500.5	58.7	116	6	ADA46053	Ada46053 Novel hum
23	500.5	58.7	116	6	ADA76484	Ada76484 Human PRO
24	500.5	58.7	116	6	ADA19134	Ada19134 Human PRO
25	500.5	58.7	116	6	ADA61757	Ada61757 Homo sapi
26	500.5	58.7	116	6	ADB19542	Adb19542 Novel hum
27	500.5	58.7	116	6	ADB28083	Adb28083 Human PRO
28	500.5	58.7	116	6	ADA86562	Ada86562 Novel hum
29	500.5	58.7	116	6	ADB16126	Adb16126 Human PRO
30	500.5	58.7	116	6	ADA47912	Ada47912 Human PRO
31	500.5	58.7	116	6	ABO33692	Abo33692 Novel hum
32	500.5	58.7	116	6	ADA67707	Ada67707 Human PRO
33	500.5	58.7	116	6	ADB30714	Adb30714 Human PRO
34	500.5	58.7	116	6	ADA86010	Ada86010 Novel hum
35	500.5	58.7	116	6	ADA97222	Ada97222 Human PRO
36	500.5	58.7	116	6	ADA79526	Ada79526 Human PRO
37	500.5	58.7	116	6	ADA87665	Ada87665 Novel hum
38	500.5	58.7	116	6	ADB16867	Adb16867 Human PRO
39	500.5	58.7	116	6	ADA91959	Ada91959 Novel hum
40	500.5	58.7	116	6	ADB15022	Adb15022 Human PRO
41	500.5	58.7	116	6	ADB18983	Adb18983 Novel hum
42	500.5	58.7	116	6	ADA94198	Ada94198 Human PRO
43	500.5	58.7	116	6	ADB20094	Adb20094 Novel hum
44	500.5	58.7	116	6	ADB13406	Adb13406 Human PRO
45	500.5	58.7	116	6	ABO43415	Abo43415 Novel hum

ALIGNMENTS

RESULT 1
AAB03627
ID   AAB03627 standard; protein; 145 AA.
XX
AC   AAB03627;
XX
DT   05-OCT-2000 (first entry)
XX
DE   Human phospholipase 1 HPPL1.
XX
KW   Human; phospholipase 1; HPPL1; cancer; autoimmune disorder;
KW   inflammatory disorder; reproductive disorder; infection.
XX
OS   Homo sapiens.
XX
FH   Key   Location/Qualifiers
FT   Peptide   1..21
FT   /label= putative_signal_peptide
FT   Peptide   1..16
FT   /label= putative_signal_peptide
FT   Protein   17..145
FT   /label= putative_mature_HPPL1
FT   Active-site   21..145
FT   /label= phospholipase_A2_active_site_signature
FT   Protein   22..145
FT   /label= putative_mature_HPPL1
FT   Modified-site   33
FT   /label= potential_phosphorylation_site
FT   Region   44..92
FT   /label= active_site_histidine_region
FT   Region   88..140
FT   /label= active_site_aspartic_acid_region
FT   Modified-site   89
FT   /label= potential_glycosylation_site
FT   Modified-site   98
FT   /label= potential_phosphorylation_site
FT   Modified-site   102
FT   /label= potential_phosphorylation_site
XX
PN   WO200024911-A2.
XX
PD   04-MAY-2000.
XX
PF   27-OCT-1999; 99WO-US025021.
XX
PR   27-OCT-1998; 98US-00181317.
PR   21-JAN-1999; 99US-00234726.
XX

RESULT 2
AAB12537
ID   AAB12537 standard; protein; 145 AA.
XX
AC   AAB12537;
XX
DT   02-NOV-2000 (first entry)
XX
DE   Human secretory phospholipase A2 protein sequence SEQ ID NO:27.
XX
KW   Secretory phospholipase A2; PLA2; antiallergic; antiinflammatory;
KW   antibacterial; immunosuppressive; tranquiliser; vulnerary; antirheumatic;
KW   antiarthritic; septic shock; trauma; pancreatitis; allergic rhinitis;
KW   chronic rheumatoid arthritis.
XX
OS   Homo sapiens.
XX
FH   Key   Location/Qualifiers
FT   Peptide   1..10
FT   /label= signal
FT   Protein   21..145
FT   /label= PLA2
XX
PN   WO200034486-A1.
XX
PD   15-JUN-2000.
XX
PA   (INCY-) INCYTE PHARM INC.
XX
PI   Hillman JL, Bandman O, Guegler KJ, Corley NC, Baughn MR;
PI   Azimzai Y, Lal P, Lu DAM;
XX
DR   WPI; 2000-350750/30.
DR   N-PSDB; AAA53269.
XX
PT   Human phospholipase genes and proteins useful to diagnose, prevent or
PT   treat cancer, autoimmune or inflammatory or reproductive disorders.
XX
PS   Claim 1; Page 70-71; 80pp; English.
XX
CC   The present sequence is human phospholipase 1 (HPPL1). This protein is
CC   involved in the hydrolysis of membrane phospholipids. The protein and its
CC   coding sequence can be used to diagnose and treat the following: cancers
CC   such as prostate, breast and testicular cancers, autoimmune and
CC   inflammatory disorders such as AIDS, allergies, anaemia, asthma,
CC   atherosclerosis, Crohn's disease, diabetes mellitus, emphysema, Graves'
CC   disease, irritable bowel syndrome, multiple sclerosis, myasthenia gravis,
CC   psoriasis, rheumatoid arthritis and systemic lupus erythematosus,
CC   infection caused by viruses, fungi, bacteria, parasites and protozoa, and
CC   reproductive disorders including infertility, disruptions of the
CC   menstrual cycle, polycystic ovary syndrome, ectopic pregnancies,
CC   disruptions of spermatogenesis, cancers within the reproductive tract and
CC   impotence
XX
SQ   Sequence 145 AA;

Query Match   100.0%; Score 852; DB 3; Length 145;
Best Local Similarity   100.0%; Pred. No. 7e-77;
Matches 145; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   1 MELALLCGLVVMAGVIPIQGGIINLNKMVKQVTGKMPILSYWPYGCHCGLGGRGQPKDAT 60
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Db   1 MELALLCGLVVMAGVIPIQGGIINLNKMVKQVTGKMPILSYWPYGCHCGLGGRGQPKDAT 60

Qy   61 DWCCQTHDCCYDHLKTQGCGIYKDYRYRNFSQGNIHCSDKGSWCEQQLCACDKEVAFCLK 120
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 DWCCQTHDCCYDHLKTQGCGIYKDYRYRNFSQGNIHCSDKGSWCEQQLCACDKEVAFCLK 120

Qy 121 RNLDTYQKRLRFYWRPHCRGQTPGC 145
         |||||||||||||||||||||||||
Db 121 RNLDTYQKRLRFYWRPHCRGQTPGC 145

PF   07-DEC-1999; 99WO-JP006844.
XX
PR   09-DEC-1998; 98JP-00349608.
XX
PA   (SHIO) SHIONOGI & CO LTD.
XX
PI   Ishizaki J, Suzuki N, Hanasaki K;
XX
DR   WPI; 2000-423429/36.
DR   N-PSDB; AAA60878.
XX
PT   Human secretory phospholipase A2 (PLA2) and its encoded gene for
PT   diagnosis and treatment of secretory PLA2-associated diseases e.g. septic
PT   shock, trauma, pancreatitis, allergic rhinitis and chronic rheumatoid
PT   arthritis.
XX
PS   Claim 1; Page 41; 45pp; Japanese.
XX
CC   The present invention describes human secretory phospholipase A2 (PLA2).
CC   PLA2 has antiallergic, antiinflammatory, antibacterial, tranquiliser,
CC   immunosuppressive, vulnerary, antirheumatic and antiarthritic activities.
CC   Human secretory phospholipase A2 (PLA2), the gene encoding it and
CC   antibodies against it are useful for the diagnosis and treatment of
CC   secretory PLA2-associated diseases e.g. septic shock, trauma,
CC   pancreatitis, allergic rhinitis and chronic rheumatoid arthritis. The
CC   present sequence represents human PLA2
XX
SQ   Sequence 145 AA;

Query Match   100.0%; Score 852; DB 3; Length 145;
Best Local Similarity   100.0%; Pred. No. 7e-77;
Matches 145; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   1 MELALLCGLVVMAGVIPIQGGIINLNKMVKQVTGKMPILSYWPYGCHCGLGGRGQPKDAT 60
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 MELALLCGLVVMAGVIPIQGGIINLNKMVKQVTGKMPILSYWPYGCHCGLGGRGQPKDAT 60

Qy   61 DWCCQTHDCCYDHLKTQGCGIYKDYRYRNFSQGNIHCSDKGSWCEQQLCACDKEVAFCLK 120
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 DWCCQTHDCCYDHLKTQGCGIYKDYRYRNFSQGNIHCSDKGSWCEQQLCACDKEVAFCLK 120

Qy 121 RNLDTYQKRLRFYWRPHCRGQTPGC 145
         |||||||||||||||||||||||||
Db 121 RNLDTYQKRLRFYWRPHCRGQTPGC 145

RESULT 3
AAM24100
ID   AAM24100 standard; protein; 145 AA.
XX
AC   AAM24100;
XX
DT   12-OCT-2001 (first entry)
XX
DE   Human EST encoded protein SEQ ID NO: 1625.
XX
KW   Human; sheep; pig; cow; fruit fly; yeast; hamster; macaque; horse;
KW   tomato; monkey; dog; sea urchin; expressed sequence tag; EST;
KW   diagnostics; forensic test; gene mapping; genetic disorder; biodiversity;
KW   gene therapy; nutrition.
XX
OS   Homo sapiens.
XX
PN   WO200154477-A2.
XX
PD   02-AUG-2001.
XX
PF   25-JAN-2001; 2001WO-US002687.
XX
PR   25-JAN-2000; 2000US-00491404.
PR   17-JUL-2000; 2000US-00617746.
PR   03-AUG-2000; 2000US-00631451.
PR   15-SEP-2000; 2000US-00663870.
XX

XX
PA (HYSE-) HYSEQ INC.
XX
PI Tang YT, Liu C, Zhou P, Qian XB, Wang Z, Chen R, Asundi V;
PI Cao Y, Drmanac RA, Zhang J, Werhman T;
XX
DR WPI; 2001-476164/51.
DR N-PSDB; AAH98759.
XX
PT Isolated polypeptide for treatment of diseases, diagnostics, raising
PT antibodies and research use.
XX
PS Claim 20; Page 1102; 1275pp; English.
XX
CC The present invention provides the protein and coding sequences of novel
CC proteins from a variety of organisms, including human, dog, cat, horse,
CC cow, pig, hamster, monkey, macaque, yeast, bacteria, fruit fly, sea
CC urchin and tomato. These were derived from expressed sequence tags (ESTs)
CC from the organism of interest. They can be used in diagnostics,
CC forensics, gene mapping, identification of mutations, to assess
CC biodiversity and for nutritional purposes. The present sequence is a
CC protein of the invention
XX
SQ Sequence 145 AA;

Query Match   100.0%; Score 852; DB 4; Length 145;
Best Local Similarity 100.0%; Pred. No. 7e-77;
Matches 145; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy   1 MELALLCGLVVMAGVIPIQGGILNLNKMVKQVTGKMPILSYWPYGCHCGLGGRGQPKDAT 60
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 MELALLCGLVVMAGVIPIQGGILNLNKMVKQVTGKMPILSYWPYGCHCGLGGRGQPKDAT 60

Qy   61 DWCCQTHDCCYDHLKTQGCGIYKDYYRYNFSQGNIHCSDKGSWCEQQLCACDKEVAFCLK 120
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 DWCCQTHDCCYDHLKTQGCGIYKDYYRYNFSQGNIHCSDKGSWCEQQLCACDKEVAFCLK 120

Qy 121 RNLDTYQKRLRFYWRPHCRGQTPGC 145
         |||||||||||||||||||||||||
Db 121 RNLDTYQKRLRFYWRPHCRGQTPGC 145

RESULT 4
AAEI1924
ID AAEI1924 standard; protein; 145 AA.
XX
AC AAEI1924;
XX
DT 18-DEC-2001 (first entry)
XX
DE Human CG95 (or C870) lipase protein.
XX
KW Human; apolipoprotein; lipase; lipoprotein receptor; ALLr; angina;
KW cardiovascular disease; lipid metabolism; myocardial infarction;
KW cerebral ischaemia; arterial thrombosis; thrombolytic; antilipaemic;
KW coronary artery thrombosis; cerebral artery thrombosis; stroke;
KW intracardiac thrombosis; gene therapy; cardiovascular; vasodilator;
KW neuroprotectant; cerebroprotective.
XX
OS Homo sapiens.
XX
FH Key   Location/Qualifiers
FT Peptide   1..24
FT   /label= Signal_peptide
FT Domain   21..145
FT   /note= "Phospholipase A2 domain"
FT Protein   25..145
FT   /note= "Human mature CG95 (or C870) protein"
XX
PN WO200179446-A2.
XX
PD 25-OCT-2001.
XX

PF 16-APR-2001; 2001WO-US012529.
XX
PR 14-APR-2000; 2000US-0197137P.
PR 20-JUN-2000; 2000US-00598042.
PR 03-AUG-2000; 2000US-00631451.
PR 22-SEP-2000; 2000US-00667298.
PR 17-NOV-2000; 2000US-00714936.
XX
PA (HYSE-) HYSEQ INC.
XX
PI Ballinger DG, Loeb D, Montgomery JR, Tang TY, Zhou P, Goodrich R;
PI Liu C, Asundi V, Zhao QA, Wehrman T, Drmanac RT, Ren F, Qian XB;
PI Wang D;
XX
DR WPI; 2001-611724/70.
DR N-PSDB; AAD19218.
XX
PT Nucleic acids encoding human apolipoproteins, lipases, and lipoprotein
PT receptor polypeptides, useful for preventing diagnosing and treating
PT lipid metabolism disorders, thrombosis and cardiovascular diseases.
XX
PS Claim 10; Fig 1; 266pp; English.
XX
CC The invention relates to polynucleotides encoding proteins CG122, CG179,
CC CG95, CG121, CG162, CG27, CG153 and CG168 which are related to proteins
CC involved in lipid metabolism and cardiovascular disease such as human
CC apolipoproteins, lipases and lipoprotein receptor proteins. These DNA and
CC protein sequences are useful for treating or preventing disorders (ALLr)
CC associated with apolipoproteins, lipases and lipoprotein receptor (ALLr)
CC expression and for treating lipid metabolism, cardiovascular diseases and
CC thrombosis. Antibodies against these proteins are useful for determining
CC the presence of or predisposition to a disease associated with altered
CC levels of these sequences. ALLr polypeptides are also useful for
CC identifying agents (agonists and antagonists) that bind to them and cells
CC expressing ALLr proteins are useful for identifying a therapeutic agent
CC for use in treatment of a pathology related to aberrant expression or
CC physiological interactions of this polypeptide. Vectors comprising these
CC DNA and protein sequences are also useful for producing ALLr proteins.
CC The nucleic acids and polypeptides of the invention are also useful for
CC the treatment of occlusive cardiovascular diseases, myocardial
CC infarction, cerebral ischaemia, angina, arterial thrombosis, coronary
CC artery thrombosis and cerebral artery thrombosis or intracardiac
CC thrombosis and stroke. The nucleotides of the invention are used in gene
CC therapy. The present sequence is human CG95 (or C870) lipase protein
XX
SQ Sequence 145 AA;

Query Match   100.0%; Score 852; DB 4; Length 145;
Best Local Similarity 100.0%; Pred. No. 7e-77;
Matches 145; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy   1 MELALLCGLVVMAGVIPIQGGILNLNKMVKQVTGKMPILSYWPYGCHCGLGGRGQPKDAT 60
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 MELALLCGLVVMAGVIPIQGGILNLNKMVKQVTGKMPILSYWPYGCHCGLGGRGQPKDAT 60

Qy   61 DWCCQTHDCCYDHLKTQGCGIYKDYYRYNFSQGNIHCSDKGSWCEQQLCACDKEVAFCLK 120
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 DWCCQTHDCCYDHLKTQGCGIYKDYYRYNFSQGNIHCSDKGSWCEQQLCACDKEVAFCLK 120

Qy 121 RNLDTYQKRLRFYWRPHCRGQTPGC 145
         |||||||||||||||||||||||||
Db 121 RNLDTYQKRLRFYWRPHCRGQTPGC 145

RESULT 5
AAM25827
ID AAM25827 standard; protein; 150 AA.
XX
AC AAM25827;
XX
DT 16-OCT-2001 (first entry)
XX
DE Human protein sequence SEQ ID NO:1342.

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Qy   61 DWCCQTHDCCYDHLKTQGCGIYKDYRYRNFSQGNIHCSDKGSWCEQQLCACDKEVAFCLK 120
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   66 DWCCQTHDCCYDHLKTQGCGIYKDYRYRNFSQGNIHCSDKGSWCEQQLCACDKEVAFCLK 125

Qy  121 RNLDTYQKRLRFYWRPHCRGQTPGC 145
          |||||||||||||||||||||||||
Db  126 RNLDTYQKRLRFYWRPHCRGQTPGC 150
```

RESULT 6
AAU09096
ID   AAU09096 standard; protein; 145 AA.
XX
AC   AAU09096;
XX
DT   20-DEC-2001 (first entry)
XX
DE   Novel human protein NHP #5.
XX
KW   Human; novel human protein; NHP; antidiabetic; antirheumatic;
KW   antiarthritic; cytostatic; antiarteriosclerotic; vulnerary;
KW   neuroprotective; nootropic; antiparkinsonian;
KW   anti-human immunodeficiency virus; antiasthmatic; vasotropic; cardiant;
KW   hypotensive; anorectic; antiinfertility; neuroleptic; anticonvulsant;
KW   antimanic; immunosuppressive; cerebroprotective; antimicrobial;
KW   antiinflammatory; antibacterial; antipsoriatic; thyromimetic;
KW   immunomodulator; antiseborrheic; dermatological; vasoconstriction;
KW   gastrointestinal disorder; cardiovascular disorder; hypertension;
KW   coronary heart disease; arteriosclerosis; anorexia; obesity; bulimia;
KW   cachexia; male infertility; impotence; testicular cancer; lung tumour;
KW   hyperproliferative disorder; pulmonary system disorder;
KW   central nervous system disorder; bone disorder;
KW   neurodegenerative disease; Alzheimer's disease; Parkinson's disease;
KW   Huntington's disease; schizophrenia; mania; dementia; paranoia;
KW   panic disorder; learning disability; amyotropic lateral sclerosis;
KW   psychosis; autism; sleep disorder; immune system disorder;
KW   Hashimoto's thyroiditis; musculo-skeletal system disorders;
KW   multiple sclerosis; ischaemic brain injury; stroke; infectious disease;
KW   diabetes mellitus; immunological disorder; asthma; AIDS; immunogen;
KW   acquired immunodeficient syndrome; leukaemia; rheumatoid arthritis;
KW   inflammatory bowel disease; sepsis; acne; psoriasis; lupus erythematosus;
KW   neural system disorder; respiratory disorder; olfactory disorder;
KW   wound healing.
XX
OS   Homo sapiens.
XX
FH   Key   Location/Qualifiers
FT   Region   52..65
FT   /label= Immunogenic_epitope
FT   Region   67..78
FT   /label= Immunogenic_epitope
FT   Region   87..105
FT   /label= Immunogenic_epitope
FT   Region   121..129
FT   /label= Immunogenic_epitope
FT   Region   136..141
FT   /label= Immunogenic_epitope
XX
PN   WO200174896-A1.
XX
PD   11-OCT-2001.
XX
PF   02-APR-2001; 2001WO-US010542.
XX
PR   03-APR-2000; 2000US-0194118P.
PR   29-SEP-2000; 2000US-0236384P.
XX
PA   (HUMA-) HUMAN GENOME SCI INC.
XX
PI   Moore PA, Ni J, Soppet DR, Coleman TA, Gentz RL, Endress GA,
PI   Li Y, Dillon PJ;
XX
DR   WPI; 2001-626394/72.
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XX
KW   Human; cancer; ulcer; HIV infection; human immunodeficiency virus;
KW   antiinflammatory; antirheumatic; antiarthritic; immunosuppressive;
KW   antibacterial; endocrine; cardiant; central nervous system; virucide;
KW   anti-HIV; fungicide; antimutagen; cardiovascular; antianaemic; anaemia;
KW   antiaggregant; haemostatic; vulnerary; antiulcer; osteopathic; eczema;
KW   dermatological; antiallergic; antiasthmatic; antidiabetic; cytostatic;
KW   neuroprotective; antidepressant; nootropic; antiparkinsonian; infection;
KW   immunostimulant; gene therapy; antisense therapy; vaccine; inflammation;
KW   antianaphylactic; rheumatoid arthritis; septic shock; pancreatitis;
KW   cardiac dysfunction; neuropathology; cardiac anaphylaxis; autoimmunity;
KW   genetic disease; haematopoietic disorder; platelet disorder; asthma;
KW   thrombocytopaenia; osteoporosis; severe combined immunodeficiency;
KW   allergic rhinitis; diabetes; multiple sclerosis; depression;
KW   Alzheimer's disease; Parkinson's disease; neurodegenerative disorder;
KW   neurological disorder.
XX
OS   Homo sapiens.
XX
PN   WO200153455-A2.
XX
PD   26-JUL-2001.
XX
PF   22-DEC-2000; 2000WO-US035017.
XX
PR   23-DEC-1999;     99US-00471275.
PR   21-JAN-2000; 2000US-0048725.
PR   25-APR-2000; 2000US-0055231?.
XX
PA   (HYSE-) HYSEQ INC.
XX
PI   Tang YT, Liu C, Drmanac RT;
XX
DR   WPI; 2001-457603/49.
DR   N-PSDB; AAH99768.
XX
PT   Isolated human polynucleotides encoding polypeptides, useful for the
PT   treatment and diagnosis of e.g. cancer, ulcers and HIV infection.
XX
PS   Claim 20; Page 278; 1217pp; English.
XX
CC   AAH99166 to AAH99904 encode the human proteins given in AAM25225 to
CC   AAM25963. The proteins can have activities based on the tissues and cells
CC   they are expressed in, such as: antiinflammatory; antirheumatic;
CC   antiarthritic; immunosuppressive; antibacterial; endocrine; cardiant;
CC   central nervous system; virucide; immunomodulatory; anti-HIV; fungicide; antimutagen;
CC   cardiovascular; antianaemic; antiaggregant; haemostatic; vulnerary;
CC   antiulcer; osteopathic; dermatological; antiallergic; antiasthmatic;
CC   antidiabetic; cytostatic; neuroprotective; antidepressant; nootropic;
CC   antiparkinsonian; and immunostimulant. The proteins and polynucleotides
CC   encoding them can be used in gene therapy, antisense therapy and vaccine
CC   production. The proteins and polynucleotides are useful for screening for
CC   agonists or antagonists of a protein and for the treatment and diagnosis
CC   of disorders associated with the activity of a protein e.g. inflammation,
CC   rheumatoid arthritis, septic shock, pancreatitis, cardiac dysfunction,
CC   neuropathology, cardiac anaphylaxis, viral, bacterial, HIV and fungal
CC   infections, autoimmunity, genetic diseases, haematopoietic disorders,
CC   anaemia, platelet disorders, thrombocytopaenia, wounds, burns, ulcers,
CC   osteoporosis, severe combined immunodeficiency, eczema, allergic
CC   rhinitis, asthma, diabetes, cancer, multiple sclerosis, depression,
CC   Alzheimer's disease, Parkinson's disease, neurodegenerative and
CC   neurological disorders
XX
SQ   Sequence 150 AA;

Query Match             100.0%;  Score 852; DB 4; Length 150;
Best Local Similarity   100.0%;  Pred. No. 7.3e-77;
Matches  145; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy    1 MELALLCGLVVMAGVIPIQGGIlNLNRMVKQVTGKMPILSYWPYGGHCGLGGRGQPKDAT 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    6 MELALLCGLVVMAGVIPIQGGIlNLNRMVKQVTGKMPILSYWPYGGHCGLGGRGQPKDAT 65
```

DR N-PSDB; AAS14884.
XX
PT New human proteins, useful for diagnosing, treating, preventing and/or
PT prognosing disorders related to the proteins, including cardiovascular
PT disorders, autoimmune disorders and reproductive disorders.
XX
PS Claim 11; Page 306-307; 318pp; English.
XX
CC The invention relates to novel human proteins (NHP) and the nucleic acids
CC that encode them and antibodies raised against them. The proteins,
CC antibodies and nucleic acids are useful in the diagnosis, prognosis,
CC prevention and/or treatment or diseases and/or disorders involving
CC vasoconstriction, gastrointestinal disorders, cardiovascular disorders
CC (e.g. hypertension, erectile dysfunction, high blood pressure, coronary
CC heart disease and arteriosclerosis), anorexia, obesity, bulimia,
CC cachexia, disorders of small intestine, disorders of reproductive system
CC (e.g. male infertility and/or impotence), testicular cancer, lung tumours
CC and other hyperproliferative disorders, disorders of pulmonary system,
CC central nervous system disorders, bone disorders, neurodegenerative
CC diseases and behavioural disorders (e.g. Alzheimer's disease, Parkinson's
CC disease, Huntington's disease, schizophrenia, mania, dementia, paranoia,
CC panic disorder, learning disabilities, amyotrophic lateral sclerosis,
CC psychoses, autism, sleep disorders), immune system disorders (e.g.
CC Hashimoto's thyroiditis), renal and musculo-skeletal system disorders,
CC central nervous system disorders (e.g. multiple sclerosis, ischaemic
CC brain injury and/or stroke), infectious diseases, diabetes mellitus,
CC immunological disorders (e.g. asthma, acquired immunodeficient syndrome
CC (AIDS), leukaemia, rheumatoid arthritis, inflammatory bowel disease,
CC sepsis, acne, psoriasis and lupus erythematosus), neural system
CC disorders, respiratory disorders, olfactory disorders and wound healing.
CC The present sequence represents an NHP of the invention
XX
SQ Sequence 145 AA;

Query Match   99.3%; Score 846; DB 4; Length 145;
Best Local Similarity   99.3%; Pred. No. 2.8e-76;
Matches 144; Conservative   0; Mismatches   1; Indels   0; Gaps   0;

Qy   1 MELALLCGLVVMAGVIPIQGGILNLNKMVKQVTGKMPILSYWPYGCHCGLGGRGQPKDAT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 MELALLCGLVVMAGVIPIQGGILNLNKMVKQVTGKMPILSYWPYGCHCGLGGRGQPKDAT 60

Qy   61 DWCCQTHDCCYDHLKTQGCGIYKDYRYNFSQGNIHCSDKGSWCEQQLCACDKEVAFCLK 120
              ||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||
Db   61 DWCCQTHDCCYDHLKTQGCSIYKDYRYNFSQGNIHCSDKGSWCEQQLCACDKEVAFCLK 120

Qy   121 RNLDTYQKRLRFYWRPHCRGQTPGC 145
              |||||||||||||||||||||||||
Db   121 RNLDTYQKRLRFYWRPHCRGQTPGC 145

RESULT 7
ABR44234
ID ABR44234 standard; protein; 145 AA.
XX
AC ABR44234;
XX
DT 18-AUG-2003 (first entry)
XX
DE Human secreted group IID phospholipase A2 (sPLA2) enzyme.
XX
KW Group IIF secreted phospholipase A2; sPLA2; phosphatidylglycerol; human;
KW phosphatidylcholine; antibacterial; virucide; cytostatic; vasotropic;
KW antiinflammatory; vulnerary; cardiant; chromosome 1p35; transgenic;
KW enzyme.
XX
OS Homo sapiens.
XX
PN WO200303689-A1.
XX
PD 24-APR-2003.
XX
PF 12-OCT-2001; 2001WO-IB002407.

XX
PR 12-OCT-2001; 2001WO-IB002407.
XX
PA (CNRS) CNRS CENT NAT RECH SCI.
XX
PI Lazdunski M, Lambeau G, Valentin E;
XX
DR WPI; 2003-403216/38.
XX
PT Novel mammalian secreted group IIF secreted phospholipase A2, useful for
PT preventing and treating bacterial and viral infections, and cancers.
XX
PS Disclosure; Fig 1; 33pp; English.
XX
CC The invention relates to a mammalian secreted group IIF secreted
CC phospholipase A2 (sPLA2) (I), where the enzyme is Ca2+ dependent,
CC maximally active at pH 7-8 and hydrolyzes phosphatidylglycerol versus
CC phosphatidylcholine with a 15-fold preference. A pharmaceutical
CC composition comprising (I) is useful for treating or preventing viral and
CC bacterial infections, and cancers. A pharmaceutical composition
CC containing compounds capable of inhibiting catalytic activity of (I),
CC biologically active compounds that bind sPLA_2 receptors, or a compound
CC that modulates cell roliferation, cell migration, cell contraction or
CC apoptosis is useful for treating disease states or disorders involving
CC group IIF sPLA2, such as inflammatory disease, cancers, cardiac and brain
CC ischaemia, acute lung injury, acute respiratory distress syndrome or
CC Crohn's disease. Specific antibodies are useful for searching new
CC secreted mammalian group IIF sPLA2 or the homologues of the enzyme in
CC other mammals. The encoding polynucleotides and vectors are useful for
CC transforming animals and establishing a line of transgenic animals.
CC Sequences ABR44232-238 represent various human secreted sPLA2 enzymes
CC used in alignment studies with the GIIF sPLA2 enzyme
XX
SQ Sequence 145 AA;

Query Match   99.3%; Score 846; DB 6; Length 145;
Best Local Similarity   99.3%; Pred. No. 2.8e-76;
Matches 144; Conservative   0; Mismatches   1; Indels   0; Gaps   0;

Qy   1 MELALLCGLVVMAGVIPIQGGILNLNKMVKQVTGKMPILSYWPYGCHCGLGGRGQPKDAT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 MELALLCGLVVMAGVIPIQGGILNLNKMVKQVTGKMPILSYWPYGCHCGLGGRGQPKDAT 60

Qy   61 DWCCQTHDCCYDHLKTQGCGIYKDYRYNFSQGNIHCSDKGSWCEQQLCACDKEVAFCLK 120
              ||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||
Db   61 DWCCQTHDCCYDHLKTQGCSIYKDYRYNFSQGNIHCSDKGSWCEQQLCACDKEVAFCLK 120

Qy   121 RNLDTYQKRLRFYWRPHCRGQTPGC 145
              |||||||||||||||||||||||||
Db   121 RNLDTYQKRLRFYWRPHCRGQTPGC 145

RESULT 8
ABR58706
ID ABR58706 standard; protein; 145 AA.
XX
AC ABR58706;
XX
DT 09-JUL-2003 (first entry)
XX
DE Human cancer related protein SEQ ID NO:363.
XX
KW Human; cancer; diagnosis; screening; modulator; leukaemia; ischaemia;
KW heart disease; atherosclerosis; endometriosis.
XX
OS Homo sapiens.
XX
PN WO200305138-A2.
XX
PD 27-MAR-2003.
XX
PF 17-SEP-2002; 2002WO-US029560.
XX

```
PR   17-SEP-2001; 2001US-0323469P.
PR   20-SEP-2001; 2001US-0323887P.
PR   13-NOV-2001; 2001US-0350666P.
PR   08-FEB-2002; 2002US-0355145P.
PR   08-FEB-2002; 2002US-0355257P.
PR   12-APR-2002; 2002US-0372246P.
XX
PA   (EOSB-) EOS BIOTECHNOLOGY INC.
XX
PI   Afar D, Aziz N, Gish KC, Hevezi PA, Mack DH, Wilson KE;
PI   Zlotnik A;
XX
DR   WPI; 2003-354600/33.
DR   N-PSDB: ACC72857.
XX
PT   New genes that are up-regulated or down-regulated in cancers, useful as
PT   markers for diagnosing e.g. cancer, ischemia or heart diseases, or as
PT   therapeutic targets for screening drugs for treating these diseases.
XX
PS   Claim 12; Page 763; 767pp; English.
XX
CC   The present invention describes an isolated nucleic acid molecule, which
CC   comprises the sequence of any of the genes that are up-regulated or down-
CC   regulated in specific cancers (e.g. about 1031 genes up-regulated in
CC   acute lymphocytic leukemia). ACC72641 to ACC72860 represent cancer
CC   related gene nucleotide sequences which encode the proteins given in
CC   ABR58821 to ABR58709. Also described: (1) determining the presence or
CC   absence of a pathological cell in a patient; (2) an expression vector
CC   comprising a nucleic acid molecule described above; (3) a host cell
CC   comprising the vector; (4) an isolated polypeptide, which is encoded by
CC   the nucleic acid; (5) an antibody that specifically binds the polypeptide
CC   of (4); (6) specifically targeting a compound to a pathological cell in a
CC   patient by administering to the patient the antibody above; and (7) a
CC   drug screening assay. The nucleic acid is useful as diagnostic markers or
CC   therapeutic targets. In particular, the nucleic acid is useful for
CC   diagnosing a pathology, e.g. cancer (e.g. cancer of the bone marrow,
CC   bladder, brain, breast, cervix, colon/rectum, kidney, lung, ovary,
CC   pancreas, prostate, skin and uterus), wounds, ischaemia, heart diseases,
CC   atherosclerosis and endometriosis. The nucleic acid is also useful in
CC   drug screening, particularly for identifying agents for treating these
CC   pathologies
XX
SQ   Sequence 145 AA;

Query Match             99.3%;  Score 846;  DB 6;  Length 145;
Best Local Similarity   99.3%;  Pred. No. 2.8e-76;
Matches  144;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps     0;

Qy          1 MELALLCGLVVMAGVIPIQGGILNLNKMVKQVTGKMPILSYWPYGCHCGLGGRGQOPKDAT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MELALLCGLVVMAGVIPIQGGILNLNKMVKQVTGKMPILSYWPYGCHCGLGGRGQOPKDAT 60

Qy         61 DWCCQTHDCCYDHLKTQGCIYKDYYRYNFSQGNIHCSDKGSWCEQQLCACDKEVAFCLK 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 DWCCQTHDCCYDHLKTQGCIYKDYYRYNFSQGNIHCSDKGSWCEQQLCACDKEVAFCLK 120

Qy        121 RNLDTYQKRLRFYWRPHCRGQTPGC 145
              |||||||||||||||||||||||||
Db        121 RNLDTYQKRLRFYWRPHCRGQTPGC 145

RESULT 9
ABU63124
ID   ABU63124 standard; protein; 145 AA.
XX
AC   ABU63124;
XX
DT   25-SEP-2003  (first entry)
XX
DE   Human group IID secreted phospholipase A2.
XX
KW   Human; group IID secreted phospholipase A2; virucide; antibacterial;
KW   cytostatic; antiinflammatory; vasotropic; cerebroprotective; sPLA2;
```

```
KW   phosphatidylglycerol hydrolysis; phosphatidylcholine hydrolysis;
KW   viral infection; bacterial infection; cancer; inflammatory disease;
KW   cardiac ischaemia; brain ischaemia; acute lung injury;
KW   acute respiratory distress syndrome; Crohn's disease; enzyme.
XX
OS   Homo sapiens.
XX
PN   US200307087-A1.
XX
PD   17-APR-2003.
XX
PF   11-OCT-2001; 2001US-00975456.
XX
PR   11-OCT-2000; 2000US-0239491P.
XX
PA   (LAZD/) LAZDUNSKI M.
PA   (LAMB/) LAMBEAU G.
PA   (VALE/) VALENTIN E.
XX
PI   Lazdunski M, Lambeau G, Valentin E;
XX
DR   WPI; 2003-567302/53.
XX
PT   New mammalian secreted group IIF phospholipase A2 or nucleic acid, useful
PT   for treating or preventing viral or bacterial infections, or cancers, or
PT   screening inhibitors of the enzyme for treating e.g. inflammatory
PT   diseases or ischemia.
XX
PS   Disclosure; Fig 1; 16pp; English.
XX
CC   The invention describes a mammalian secreted group IIF phospholipase A2
CC   (sPLA2), which is Ca2-dependent, maximally active at pH of about 7-8,
CC   and hydrolyses phosphatidylglycerol versus phosphatidylcholine with about
CC   a 15-fold preference. The mammalian secreted group IIF sPLA2 protein or
CC   nucleic acid, or a pharmaceutical composition is useful for treating
CC   and/or preventing viral infections, bacterial infections, or cancers. The
CC   inhibitors of sPLA2 or a composition comprising sPLA2 inhibitors is
CC   useful for treating disease states or disorders involving group IIF
CC   sPLA2, e.g. inflammatory diseases, cancer, cardiac and brain ischaemia,
CC   acute lung injury, acute respiratory distress syndrome, or Crohn's
CC   disease. The enzyme is also useful for screening various chemical
CC   compounds for treating these diseases. This is the amino acid sequence of
CC   human group IID phospholipase A2 used to determine a consensus sequence
CC   for human sPLA2s
XX
SQ   Sequence 145 AA;

Query Match             99.3%;  Score 846;  DB 6;  Length 145;
Best Local Similarity   99.3%;  Pred. No. 2.8e-76;
Matches  144;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps     0;

Qy          1 MELALLCGLVVMAGVIPIQGGILNLNKMVKQVTGKMPILSYWPYGCHCGLGGRGQOPKDAT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MELALLCGLVVMAGVIPIQGGILNLNKMVKQVTGKMPILSYWPYGCHCGLGGRGQOPKDAT 60

Qy         61 DWCCQTHDCCYDHLKTQGCIYKDYYRYNFSQGNIHCSDKGSWCEQQLCACDKEVAFCLK 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 DWCCQTHDCCYDHLKTQGCIYKDYYRYNFSQGNIHCSDKGSWCEQQLCACDKEVAFCLK 120

Qy        121 RNLDTYQKRLRFYWRPHCRGQTPGC 145
              |||||||||||||||||||||||||
Db        121 RNLDTYQKRLRFYWRPHCRGQTPGC 145

RESULT 10
AAB12536
ID   AAB12536 standard; protein; 144 AA.
XX
AC   AAB12536;
XX
DT   02-NOV-2000  (first entry)
XX
DE   Mouse secretory phospholipase A2 protein sequence SEQ ID NO:14.
```

```
XX
KW   Secretory phospholipase A2; PLA2; antiallergic; antiinflammatory;
KW   antibacterial; immunosuppressive; tranquiliser; vulnerary; antirheumatic;
KW   antiarthritic; septic shock; trauma; pancreatitis; allergic rhinitis;
KW   chronic rheumatoid arthritis.
XX
OS   Mus musculus.
XX
FH   Key            Location/Qualifiers
FT   Peptide        1..19
FT                  /label= signal
FT   Protein        20..144
FT                  /label= PLA2
XX
PN   WO200034486-A1.
XX
PD   15-JUN-2000.
XX
PF   07-DEC-1999;   99WO-JP006844.
XX
PR   09-DEC-1998;   98JP-00349608.
XX
PA   (SHIO ) SHIONOGI & CO LTD.
XX
PI   Ishizaki J, Suzuki N, Hanasaki K;
XX
DR   WPI; 2000-423429/36.
DR   N-PSDB; AAA60866.
XX
PT   Human secretory phospholipase A2 (PLA2) and its encoded gene for
PT   diagnosis and treatment of secretory PLA2-associated diseases e.g. septic
PT   shock, trauma, pancreatitis, allergic rhinitis and chronic rheumatoid
PT   arthritis.
XX
PS   Example 3; Page 37; 45pp; Japanese.
XX
CC   The present invention describes human secretory phospholipase A2 (PLA2).
CC   PLA2 has antiallergic, antiinflammatory, antibacterial, tranquiliser,
CC   immunosuppressive, vulnerary, antirheumatic and antiarthritic activities.
CC   Human secretory phospholipase A2 (PLA2), the gene encoding it and
CC   antibodies against it are useful for the diagnosis and treatment of
CC   secretory PLA2-associated diseases e.g. septic shock, trauma,
CC   pancreatitis, allergic rhinitis and chronic rheumatoid arthritis. The
CC   present sequence represents mouse PLA2, which is used in an example from
CC   the present invention
XX
SQ   Sequence 144 AA;

     Query Match             73.3%;  Score 624.5;  DB 3;  Length 144;
     Best Local Similarity   71.0%;  Pred. No. 3.2e-54;
     Matches   103;  Conservative    14;  Mismatches    27;  Indels     1;  Gaps     1;

Qy          1 MELALLCGLVVMAGVIPIQGGILNLNKMVKQVTGKMPILSYWPYGCHCGLGGRGQPKDAT 60
              ||||||||:|:|||||||||||||||||||||||||||:|||||||||||||||||||||
Db          1 MRLALLCGL-LLAGITATQGGLLNLNKMVTHMTGKKAFFSYWPYGCHCGLGGKGQPKDAT 59

Qy         61 DWCCQTHDCCYDHLKTQGCGIYKDYIRYNFSQGNIHCSDKGSWCEQQLCACDKEVAFCLK 120
              |||||||||:||||||||||||||||||:||||||:|||||:||||||||:||||||:||
Db         60 DWCCQKHDCCYAHLKIDGCKSLTDNYKYSISQGTIQCSDNGSWCERQLCACDKEVALCLK 119

Qy        121 RNLDTYQKRLRFYWRPHCRGQTPGC 145
              :||||:||||||||||||:|:||:|
Db        120 QNLDSYNKRLRYYWRPRCKGKTPAC 144

RESULT 11
AAB11994
ID   AAB11994 standard; protein; 144 AA.
XX
AC   AAB11994;
XX
DT   24-NOV-2000  (first entry)
XX
```

```
DE   Mouse secreted phospholipase A2.
XX
KW   Secreted phospholipase A2; PLA2; mouse; murine; recombinant production;
KW   antibody; diagnosis; drug screening; expressed sequence tag; EST.
XX
OS   Mus musculus.
XX
FH   Key            Location/Qualifiers
FT   Peptide        1..19
FT                  /note= "Signal peptide"
FT   Protein        20..144
FT                  /note= "Mouse mature secreted phospholipase A2"
XX
PN   JP200016544-A.
XX
PD   20-JUN-2000.
XX
PF   09-DEC-1998;   98JP-00349602.
XX
PR   09-DEC-1998;   98JP-00349602.
XX
PA   (SHIO ) SHIONOGI & CO LTD.
XX
DR   WPI; 2000-458171/40.
DR   N-PSDB; AAA72076.
XX
PT   Mouse secretion type phospholipase A2.
XX
PS   Claim 1; Page 10-11; 12pp; Japanese.
XX
CC   This sequence represents a mouse secreted phospholipase A2 (secreted
CC   PLA2). A cDNA was initially identified in an EST (expressed sequence tag)
CC   database, and a fragment (AAA72077) was isolated from cDNA derived from
CC   several mouse tissue types using primers AAA72078-A72081). The full
CC   length cDNA was generated using primers AAA72082-A72088. The invention
CC   relates to the novel secreted PLA2, nucleic acids encoding it, and
CC   variants of the protein which retain phospholipase A2 activity. It also
CC   encompasses an expression vector and host cells comprising DNA encoding
CC   murine secreted PLA2, a method for the recombinant production of the
CC   protein, a method of screening potential inhibitors of the protein and
CC   the compounds thus identified, and an antibody specific for murine PLA2.
CC   The antibody can be used for the diagnosis of a variety of diseases
XX
SQ   Sequence 144 AA;

     Query Match             73.3%;  Score 624.5;  DB 3;  Length 144;
     Best Local Similarity   71.0%;  Pred. No. 3.2e-54;
     Matches   103;  Conservative    14;  Mismatches    27;  Indels     1;  Gaps     1;

Qy          1 MELALLCGLVVMAGVIPIQGGILNLNKMVKQVTGKMPILSYWPYGCHCGLGGRGQPKDAT 60
              ||||||||:|:|||||||||||||||||||||||||||:|||||||||||||||||||||
Db          1 MRLALLCGL-LLAGITATQGGLLNLNKMVTHMTGKKAFFSYWPYGCHCGLGGKGQPKDAT 59

Qy         61 DWCCQTHDCCYDHLKTQGCGIYKDYIRYNFSQGNIHCSDKGSWCEQQLCACDKEVAFCLK 120
              |||||||||:||||||||||||||||||:||||||:|||||:||||||||:||||||:||
Db         60 DWCCQKHDCCYAHLKIDGCKSLTDNYKYSISQGTIQCSDNGSWCERQLCACDKEVALCLK 119

Qy        121 RNLDTYQKRLRFYWRPHCRGQTPGC 145
              :||||:||||||||||||:|:||:|
Db        120 QNLDSYNKRLRYYWRPRCKGKTPAC 144

RESULT 12
AAB24434
ID   AAB24434 standard; protein; 116 AA.
XX
AC   AAB24434;
XX
DT   07-NOV-2000  (first entry)
XX
DE   Human PRO1561 protein sequence SEQ ID NO:222.
XX
KW   Human; PRO; promotion; inhibition; angiogenesis; cardiovascularisation;
```

```
KW   diagnosis; trauma; wound; cancer; atherosclerosis; cardiac hypertrophy;
KW   angiogenic; proliferative; cardiant; cardiovascular; antiatherosclerotic;
KW   cytostatic; gene therapy; vaccine.
OS   Homo sapiens.
XX
PN   WO200032221-A2.
XX
PD   08-JUN-2000.
XX
PF   30-NOV-1999;        99WO-US028313.
XX
PR   01-DEC-1998;        98WO-US025108.
PR   16-DEC-1998;        98US-0112850P.
PR   12-JAN-1999;        99US-0115554P.
PR   08-MAR-1999;        99WO-US005028.
PR   12-MAR-1999;        99US-0123957P.
PR   28-APR-1999;        99US-0131445P.
PR   14-MAY-1999;        99US-0134287P.
PR   02-JUN-1999;        99US-0012252.
PR   23-JUN-1999;        99US-0141037P.
PR   20-JUL-1999;        99US-0144758P.
PR   26-JUL-1999;        99US-0145698P.
PR   01-SEP-1999;        99WO-US020111.
PR   08-SEP-1999;        99WO-US020594.
PR   13-SEP-1999;        99WO-US020944.
PR   15-SEP-1999;        99WO-US021090.
PR   15-SEP-1999;        99WO-US021547.
PR   05-OCT-1999;        99WO-US023089.
PR   29-OCT-1999;        99US-0162506P.
XX
PA   (GETH ) GENENTECH INC.
XX
PI   Ashkenazi AJ,  Baker KP,  Ferrara N,  Gerber H,  Hillan KJ;
PI   Goddard A,  Godowski PJ,  Gurney AL,  Klein RD,  Kuo SS,  Paoni NF;
PI   Smith V,  Watanabe CK,  Williams PM,  Wood WI;
XX
DR   WPI; 2000-412154/35.
DR   N-PSDB; AAA77684.
XX
PT   Nucleic acids encoding PRO polypeptides useful for preventing, diagnosing
PT   and treating diagnosing a cardiovascular, endothelial or angiogenic
PT   disorders in mammals.
XX
PS   Claim 72; Fig 94; 315pp; English.
XX
CC   The present invention describes nucleic acids encoding PRO polypeptides
CC   useful for preventing, diagnosing and treating diagnosing a
CC   cardiovascular, endothelial or angiogenic disorder in mammals by
CC   modulating cell proliferation, angiogenesis and cardiovascularisation,
CC   and for identifying agonists and antagonists of these processes. The
CC   nucleic acids and the proteins they encode may be used in the prevention,
CC   treatment and diagnosis of diseases associated with inappropriate PRO
CC   expression such as cardiovascular, endothelial or angiogenic disorders in
CC   mammals (e.g. atherosclerosis, cancers and cardiac hypertrophy). For
CC   example, the nucleic acids (NCs) and vectors containing them and the PRO
CC   polypeptide may be used to treat disorders associated with decreased PRO
CC   expression. AAA77510 to AAA77721 and AAB24388 to AAB24435 represent
CC   nucleotide and protein sequences used in the exemplification of the
CC   present invention
XX
SQ   Sequence 116 AA;

Query Match             58.7%;  Score 500.5;  DB 3;  Length 116;
Best Local Similarity   82.6%;  Pred. No. 5.5e-42;
Matches   90;  Conservative    4;  Mismatches    6;  Indels    9;  Gaps    2;

Qy     1 MELALLCGLVVMAGVIPIQGGIINLNKMVKQVTGKMPILSTWPYGCHCGLGGRGQPKDAT 60
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1 MELALLCGLVVMAGVIPIQGGIINLNKMVKQVTGKMPILSTWPYGCHCGLGGRGQPKDAT 60

Qy    61 DWCCQTHDCCYDHLKTQGCGIYKDYYRYNFSQGNIHCSDKGSWCEQQLC 109
         ::  :|||| |  ||||||||    || |
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```
Db          61 DWCCQTHDCCYDHLKTQGCGIYKDN----NKSSIHCMD----LSQRYC 100

RESULT 13
AAY99450
ID   AAY99450 standard; protein; 116 AA.
XX
AC   AAY99450;
XX
DT   08-AUG-2000  (first entry)
XX
DE   Human PRO1561 (UNQ768) amino acid sequence SEQ ID NO:378.
XX
KW   Human; PRO polypeptide; membrane bound protein; receptor; diagnosis;
KW   transmembrane; secretion; immunoadhesion; pharmaceutical; screening.
XX
OS   Homo sapiens.
XX
PN   WO200012708-A2.
XX
PD   09-MAR-2000.
XX
PF   01-SEP-1999;        99WO-US020111.
XX
PR   01-SEP-1998;        98US-0098716P.
PR   01-SEP-1998;        98US-0098749P.
PR   01-SEP-1998;        98US-0098750P.
PR   02-SEP-1998;        98US-0098803P.
PR   02-SEP-1998;        98US-0098821P.
PR   02-SEP-1998;        98US-0098843P.
PR   09-SEP-1998;        98US-0099536P.
PR   09-SEP-1998;        98US-0099596P.
PR   09-SEP-1998;        98US-0099598P.
PR   09-SEP-1998;        98US-0099602P.
PR   09-SEP-1998;        98US-0099642P.
PR   10-SEP-1998;        98US-0099741P.
PR   10-SEP-1998;        98US-0099754P.
PR   10-SEP-1998;        98US-0099763P.
PR   10-SEP-1998;        98US-0099792P.
PR   10-SEP-1998;        98US-0099808P.
PR   10-SEP-1998;        98US-0099812P.
PR   10-SEP-1998;        98US-0099815P.
PR   10-SEP-1998;        98US-0099816P.
PR   15-SEP-1998;        98US-0100385P.
PR   15-SEP-1998;        98US-0100388P.
PR   15-SEP-1998;        98US-0100390P.
PR   16-SEP-1998;        98US-0100584P.
PR   16-SEP-1998;        98US-0100627P.
PR   16-SEP-1998;        98US-0100661P.
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PR   16-SEP-1998;        98US-0100664P.
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PR   17-SEP-1998;        98US-0100710P.
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PR   17-SEP-1998;        98US-0100919P.
PR   17-SEP-1998;        98US-0100930P.
PR   18-SEP-1998;        98US-0100848P.
PR   18-SEP-1998;        98US-0100499P.
PR   18-SEP-1998;        98US-0101014P.
PR   18-SEP-1998;        98US-0101068P.
PR   22-SEP-1998;        98US-0101071P.
PR   22-SEP-1998;        98US-0101279P.
PR   23-SEP-1998;        98US-0101471P.
PR   23-SEP-1998;        98US-0101472P.
PR   23-SEP-1998;        98US-0101474P.
PR   23-SEP-1998;        98US-0101475P.
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PR   24-SEP-1998;        98US-0101738P.
PR   24-SEP-1998;        98US-0101741P.
PR   24-SEP-1998;        98US-0101743P.
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XX
PA   (GETH ) GENENTECH INC.
XX
PI   Baker K, Goddard A, Gurney AL, Smith V, Watanabe CK, Wood WI;
XX
DR   WPI; 2000-237871/20.
DR   N-PSDB; AAA37132.
XX
PT   New mammalian DNA sequences encoding transmembrane, receptor or secreted
PT   PRO polypeptides, useful for screening of potential peptide or small
PT   molecule inhibitors of the relevant receptor/ligand interactions.
XX
PS   Claim 12; Fig 222; 773pp; English.
XX
CC   AAA37022 to AAA37144 encode the new isolated human transmembrane,
CC   receptor or secreted PRO polypeptides given in AAY99340 to AAY99462. The
CC   transmembrane and receptor PRO proteins can be used for screening of
CC   potential peptide or small molecule inhibitors of the relevant
CC   receptor/ligand interactions. The polypeptides and nucleotide sequences
CC   encoding then have various industrial applications, including uses as
CC   pharmaceutical and diagnostic agents. AAA37145 to AAA37330 represent PCR
CC   primers and hybridisation probes used in the isolation of the PRO
CC   polypeptides from the present invention
XX
SQ   Sequence 116 AA;

Query Match             58.7%;  Score 500.5;  DB 3;  Length 116;
                                Pred. No. 5.5e-42;
Best Local Similarity   82.6%;
Matches   90;  Conservative    4;  Mismatches    6;  Indels    9;  Gaps    2;

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Db         61 DWCCQTHDCCYDHLKTQGCGIYKDN----NKSSIHCMD----LSQRYC 100


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AC   AAB66199;
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DT   02-APR-2001  (first entry)
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OS   Unidentified.
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PN   WO200078961-A1.
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PD   28-DEC-2000.
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PF   18-FEB-2000; 2000WO-US004342.
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PR   23-JUN-1999;   99US-0141037P.
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XX
PA   (GETH ) GENENTECH INC.
XX
PI   Baker KP, Botstein D, Desnoyers L, Eaton DL, Ferrara N, Fong S;
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PR   24-SEP-1998;   98US-0101915P.
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PR   18-NOV-1998;   98US-0108858P.
PR   18-NOV-1998;   98US-0108904P.
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PI   Gao W, Goddard A, Godowski PJ, Grimaldi CJ, Gurney AL, Hillan KJ;
PI   Pan J, Paoni NF, Roy MA, Smith V, Stewart TA, Tumas D, Watanabe CK;
PI   Williams PM, Wood WI;
XX
DR   WPI; 2001-071395/08.
XX
PT   Secreted and transmembrane proteins and nucleic acids designated PRO,
PT   useful as hybridization probes, in chromosome and gene mapping and gene
PT   therapy.
XX
PS   Claim 1; Fig 222; 787pp; English.
XX
CC   The present invention relates to secreted and transmembrane proteins.
CC   These proteins and the DNA encoding them may be used as hybridization
CC   probes, in chromosome and gene mapping and in the generation of anti-
CC   sense RNA and DNA. They may also be used to generate either
CC   transgenic animals or knockout animals which are in turn useful for
CC   development and screening of therapeutically useful reagents. The nucleic
CC   acids may also be used in gene therapy
XX
SQ   Sequence 116 AA;

Query Match   58.7%;   Score 500.5; DB 4; Length 116;
Best Local Similarity 82.6%;   Pred. No. 5.5e-42;
Matches 90; Conservative   4; Mismatches   6; Indels   9; Gaps   2;

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AC   AAU12438;
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DT   24-OCT-2001 (first entry)
XX
DE   Human PRO1561 polypeptide sequence.
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KW   Human secretory and transmembrane; PRO; mammalian; cancer; lung; breast;
KW   prostate; cervical; tumour necrosis factor-alpha; TNF-alpha; cartilage;
KW   ear; proliferation; glucose; free fatty acid; skeletal muscle; adipocyte;
KW   A-peptide; factor VIIA; gene therapy.
XX
OS   Homo sapiens.
XX
PN   WO200140466-A2.
XX
PD   07-JUN-2001.
XX
PF   01-DEC-2000; 2000WO-US032678.
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PR   01-DEC-1999; 99WO-US028301.
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PR   20-DEC-1999; 99WO-US030911.
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PR   30-DEC-1999; 99WO-US031243.
PR   30-DEC-1999; 99WO-US031274.
PR   05-JAN-2000; 2000WO-US000219.
PR   06-JAN-2000; 2000WO-US000377.
PR   06-JAN-2000; 2000WO-US000376.
PR   11-FEB-2000; 2000WO-US003565.

PR   18-FEB-2000; 2000WO-US004341.
PR   18-FEB-2000; 2000WO-US004342.
PR   22-FEB-2000; 2000WO-US004414.
PR   24-FEB-2000; 2000WO-US004914.
PR   24-FEB-2000; 2000WO-US005004.
PR   01-MAR-2000; 2000WO-US005601.
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PR   03-MAR-2000; 2000US-0187202P.
PR   10-MAR-2000; 2000WO-US006319.
PR   15-MAR-2000; 2000WO-US006884.
PR   20-MAR-2000; 2000WO-US007377.
PR   21-MAR-2000; 2000WO-US007532.
PR   30-MAR-2000; 2000WO-US008439.
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PR   28-JUL-2000; 2000WO-US020710.
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PR   23-AUG-2000; 2000WO-US023522.
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PR   10-NOV-2000; 2000WO-US030873.
XX
PA   (GETH) GENENTECH INC.
XX
PI   Baker KP, Beresini M, Deforge L, Desnoyers L, Filvaroff E, Gao W;
PI   Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S;
PI   Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;
XX
DR   WPI; 2001-408281/43.
DR   N-PSDB; AAS21510.
XX
PT   Isolated, secretory and transmembrane PRO polypeptide used to detect
PT   other PRO polypeptides, link bioactive molecules to cells expressing PRO
PT   polypeptides, and detect the presence of mammalian tumors e.g. lung,
PT   breast, prostate, cervical.
XX
PS   Claim 12; Fig 534; 813pp; English.
XX
CC   AAU2172-AAU12446 represent novel human secretory and transmembrane PRO
CC   polypeptides. The PRO polypeptides are useful to detect other PRO
CC   polypeptides, to link bioactive molecules to cells expressing PRO
CC   polypeptides, to modulate biological activities of cells expressing PRO
CC   polypeptides, and to detect the presence of mammalian lung, colon,
CC   breast, prostate, rectal, cervical or liver tumours by comparing PRO
CC   polypeptide expression in a cell sample to that in a control sample. Some
CC   of the 275 sequences are also useful to stimulate the release of tumour
CC   necrosis factor-alpha (TNF-alpha) from human blood, the proliferation or
CC   differentiation of chondrocytes, the proliferation or gene expression in
CC   pericyte cells, the release of proteoglycans from cartilage, the
CC   proliferation of inner ear utricular supporting cells or of T-
CC   lymphocytes, the release of a cytokine from peripheral blood monocytes
CC   (PBMCs), or the proliferation of endothelial cells. Some of the PRO
CC   polypeptides may modulate glucose or free fatty acid uptake by skeletal
CC   muscle cells or by adipocytes; or inhibit binding of A-peptide to factor
CC   VIIA. The PRO polypeptides can be used in assays to identify molecules
CC   involved in binding interactions. The polynucleotides encoding PRO
CC   polypeptides can be used to generate probes, antisense RNA/DNA,
CC   transgenic or knock out animals and can be used in gene therapy
XX
SQ   Sequence 116 AA;

Query Match   58.7%;   Score 500.5; DB 4; Length 116;
Best Local Similarity 82.6%;   Pred. No. 5.5e-42;
Matches 90; Conservative   4; Mismatches   6; Indels   9; Gaps   2;

Qy   1 MELALLCGLVVMAGVIPIQGGILNLNKMVKQVTGKMPILSYWPYGCHCGLGGRGQPKDAT 60
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Qy   61 DWCCQTHDCCYDHLKTQGCGIYKDYYRYNFSQGNIHCSDKGSWCEQQLC 109

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Copyright   GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd.

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Pred. No. is the number of results predicted by chance to have a
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and is derived by analysis of the total score distribution.

SUMMARIES

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2	401.5	47.1	146	4	US-09-489-770-4	Sequence 4, Appli
3	400.5	47.0	146	4	US-08-888-497-35	Sequence 35, Appl
4	400.5	47.0	146	4	US-09-362-230-35	Sequence 35, Appl
5	400.5	47.0	146	5	PCT-US94-07926-35	Sequence 35, Appl
6	395.5	46.4	144	2	US-08-186-895-10	Sequence 10, Appli
7	395.5	46.4	144	4	US-08-888-497-37	Sequence 37, Appl
8	395.5	46.4	144	4	US-09-362-230-37	Sequence 37, Appl
9	395.5	46.4	144	3	PCT-US94-07926-37	Sequence 37, Appl
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12	367.5	43.1	124	2	US-08-170-360-4	Sequence 4, Appli
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42	263.5	30.9	165	2	US-09-489-770-1	Sequence 1, Appli
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ALIGNMENTS

RESULT 1
US-08-966-317-4
; Sequence 4, Application US/08966317
; Patent No. 6103469
; GENERAL INFORMATION:
; APPLICANT: Hawkins, Phillip R.
; APPLICANT: Bandman, Olga
; APPLICANT: Guegler, Karl J.
; APPLICANT: Shah, Purvi
; APPLICANT: Corley, Neil C.
; TITLE OF INVENTION: HUMAN PHOSPHOLIPASE A2 PROTEIN
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Dr.
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/966,317
; FILING DATE: Filed Herewith
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0403 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-855-0555
; TELEFAX: 650-845-4166
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 146 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GenBank
; CLONE: 204319
US-08-966-317-4

11/7/1997 (filing)

Query Match   47.1%;   Score 401.5; DB 3; Length 146;
Best Local Similarity 47.9%;   Pred. No. 1.1e-34;

Matches 70; Conservative 23; Mismatches 52; Indels 1; Gaps 1;

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RESULT 2
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; Sequence 4, Application US/09489770
; Patent No. 6399301
; GENERAL INFORMATION:
; APPLICANT: Hawkins, Phillip R.
; APPLICANT: Bandman, Olga
; APPLICANT: Guegler, Karl J.
; APPLICANT: Shah, Purvi
; APPLICANT: Corley, Neil C.
; TITLE OF INVENTION: HUMAN PHOSPHOLIPASE A2 PROTEIN
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Dr.
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/489,770
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/966,317
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERRENCE/DOCKET NUMBER: PF-0403 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-855-0555
; TELEFAX: 650-845-4166
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 146 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GenBank
; CLONE: 204319
US-09-489-770-4

Query Match 47.1%; Score 401.5; DB 4; Length 146;
Best Local Similarity 47.9%; Pred. No. 1.1e-34;
Matches 70; Conservative 23; Mismatches 52; Indels 1; Gaps 1;

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Qy    1 MELALLCGLVVMA-GVIPIQGGILNLNKMVKQVTGKMPILSYWPYGCHCGLGGRGQPKDA 59
        |::  ||.:|.|||   |:|||||||||||||||:||||:  ||||||||||:||:||||
Db    1 MKVLLLLAVVIMAFGSIQVQGSLLEFGQMILFKTGKRADVSYGFYGCHCGVGGRGSPKDA 60

Qy   60 TDWCCQTHDCCYDHLKTQGCGIYKDYYRYNFSQGNIHCSDKGSWSEQQLCACDKEVAFCL 119
        |||||.|||||  |.:| |:||  ||||  :||  :::: ||||||.||||  || |||:|||
Db   61 TDWCCVTHDCCYNRLEKRGCGTKFLTYKFSYRGGQISCSTNQDSCRKQLCQCDKAAAECF 120

Qy  120 KRNLDTYQKRLRFYWRPHCRGQTPGC 145
         || || || ||  |.|:|:|
Db  121 ARNKKSYSLKYQFYLNKFCKGKTPSC 146
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RESULT 3
US-08-888-497-35
; Sequence 35, Application US/08888497
; Patent No. 5972677
; GENERAL INFORMATION:
; APPLICANT: Tischfield, Jay A.
; APPLICANT: Seilhamer, Jeffrey J.
; TITLE OF INVENTION: Mammalian Phospholipase A2 Nucleotide
; TITLE OF INVENTION: Sequences and Low Molecular Weight Amino Acid Sequences
; TITLE OF INVENTION: Encoded Thereby, Antisense Sequences and Nucleotide
; TITLE OF INVENTION: Sequences Having Internal Ribosome Binding Sites
; NUMBER OF SEQUENCES: 44
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Ruden, Barnett, McClosky, Smith, Schuster &
; ADDRESSEE: Russell PA
; STREET: 200 East Broward Boulevard
; CITY: Fort Lauderdale
; STATE: FL
; COUNTRY: USA
; ZIP: 33301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/888,497
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/651,405
; FILING DATE:
; APPLICATION NUMBER: US 08/097,354
; FILING DATE: 26-JUL-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Manso, Peter J.
; REGISTRATION NUMBER: 32,264
; REFERENCE/DOCKET NUMBER: IN21044-5
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 305-527-2498
; TELEFAX: 305-764-4996
; INFORMATION FOR SEQ ID NO: 35:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 146 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-888-497-35

Query Match 47.0%; Score 400.5; DB 2; Length 146;
Best Local Similarity 47.9%; Pred. 1.4e-34;
Matches 70; Conservative 23; Mismatches 52; Indels 1; Gaps 1;

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Qy    1 MELALLCGLVVMA-GVIPIQGGILNLNKMVKQVTGKMPILSYWPYGCHCGLGGRGQPKDA 59
        |::  ||.:|.|||   |:|||||||||||||||:||||:  ||||||||||:||:||||
Db    1 MKVLLLLAVVIMAFGSIQVQGSLLEFGQMILFKTGKRADVSYGFYGCHCGVGGRGSPKDA 60

Qy   60 TDWCCQTHDCCYDHLKTQGCGIYKDYYRYNFSQGNIHCSDKGSWSEQQLCACDKEVAFCL 119
        |||||.|||||  |.:| |:||  ||||  :|| :::: ||||||.||||  || |||:|||
Db   61 TDWCCVTHDCCYNRLEKRGCGTKFLTYKFSYRGGQISCSTNQDSCRKQLCQCDKAAAECF 120

Qy  120 KRNLDTYQKRLRFYWRPHCRGQTPGC 145
         || || || ||  |.|:|:|
Db  121 ARNKKSYSLKYQFYPNKFCKGKTPSC 146
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RESULT 4
US-09-362-230-35
; Sequence 35, Application US/09362230
; Patent No. 6352849
; GENERAL INFORMATION:
;   APPLICANT: Tischfield, Jay A.
;   APPLICANT: Seilhamer, Jeffrey J.
;   TITLE OF INVENTION: Mammalian Phospholipase A2 Nucleotide
;   TITLE OF INVENTION: Sequences and Low Molecular Weight Amino Acid Sequences
;   TITLE OF INVENTION: Encoded Thereby, Antisense Sequences and Nucleotide
;   TITLE OF INVENTION: Sequences Having Internal Ribosome Binding Sites
;   NUMBER OF SEQUENCES: 44
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE: Ruden, Barnett, McClosky, Smith, Schuster &
;   ADDRESSEE: Russell PA
;   STREET: 200 East Broward Boulevard
;   CITY: Fort Lauderdale
;   STATE: FL
;   COUNTRY: USA
;   ZIP: 33301
;   COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: PatentIn Release #1.0, Version #1.25
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/09/362,230
;   FILING DATE:
;   CLASSIFICATION:
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: 08/888,497
;   FILING DATE:
;   APPLICATION NUMBER: US 08/097,354
;   FILING DATE: 26-JUL-1993
;   ATTORNEY/AGENT INFORMATION:
;   NAME: Manso, Peter J.
;   REGISTRATION NUMBER: 32,264
;   REFERENCE/DOCKET NUMBER: IN21044-5
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE: 305-527-2498
;   TELEFAX: 305-764-4996
; INFORMATION FOR SEQ ID NO: 35:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH: 146 amino acids
;   TYPE: amino acid
;   STRANDEDNESS: single
;   TOPOLOGY: linear
;   MOLECULE TYPE: protein
US-09-362-230-35

Query Match   47.0%; Score 400.5; DB 4; Length 146;
Best Local Similarity   47.9%; Pred. No. 1.4e-34;
Matches   70; Conservative   23; Mismatches   52; Indels   1; Gaps   1;

Qy   1 MELALLCGLVVMA-GVIPIQGGILNLNKMVKQVTGKMPILSYWPYGCHCGLGGRGQPKDA 59
Db   1 MKVLLLLAVVIMAFGSIQVQGSLLEFGQMILFKTGKRADVSYGFYGCHCGVGGRGSPKDA 60

Qy   60 TDWCCQTHDCCYDHLKTQGCGIYKDYYRYNFSQGNIHCSDKGSWCEQQLCACDKEVAFCL 119
Db   61 TDWCCVTHDCCYNRLEKRGCGTKFVTYKFSYRGGQISCSTNQDSCRKQLCQCDKAAAECF 120

Qy   120 KRNLDTYQKRLRFYWRPHCRGQTPGC 145
Db   121 ARNKKSYSLKYQFYPNKFCKGKTPSC 146

RESULT 5
PCT-US94-07926-35
; Sequence 35, Application PC/TUS9407926
; GENERAL INFORMATION:
;   APPLICANT: Tischfield, Jay A.
;   APPLICANT: Seilhamer, Jeffrey J.
;   TITLE OF INVENTION: Mammalian Phospholipase A2 Nucleotide
;   TITLE OF INVENTION: Sequences and Low Molecular Weight Amino Acid Sequences
;   TITLE OF INVENTION: Encoded Thereby, Antisense Sequences and Nucleotide
;   TITLE OF INVENTION: Sequences Having Internal Ribosome Binding Sites
;   NUMBER OF SEQUENCES: 44
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE: Ruden, Barnett, McClosky, Smith, Schuster &
;   ADDRESSEE: Russell PA
;   STREET: 200 East Broward Boulevard
;   CITY: Fort Lauderdale
;   STATE: FL
;   COUNTRY: USA
;   ZIP: 33301
;   COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: PatentIn Release #1.0, Version #1.25
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: PCT/US94/07926
;   FILING DATE: 15-JUL-1994
;   CLASSIFICATION:
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: US 08/097,354
;   FILING DATE: 26-JUL-1993
;   ATTORNEY/AGENT INFORMATION:
;   NAME: Manso, Peter J.
;   REGISTRATION NUMBER: 32,264
;   REFERENCE/DOCKET NUMBER: IN21044-5
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE: 305-527-2498
;   TELEFAX: 305-764-4996
; INFORMATION FOR SEQ ID NO: 35:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH: 146 amino acids
;   TYPE: amino acid
;   STRANDEDNESS: single
;   TOPOLOGY: linear
;   MOLECULE TYPE: protein
PCT-US94-07926-35

Query Match   47.0%; Score 400.5; DB 5; Length 146;
Best Local Similarity   47.9%; Pred. No. 1.4e-34;
Matches   70; Conservative   23; Mismatches   52; Indels   1; Gaps   1;

Qy   1 MELALLCGLVVMA-GVIPIQGGILNLNKMVKQVTGKMPILSYWPYGCHCGLGGRGQPKDA 59
Db   1 MKVLLLLAVVIMAFGSIQVQGSLLEFGQMILFKTGKRADVSYGFYGCHCGVGGRGSPKDA 60

Qy   60 TDWCCQTHDCCYDHLKTQGCGIYKDYYRYNFSQGNIHCSDKGSWCEQQLCACDKEVAFCL 119
Db   61 TDWCCVTHDCCYNRLEKRGCGTKFVTYKFSYRGGQISCSTNQDSCRKQLCQCDKAAAECF 120

Qy   120 KRNLDTYQKRLRFYWRPHCRGQTPGC 145
Db   121 ARNKKSYSLKYQFYPNKFCKGKTPSC 146

RESULT 6
US-08-186-895-10
; Sequence 10, Application US/08186895
; Patent No. 5538885
; GENERAL INFORMATION:
;   APPLICANT: Hollis, Melvyn
;   APPLICANT: Needham, Maurice R.C.
;   APPLICANT: Gooding, Clare
;   APPLICANT: Grosveld, Franklin G.
;   TITLE OF INVENTION: Expression Systems
;   NUMBER OF SEQUENCES: 10
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE: Cushman, Darby & Cushman
;   STREET: 1615 L Street, N.W.

```
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20036-5601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/186,895
FILING DATE: 27-JAN-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/046,383
FILING DATE: 09-APR-1993
APPLICATION NUMBER: US/07/810,414
ATTORNEY/AGENT INFORMATION:
NAME: Kokulis, Paul N.
REGISTRATION NUMBER: 16,773
REFERENCE/DOCKET NUMBER: PNK/3893/93802/MJW
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-861-3000
TELEFAX: 202-822-0944
TELEX: 6714627 CUSH
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 144 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-186-895-10

Query Match            46.4%;   Score 395.5; DB 1; Length 144;
Best Local Similarity  47.6%;   Pred. No. 4.7e-34;
Matches   69;  Conservative  23;  Mismatches  52;  Indels  1;  Gaps  1;

Qy    1 MELALLCGLVVMAGVIPIQGGILNLNKMVKQVTGKMPILSYWPYGCHCGLGGRGQPKDAT 60
          || |||| ::::: |:: :||:||||||| ||||||||||||| ||||||||||||
Db    1 MKTLLLLAVIMIFGLLQAHGNLVNFHRMKLTTGKEAALSYGFYGCHCGVGGRGSPKDAT 60

Qy   61 DWCCQTHDCCYDHLKTQGCGIYKDYYRYNFSQGNIHCSDKGSWCEQQLCACDKEVAFCLK 120
          || ||||| |||  :|| ||  ||| :::| |||||  ||| ||| | ||||  | |||
Db   61 DRCCVTHDCCYKRLEKRGCGTKFLSYKFSNSGSRITCAKQDS-CRSQLCECDKAAATCFA 119

Qy  121 RNLDTYQKRLRFYWRPHCRGQTPGC 145
          || |||  ||||| |||||
Db  120 RNKTTYNKKYQYYSNKHCRGSTPRC 144

RESULT 7
US-08-888-497-37
; Sequence 37, Application US/08888497
; Patent No. 5972677
; GENERAL INFORMATION:
; APPLICANT: Tischfield, Jay A.
; APPLICANT: Seilhamer, Jeffrey J.
; TITLE OF INVENTION: Mammalian Phospholipase A2 Nucleotide
; TITLE OF INVENTION: Sequences and Low Molecular Weight Amino Acid Sequences
; TITLE OF INVENTION: Encoded Thereby, Antisense Sequences and Nucleotide
; TITLE OF INVENTION: Sequences Having Internal Ribosome Binding Sites
; NUMBER OF SEQUENCES: 44
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Ruden, Barnett, McClosky, Smith, Schuster &
; ADDRESSEE: Russell PA
; STREET: 200 East Broward Boulevard
; CITY: Fort Lauderdale
; STATE: FL
; COUNTRY: USA
; ZIP: 33301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/888,497
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/651,405
FILING DATE:
APPLICATION NUMBER: US 08/097,354
FILING DATE: 26-JUL-1993
ATTORNEY/AGENT INFORMATION:
NAME: Manso, Peter J.
REGISTRATION NUMBER: 32,264
REFERENCE/DOCKET NUMBER: IN21044-5
TELECOMMUNICATION INFORMATION:
TELEPHONE: 305-527-2498
TELEFAX: 305-764-4996
INFORMATION FOR SEQ ID NO: 37:
SEQUENCE CHARACTERISTICS:
LENGTH: 144 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-888-497-37

Query Match            46.4%;   Score 395.5; DB 2; Length 144;
Best Local Similarity  47.6%;   Pred. No. 4.7e-34;
Matches   69;  Conservative  23;  Mismatches  52;  Indels  1;  Gaps  1;

Qy    1 MELALLCGLVVMAGVIPIQGGILNLNKMVKQVTGKMPILSYWPYGCHCGLGGRGQPKDAT 60
          || |||| ::::: |:: :||:||||||| ||||||||||||| ||||||||||||
Db    1 MKTLLLLAVIMIFGLLQAHGNLVNFHRMKLTTGKEAALSYGFYGCHCGVGGRGSPKDAT 60

Qy   61 DWCCQTHDCCYDHLKTQGCGIYKDYYRYNFSQGNIHCSDKGSWCEQQLCACDKEVAFCLK 120
          || ||||| |||  :|| ||  ||| :::| |||||  ||| ||| | ||||  | |||
Db   61 DRCCVTHDCCYKRLEKRGCGTKFLSYKFSNSGSRITCAKQDS-CRSQLCECDKAAATCFA 119

Qy  121 RNLDTYQKRLRFYWRPHCRGQTPGC 145
          || |||  ||||| |||||
Db  120 RNKTTYNKKYQYYSNKHCRGSTPRC 144

RESULT 8
US-09-362-230-37
; Sequence 37, Application US/09362230
; Patent No. 6352849
; GENERAL INFORMATION:
; APPLICANT: Tischfield, Jay A.
; APPLICANT: Seilhamer, Jeffrey J.
; TITLE OF INVENTION: Mammalian Phospholipase A2 Nucleotide
; TITLE OF INVENTION: Sequences and Low Molecular Weight Amino Acid Sequences
; TITLE OF INVENTION: Encoded Thereby, Antisense Sequences and Nucleotide
; TITLE OF INVENTION: Sequences Having Internal Ribosome Binding Sites
; NUMBER OF SEQUENCES: 44
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Ruden, Barnett, McClosky, Smith, Schuster &
; ADDRESSEE: Russell PA
; STREET: 200 East Broward Boulevard
; CITY: Fort Lauderdale
; STATE: FL
; COUNTRY: USA
; ZIP: 33301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/362,230
; FILING DATE:
; CLASSIFICATION:
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PRIOR APPLICATION DATA:
  APPLICATION NUMBER: 08/888,497
  FILING DATE:
  APPLICATION NUMBER: US 08/097,354
  FILING DATE: 26-JUL-1993
ATTORNEY/AGENT INFORMATION:
  NAME: Manso, Peter J.
  REGISTRATION NUMBER: 32,264
  REFERENCE/DOCKET NUMBER: IN21044-5
TELECOMMUNICATION INFORMATION:
  TELEPHONE: 305-527-2498
  TELEFAX: 305-764-4996
INFORMATION FOR SEQ ID NO: 37:
  SEQUENCE CHARACTERISTICS:
  LENGTH: 144 amino acids
  TYPE: amino acid
  STRANDEDNESS: single
  TOPOLOGY: linear
  MOLECULE TYPE: protein
US-09-362-230-37

Query Match         46.4%;  Score 395.5;  DB 4;  Length 144;
Best Local Similarity 47.6%;  Pred. No. 4.7e-34;
Matches   69;  Conservative  23;  Mismatches  52;  Indels  1;  Gaps  1;

Qy    1 MELALLCGLVVMAGVIPIQGGILNLNKRMVKQVTGKMPILSYWPYGCHCGLGGRGQPKDAT 60
          | || |    | ::: | |: ::|::  | : ||: ::|:|| ||||:|| |||:|| |||
Db    1 MKTLLLLAVIMIFGLLQAHGNLVNFHRMIKLTTGKEAALSYGFYGCHCGVGGRGSPKDAT 60

Qy   61 DWCCQTHDCCYDHLKTQGCGIYKDYYRYNFSQGNIHCSDKGSWCEQQLCACDKEVAFCLK 120
          | |||| |||: | :|    :::: ||: | | | :| | |::| |: :|  |||  | |
Db   61 DRCCVTHDCCYKRLEKRGCGTKFLSYKFSNSGSRITCAKQDS-CRSQLCECDKAAATCFA 119

Qy  121 RNLDTYQKRLRFYWRPHCRGQTPGC 145
          || ||     || |: ||||| | |
Db  120 RNKTTYNKKYQYYSNKHCRGSTPRC 144

RESULT 9
PCT-US94-07926-37
; Sequence 37, Application PC/TUS9407926
; GENERAL INFORMATION:
  APPLICANT: Tischfield, Jay A.
  APPLICANT: Seilhamer, Jeffrey J.
  TITLE OF INVENTION: Mammalian Phospholipase A2 Nucleotide
  TITLE OF INVENTION: Sequences and Low Molecular Weight Amino Acid Sequences
  TITLE OF INVENTION: Encoded Thereby, Antisense Sequences and Nucleotide
  TITLE OF INVENTION: Sequences Having Internal Ribosome Binding Sites
  NUMBER OF SEQUENCES: 44
  CORRESPONDENCE ADDRESS:
    ADDRESSEE: Ruden, Barnett, McClosky, Smith, Schuster &
    ADDRESSEE: Russell PA
    STREET: 200 East Broward Boulevard
    CITY: Fort Lauderdale
    STATE: FL
    COUNTRY: USA
    ZIP: 33301
  COMPUTER READABLE FORM:
    MEDIUM TYPE: Floppy disk
    COMPUTER: IBM PC compatible
    OPERATING SYSTEM: PC-DOS/MS-DOS
    SOFTWARE: PatentIn Release #1.0, Version #1.25
  CURRENT APPLICATION DATA:
    APPLICATION NUMBER: PCT/US94/07926
    FILING DATE: 15-JUL-1994
    CLASSIFICATION:
  PRIOR APPLICATION DATA:
    APPLICATION NUMBER: US 08/097,354
    FILING DATE: 26-JUL-1993
  ATTORNEY/AGENT INFORMATION:
    NAME: Manso, Peter J.
    REGISTRATION NUMBER: 32,264
    REFERENCE/DOCKET NUMBER: IN21044-5
  TELECOMMUNICATION INFORMATION:
    TELEPHONE: 305-527-2498
    TELEFAX: 305-764-4996
INFORMATION FOR SEQ ID NO: 37:
  SEQUENCE CHARACTERISTICS:
  LENGTH: 144 amino acids
  TYPE: amino acid
  STRANDEDNESS: single
  TOPOLOGY: linear
  MOLECULE TYPE: protein
PCT-US94-07926-37

Query Match         46.4%;  Score 395.5;  DB 5;  Length 144;
Best Local Similarity 47.6%;  Pred. No. 4.7e-34;
Matches   69;  Conservative  23;  Mismatches  52;  Indels  1;  Gaps  1;

Qy    1 MELALLCGLVVMAGVIPIQGGILNLNKRMVKQVTGKMPILSYWPYGCHCGLGGRGQPKDAT 60
          | || |    | ::: | |: ::|::  | : ||: ::|:|| ||||:|| |||:|| |||
Db    1 MKTLLLLAVIMIFGLLQAHGNLVNFHRMIKLTTGKEAALSYGFYGCHCGVGGRGSPKDAT 60

Qy   61 DWCCQTHDCCYDHLKTQGCGIYKDYYRYNFSQGNIHCSDKGSWCEQQLCACDKEVAFCLK 120
          | |||| |||: | :|    :::: ||: | | | :| | |::| |: :|  |||  | |
Db   61 DRCCVTHDCCYKRLEKRGCGTKFLSYKFSNSGSRITCAKQDS-CRSQLCECDKAAATCFA 119

Qy  121 RNLDTYQKRLRFYWRPHCRGQTPGC 145
          || ||     || |: ||||| | |
Db  120 RNKTTYNKKYQYYSNKHCRGSTPRC 144

RESULT 10
US-08-966-317-3
; Sequence 3, Application US/08966317
; Patent No. 6103469
; GENERAL INFORMATION:
  APPLICANT: Hawkins, Phillip R.
  APPLICANT: Bandman, Olga
  APPLICANT: Guegler, Karl J.
  APPLICANT: Shah, Purvi
  APPLICANT: Corley, Neil C.
  TITLE OF INVENTION: HUMAN PHOSPHOLIPASE A2 PROTEIN
  NUMBER OF SEQUENCES: 4
  CORRESPONDENCE ADDRESS:
    ADDRESSEE: Incyte Pharmaceuticals, Inc.
    STREET: 3174 Porter Dr.
    CITY: Palo Alto
    STATE: CA
    COUNTRY: USA
    ZIP: 94304
  COMPUTER READABLE FORM:
    MEDIUM TYPE: Diskette
    COMPUTER: IBM Compatible
    OPERATING SYSTEM: DOS
    SOFTWARE: FastSEQ for Windows Version 2.0
  CURRENT APPLICATION DATA:
    APPLICATION NUMBER: US/08/966,317
    FILING DATE: Filed Herewith
  PRIOR APPLICATION DATA:
    APPLICATION NUMBER:
    FILING DATE:
  ATTORNEY/AGENT INFORMATION:
    NAME: Billings, Lucy J.
    REGISTRATION NUMBER: 36,749
    REFERENCE/DOCKET NUMBER: PF-0403 US
  TELECOMMUNICATION INFORMATION:
    TELEPHONE: 650-855-0555
    TELEFAX: 650-845-4166
INFORMATION FOR SEQ ID NO: 3:
  SEQUENCE CHARACTERISTICS:
  LENGTH: 146 amino acids
  TYPE: amino acid
  STRANDEDNESS: single
  TOPOLOGY: linear
  IMMEDIATE SOURCE:
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    LIBRARY: GenBank
    CLONE: 984837
US-08-966-317-3

Query Match     43.6%;  Score 371.5;  DB 3;  Length 146;
Best Local Similarity 47.3%; Pred. No. 1.6e-31;
Matches 69; Conservative 19; Mismatches 57; Indels 1; Gaps 1;

Qy    1 MELALLCGLVVMA-GVIPIQGGILNLNKMVKQVTGKMPILSYWPYGCHCGLGGRGQPKDA 59
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Db    1 MKVLLLAASIMAFGSIQVQGNIAQFGEMIRLKTGKRAELSYAFYGCHCGLGGKGSPKDA 60

Qy   60 TDWCCQTHDCCYDHLKTQGCGIYKDYRYNFSQGNIHCSDKGSWCEQQLCACDKEVAFCL 119
        || |||||||| |  :  ||| : |||  |  | | ||  |  | : |  ||||   ||
Db   61 TDRCCVTHDCCYKSLEKSGCGTKLLKYKYSHQGGQITCSANQNSCQKRLCQCDKAAAECF 120

Qy  120 KRNLDTYQKRLRFYWRPHCRGQTPGC 145
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Db  121 ARNKKTYSLKYQFYPNMFCKGKKPKC 146


RESULT 11
US-09-489-770-3
; Sequence 3, Application US/09489770
; Patent No. 6399301
; GENERAL INFORMATION:
;   APPLICANT: Hawkins, Phillip R.
;   APPLICANT: Bandman, Olga
;   APPLICANT: Guegler, Karl J.
;   APPLICANT: Shah, Purvi
;   APPLICANT: Corley, Neil C.
;   TITLE OF INVENTION: HUMAN PHOSPHOLIPASE A2 PROTEIN
;   NUMBER OF SEQUENCES: 4
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE: Incyte Pharmaceuticals, Inc.
;   STREET: 3174 Porter Dr.
;   CITY: Palo Alto
;   STATE: CA
;   COUNTRY: USA
;   ZIP: 94304
;   COMPUTER READABLE FORM:
;   MEDIUM TYPE: Diskette
;   COMPUTER: IBM Compatible
;   OPERATING SYSTEM: DOS
;   SOFTWARE: FastSEQ for Windows Version 2.0
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/09/489,770
;   FILING DATE:
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: 08/966,317
;   FILING DATE:
;   ATTORNEY/AGENT INFORMATION:
;   NAME: Billings, Lucy J.
;   REGISTRATION NUMBER: 36,749
;   REFERENCE/DOCKET NUMBER: PF-0403 US
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE: 650-855-0555
;   TELEFAX: 650-845-4166
;   INFORMATION FOR SEQ ID NO: 3:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH: 146 amino acids
;   TYPE: amino acid
;   STRANDEDNESS: single
;   TOPOLOGY: linear
;   IMMEDIATE SOURCE:
;   LIBRARY: GenBank
;   CLONE: 984837
US-09-489-770-3

Query Match     43.6%;  Score 371.5;  DB 4;  Length 146;
Best Local Similarity 47.3%; Pred. No. 1.6e-31;
Matches 69; Conservative 19; Mismatches 57; Indels 1; Gaps 1;
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Qy    1 MELALLCGLVVMA-GVIPIQGGILNLNKMVKQVTGKMPILSYWPYGCHCGLGGRGQPKDA 59
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Db    1 MKVLLLAASIMAFGSIQVQGNIAQFGEMIRLKTGKRAELSYAFYGCHCGLGGKGSPKDA 60

Qy   60 TDWCCQTHDCCYDHLKTQGCGIYKDYRYNFSQGNIHCSDKGSWCEQQLCACDKEVAFCL 119
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Db   61 TDRCCVTHDCCYKSLEKSGCGTKLLKYKYSHQGGQITCSANQNSCQKRLCQCDKAAAECF 120

Qy  120 KRNLDTYQKRLRFYWRPHCRGQTPGC 145
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Db  121 ARNKKTYSLKYQFYPNMFCKGKKPKC 146


RESULT 12
US-08-170-360-4
; Sequence 4, Application US/08170360
; Patent No. 5656602
; GENERAL INFORMATION:
;   APPLICANT: Tseng, Albert P. S.
;   APPLICANT: Inglis, Adam
;   TITLE OF INVENTION: PLA2 INHIBITORY COMPOUNDS
;   NUMBER OF SEQUENCES: 17
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE: Rothwell, Figg Ernst & Kurz
;   STREET: Suite 701-E, 555 Thirteenth St., N.W
;   CITY: Washington
;   STATE: D. C.
;   COUNTRY: U.S.A.
;   ZIP: 20004
;   COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: PatentIn Release #1.0, Version #1.25
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/08/170,360
;   FILING DATE: 03-MAR-1994
;   CLASSIFICATION: 514
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: AU PCT/AU92/00333
;   FILING DATE: 06-JUL-1992
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: AU PK 7058
;   FILING DATE: 04-JUL-1991
;   ATTORNEY/AGENT INFORMATION:
;   NAME: Ernst, Barbara G.
;   REGISTRATION NUMBER: 30,377
;   REFERENCE/DOCKET NUMBER: 1871-104A
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE: (202)783-6040
;   TELEFAX: (202)783-6031
;   INFORMATION FOR SEQ ID NO: 4:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH: 124 amino acids
;   TYPE: amino acid
;   STRANDEDNESS: single
;   TOPOLOGY: linear
;   MOLECULE TYPE: protein
;   HYPOTHETICAL: NO
;   ANTI-SENSE: NO
;   FRAGMENT TYPE: N-terminal
US-08-170-360-4

Query Match     43.1%;  Score 367.5;  DB 1;  Length 124;
Best Local Similarity 51.6%; Pred. No. 3.4e-31;
Matches 64; Conservative 16; Mismatches 43; Indels 1; Gaps 1;

Qy   22 IILNLNKMVKQVTGKMPILSYWPYGCHCGLGGRGQPKDATDWCCQTHDCCYDHLKTQGCGI 81
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Db    2 LVNFHRMIKLTTGKEAALSYGFYGCHCGVGRGSPKDATDRCCVTHDCCYKRLEKRGCGT 61

Qy   82 YKDYYRYNFSQGNIHCSDKGSWCEQQLCACDKEVAFCLKRNLDTYQKRLRFYWRPHCRGQ 141
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Db   62 KFLSYKFSNSGSRITCAKQDS-CRSQLCECDKAAATCFARNKTTYNKKYQYYSNKHCRGS 120

Qy   142 TPGC 145
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Db   121 TPRC 124

RESULT 13
US-08-888-497-39
; Sequence 39, Application US/08888497
; Patent No. 5972677
; GENERAL INFORMATION:
;   APPLICANT: Tischfield, Jay A.
;   APPLICANT: Seilhamer, Jeffrey J.
;   TITLE OF INVENTION: Mammalian Phospholipase A2 Nucleotide
;   TITLE OF INVENTION: Sequences and Low Molecular Weight Amino Acid Sequences
;   TITLE OF INVENTION: Encoded Thereby, Antisense Sequences and Nucleotide
;   TITLE OF INVENTION: Sequences Having Internal Ribosome Binding Sites
;   NUMBER OF SEQUENCES: 44
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE: Ruden, Barnett, McClosky, Smith, Schuster &
;   ADDRESSEE: Russell PA
;   STREET: 200 East Broward Boulevard
;   CITY: Fort Lauderdale
;   STATE: FL
;   COUNTRY: USA
;   ZIP: 33301
;   COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: PatentIn Release #1.0, Version #1.25
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/08/888,497
;   FILING DATE:
;   CLASSIFICATION:
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: US/08/651,405
;   FILING DATE:
;   APPLICATION NUMBER: US 08/097,354
;   FILING DATE: 26-JUL-1993
;   ATTORNEY/AGENT INFORMATION:
;   NAME: Manso, Peter J.
;   REGISTRATION NUMBER: 32,264
;   REFERENCE/DOCKET NUMBER: IN21044-5
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE: 305-527-2498
;   TELEFAX: 305-764-4996
; INFORMATION FOR SEQ ID NO: 39:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH: 124 amino acids
;   TYPE: amino acid
;   STRANDEDNESS: single
;   TOPOLOGY: linear
;   MOLECULE TYPE: protein
US-08-888-497-39

  Query Match   43.1%; Score 367.5; DB 2; Length 124;
  Best Local Similarity   51.6%; Pred. No. 3.4e-31;
  Matches   64; Conservative 16; Mismatches 43; Indels   1; Gaps   1;

Qy   22 ILNLNKMVKQVTGKMPILSYWPYGCHCGLGGRGQPKDATDWCCQTHDCCYDHLKTQGCGI 81
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Db   2 LVNFHRMIKLTTGKEAALSYGFYGCHCGVGGRGSPKDATDRCCVTHDCCYKRLEKRGCGT 61

Qy   82 YKDYYRYNFSQGNIHCSDKGSWCEQQLCACDKEVAFCLKRNLDTYQKRLRFYWRPHCRGQ 141
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Db   62 KFLSYKFSNSGSRITCAKQDS-CRSQLCECDKAAATCFARNKTTYNKKYQYYSNKHCRGS 120

Qy   142 TPGC 145
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Db   121 TPRC 124

RESULT 14
US-09-362-230-39
; Sequence 39, Application US/09362230
; Patent No. 6352849
; GENERAL INFORMATION:
;   APPLICANT: Tischfield, Jay A.
;   APPLICANT: Seilhamer, Jeffrey J.
;   TITLE OF INVENTION: Mammalian Phospholipase A2 Nucleotide
;   TITLE OF INVENTION: Sequences and Low Molecular Weight Amino Acid Sequences
;   TITLE OF INVENTION: Encoded Thereby, Antisense Sequences and Nucleotide
;   TITLE OF INVENTION: Sequences Having Internal Ribosome Binding Sites
;   NUMBER OF SEQUENCES: 44
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE: Ruden, Barnett, McClosky, Smith, Schuster &
;   ADDRESSEE: Russell PA
;   STREET: 200 East Broward Boulevard
;   CITY: Fort Lauderdale
;   STATE: FL
;   COUNTRY: USA
;   ZIP: 33301
;   COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: PatentIn Release #1.0, Version #1.25
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/09/362,230
;   FILING DATE:
;   CLASSIFICATION:
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: 08/888,497
;   FILING DATE:
;   APPLICATION NUMBER: US 08/097,354
;   FILING DATE: 26-JUL-1993
;   ATTORNEY/AGENT INFORMATION:
;   NAME: Manso, Peter J.
;   REGISTRATION NUMBER: 32,264
;   REFERENCE/DOCKET NUMBER: IN21044-5
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE: 305-527-2498
;   TELEFAX: 305-764-4996
; INFORMATION FOR SEQ ID NO: 39:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH: 124 amino acids
;   TYPE: amino acid
;   STRANDEDNESS: single
;   TOPOLOGY: linear
;   MOLECULE TYPE: protein
US-09-362-230-39

  Query Match   43.1%; Score 367.5; DB 4; Length 124;
  Best Local Similarity   51.6%; Pred. No. 3.4e-31;
  Matches   64; Conservative 16; Mismatches 43; Indels   1; Gaps   1;

Qy   22 ILNLNKMVKQVTGKMPILSYWPYGCHCGLGGRGQPKDATDWCCQTHDCCYDHLKTQGCGI 81
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Db   2 LVNFHRMIKLTTGKEAALSYGFYGCHCGVGGRGSPKDATDRCCVTHDCCYKRLEKRGCGT 61

Qy   82 YKDYYRYNFSQGNIHCSDKGSWCEQQLCACDKEVAFCLKRNLDTYQKRLRFYWRPHCRGQ 141
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Db   62 KFLSYKFSNSGSRITCAKQDS-CRSQLCECDKAAATCFARNKTTYNKKYQYYSNKHCRGS 120

Qy   142 TPGC 145
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Db   121 TPRC 124

RESULT 15
US-09-740-569-2
; Sequence 2, Application US/09740569
; Patent No.6475484
; GENERAL INFORMATION:

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; APPLICANT: Weiss, Jerrold
; APPLICANT:   Elsbach, Peter
; APPLICANT:   Liang, Ning-Sheng
; TITLE OF INVENTION: ANTIBACTERIAL GROUP IIA PHOSPHOLIPASE A2 AND METHODS OF USE THERE
; FILE REFERENCE: 5986/1E91 7US1
; CURRENT APPLICATION NUMBER: US/09/740,569
; CURRENT FILING DATE:   2000-12-18
; PRIOR APPLICATION NUMBER: US 60/172,467
; PRIOR FILING DATE: 1999-12-17
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn version 3.1
;
; SEQ ID NO 2
;   LENGTH: 124
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-740-569-2

Query Match             43.1%;  Score 367.5;  DB 4;  Length 124;
Best Local Similarity   50.8%;  Pred. No. 3.4e-31;
Matches   63;  Conservative   18;  Mismatches   42;  Indels   1;  Gaps   1;

Qy     22  IILNLNKMVKQVTGKMPILSYWPYGCHCGLGGRGQPKDATDWCCQTHDCCYDHLKTQGCGI  81
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Db      2  LVNFHRLJKLJTGKEAALSYGFYGCHCGVGGRGSPKDATDRCCVTHDCCYKRLEKRGCGT  61

Qy     82  YKDYYRYNFSQGNIHCSDKGSWCEQQLCACDKEVAFCLKRNLDTYQKRLRFYWRPHCRGQ  141
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Qy    142  TPGC  145
               || |
Db    121  TPRC  124


Search completed: October  5, 2004, 19:24:54
Job time : 10.0867 secs
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                    GenCore version 5.1.6
           Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on:    October  5, 2004, 19:25:05  ; Search time 32.8667 Seconds
                                        (without alignments)
                                        1419.702 Million cell updates/sec

Title:          US-09-830-321A-1
Perfect score:  852
Sequence:       1 MELALLCGLVVMAGVIPIQG.........YQKRLRFWRPHCRGQTPGC 145

Scoring table:  BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched:       1351062 seqs, 321799191 residues

Total number of hits satisfying chosen parameters:    1351062

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :      Published Applications AA:*
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       2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
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      14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*
      15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep:*
      16: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
      17: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep:*
      18: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	852	100.0	145	9	US-09-835-996A-6	Sequence 6, Appli
2	852	100.0	150	12	US-10-296-115-1342	Sequence 1342, Ap
3	846	99.3	145	9	US-09-969-384-17	Sequence 17, Appl
4	846	99.3	145	10	US-09-975-456B-7	Sequence 7, Appli
5	500.5	58.7	116	10	US-09-946-374-378	Sequence 378, App
6	500.5	58.7	116	12	US-10-147-493-534	Sequence 534, App
7	500.5	58.7	116	12	US-10-145-127-534	Sequence 534, App
8	500.5	58.7	116	12	US-10-160-503-534	Sequence 534, App
9	500.5	58.7	116	12	US-10-143-118-534	Sequence 534, App
10	500.5	58.7	116	12	US-10-144-993-534	Sequence 534, App
11	500.5	58.7	116	12	US-10-158-787-534	Sequence 534, App
12	500.5	58.7	116	12	US-10-140-024-534	Sequence 534, App
13	500.5	58.7	116	12	US-10-140-808-534	Sequence 534, App
14	500.5	58.7	116	12	US-10-006-485A-378	Sequence 378, App
15	500.5	58.7	116	12	US-10-013-907A-378	Sequence 378, App
16	500.5	58.7	116	12	US-10-015-499A-378	Sequence 378, App
17	500.5	58.7	116	12	US-10-013-910A-378	Sequence 378, App
18	500.5	58.7	116	12	US-10-152-405-534	Sequence 534, App
19	500.5	58.7	116	12	US-10-127-852A-534	Sequence 534, App
20	500.5	58.7	116	12	US-10-127-900A-534	Sequence 534, App
21	500.5	58.7	116	12	US-10-128-685A-534	Sequence 534, App
22	500.5	58.7	116	12	US-10-226-254A-378	Sequence 378, App
23	500.5	58.7	116	12	US-10-131-820A-534	Sequence 534, App
24	500.5	58.7	116	12	US-10-142-886-534	Sequence 534, App
25	500.5	58.7	116	12	US-10-146-728-534	Sequence 534, App
26	500.5	58.7	116	12	US-10-146-786-534	Sequence 534, App
27	500.5	58.7	116	12	US-10-147-499-534	Sequence 534, App
28	500.5	58.7	116	12	US-10-157-798-534	Sequence 534, App
29	500.5	58.7	116	12	US-10-015-395A-378	Sequence 378, App
30	500.5	58.7	116	14	US-10-028-072-534	Sequence 534, App
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32	500.5	58.7	116	14	US-10-123-904-534	Sequence 534, App
33	500.5	58.7	116	14	US-10-140-470-534	Sequence 534, App
34	500.5	58.7	116	14	US-10-175-746-534	Sequence 534, App
35	500.5	58.7	116	14	US-10-176-918-534	Sequence 534, App
36	500.5	58.7	116	14	US-10-176-921-534	Sequence 534, App
37	500.5	58.7	116	14	US-10-137-865-534	Sequence 534, App
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39	500.5	58.7	116	14	US-10-142-431-534	Sequence 534, App
40	500.5	58.7	116	14	US-10-143-114-534	Sequence 534, App
41	500.5	58.7	116	14	US-10-140-002-534	Sequence 534, App
42	500.5	58.7	116	14	US-10-006-856A-378	Sequence 378, App
43	500.5	58.7	116	14	US-10-142-419-534	Sequence 534, App
44	500.5	58.7	116	14	US-10-123-262-534	Sequence 534, App
45	500.5	58.7	116	14	US-10-142-423-534	Sequence 534, App

ALIGNMENTS

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RESULT 1
US-09-835-996A-6

; Sequence 6, Application US/09835996A
; Patent No. US2002014295A1
; GENERAL INFORMATION:
;  APPLICANT: Ballinger, Dennis
;  APPLICANT: Loeb, Debra
;  APPLICANT: Montgomery, Julie
;  APPLICANT: Tang, Y. Tom
;  APPLICANT: Zhou, Ping
;  APPLICANT: Goodrich, Ryle
;  APPLICANT: Liu, Chenghua
;  APPLICANT: Asundi, Vinod
;  APPLICANT: Zhao, Qing
;  APPLICANT: Wehrman, Tom
;  APPLICANT: Drmanac, Radoje
;  APPLICANT: Ren, Feiyan
;  APPLICANT: Qian, Xiahong
;  APPLICANT: Wang, Dunrui
;  TITLE OF INVENTION: MATERIALS AND METHODS RELATING TO LIPID METABOLISM
;  FILE REFERENCE: 28110/35915A
;  CURRENT APPLICATION NUMBER: US/09/835,996A
;  CURRENT FILING DATE:  2001-04-16
;  PRIOR APPLICATION NUMBER: US 60/197,137
;  PRIOR APPLICATION NUMBER: US 2000-04-14
;  PRIOR APPLICATION NUMBER: US 09/714,936
;  PRIOR FILING DATE: 2000-11-17
;  PRIOR APPLICATION NUMBER: US 09/667,298
;  PRIOR FILING DATE: 2000-09-22
;  PRIOR APPLICATION NUMBER: US 09/631,451
;  PRIOR FILING DATE: 2000-08-03
;  PRIOR APPLICATION NUMBER: US 09/598,042
;  PRIOR FILING DATE: 2000-06-20
;  NUMBER OF SEQ ID NOS: 45
;  SOFTWARE: Patentin version 3.0
; SEQ ID NO 6
;  LENGTH: 145
;  TYPE: PRT
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;  ORGANISM: Homo sapiens
US-09-835-996A-6

Query Match        100.0%;   Score 852;  DB 9;  Length 145;
Best Local Similarity  100.0%;  Pred. No. 1.6e-81;
Matches 145;  Conservative  0;  Mismatches  0;  Indels  0;  Gaps  0;

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Qy    61  DWCCQTHDCCYDHLKTQGCGIYKDYYRYNFSQGNIHCSDKGSWCEQQLCACDKEVAFCLK  120
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Db    61  DWCCQTHDCCYDHLKTQGCGIYKDYYRYNFSQGNIHCSDKGSWCEQQLCACDKEVAFCLK  120

Qy   121  RNLDTYQKRLRFYWRPHCRGQTPGC  145
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RESULT 2
US-10-296-115-1342
;  Sequence 1342, Application US/10296115
;  Publication No. US2004005324BA1
;  GENERAL INFORMATION:
;  APPLICANT: Hyseq Inc
;  TITLE OF INVENTION: No. US2004005324BA1e1 Nucleic Acids and Polypeptides
;  FILE REFERENCE: 784PCT
;  CURRENT APPLICATION NUMBER: US/10/296,115
;  CURRENT FILING DATE: 2002-11-18
;  PRIOR APPLICATION NUMBER: US09/488,725
;  PRIOR FILING DATE: 2000-01-21
;  PRIOR APPLICATION NUMBER: US09/552,317
;  PRIOR FILING DATE: 2000-04-25
;  NUMBER OF SEQ ID NOS: 1478
;  SEQ ID NO 1342
;  LENGTH: 150
;  TYPE: PRT
;  ORGANISM: Homo sapiens
US-10-296-115-1342

Query Match        100.0%;   Score 852;  DB 12;  Length 150;
Best Local Similarity  100.0%;  Pred. No. 1.6e-81;
Matches 145;  Conservative  0;  Mismatches  0;  Indels  0;  Gaps  0;

Qy     1  MELALLCGLVVMAGVIPIQGGILNLNKMVKQVTGKMPILSYWPYGCHCGLGGRGQPKDAT  60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     6  MELALLCGLVVMAGVIPIQGGILNLNKMVKQVTGKMPILSYWPYGCHCGLGGRGQPKDAT  65

Qy    61  DWCCQTHDCCYDHLKTQGCGIYKDYYRYNFSQGNIHCSDKGSWCEQQLCACDKEVAFCLK  120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    66  DWCCQTHDCCYDHLKTQGCGIYKDYYRYNFSQGNIHCSDKGSWCEQQLCACDKEVAFCLK  125

Qy   121  RNLDTYQKRLRFYWRPHCRGQTPGC  145
          |||||||||||||||||||||||||
Db   126  RNLDTYQKRLRFYWRPHCRGQTPGC  150


RESULT 3
US-09-969-384-17
;  Sequence 17, Application US/09969384
;  Publication No. US20020192749A1
;  GENERAL INFORMATION:
;  APPLICANT: Moore, et al.
;  TITLE OF INVENTION: Human Gene Polynucleotides, Polypeptides, and Antibodies
;  FILE REFERENCE: PT055P1
;  CURRENT APPLICATION NUMBER: US/09/969,384
;  CURRENT FILING DATE: 2001-10-03
;  PRIOR APPLICATION NUMBER: PCT/US01/10542
;  PRIOR FILING DATE: 2001-04-02
;  PRIOR APPLICATION NUMBER: 60/236,384
;  PRIOR FILING DATE: 2000-09-29
;  PRIOR APPLICATION NUMBER: 60/194,118
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;  PRIOR FILING DATE: 2000-04-03
;  NUMBER OF SEQ ID NOS: 27
;  SOFTWARE: PatentIn Ver. 2.0
;  SEQ ID NO 17
;  LENGTH: 145
;  TYPE: PRT
;  ORGANISM: Homo sapiens
US-09-969-384-17

Query Match        99.3%;   Score 846;  DB 9;  Length 145;
Best Local Similarity  99.3%;  Pred. No. 6.7e-81;
Matches 144;  Conservative  0;  Mismatches  1;  Indels  0;  Gaps  0;

Qy     1  MELALLCGLVVMAGVIPIQGGILNLNKMVKQVTGKMPILSYWPYGCHCGLGGRGQPKDAT  60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1  MELALLCGLVVMAGVIPIQGGILNLNKMVKQVTGKMPILSYWPYGCHCGLGGRGQPKDAT  60

Qy    61  DWCCQTHDCCYDHLKTQGCGIYKDYYRYNFSQGNIHCSDKGSWCEQQLCACDKEVAFCLK  120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    61  DWCCQTHDCCYDHLKTQGCGIYKDYYRYNFSQGNIHCSDKGSWCEQQLCACDKEVAFCLK  120

Qy   121  RNLDTYQKRLRFYWRPHCRGQTPGC  145
          |||||||||||||||||||||||||
Db   121  RNLDTYQKRLRFYWRPHCRGQTPGC  145


RESULT 4
US-09-975-456B-7
;  Sequence 7, Application US/09975456B
;  Publication No. US2003007308TA1
;  GENERAL INFORMATION:
;  APPLICANT: LAZDUNSKI, MICHEL
;  APPLICANT: LAMBEAU, GERARD
;  APPLICANT: VALENTIN, EMMANUEL
;  TITLE OF INVENTION: NOVEL MAMMALIAN SECRETED GROUP IIF PHOSPHOLIPASE A2
;  FILE REFERENCE: 1478-R-00
;  CURRENT APPLICATION NUMBER: US/09/975,456B
;  CURRENT FILING DATE: 2002-08-27
;  PRIOR APPLICATION NUMBER: 60/239,491
;  PRIOR FILING DATE: 2000-10-11
;  NUMBER OF SEQ ID NOS: 10
;  SOFTWARE: PatentIn version 2.1
;  SEQ ID NO 7
;  LENGTH: 145
;  TYPE: PRT
;  ORGANISM: Homo sapiens
US-09-975-456B-7

Query Match        99.3%;   Score 846;  DB 10;  Length 145;
Best Local Similarity  99.3%;  Pred. No. 6.7e-81;
Matches 144;  Conservative  0;  Mismatches  1;  Indels  0;  Gaps  0;

Qy     1  MELALLCGLVVMAGVIPIQGGILNLNKMVKQVTGKMPILSYWPYGCHCGLGGRGQPKDAT  60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1  MELALLCGLVVMAGVIPIQGGILNLNKMVKQVTGKMPILSYWPYGCHCGLGGRGQPKDAT  60

Qy    61  DWCCQTHDCCYDHLKTQGCGIYKDYYRYNFSQGNIHCSDKGSWCEQQLCACDKEVAFCLK  120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    61  DWCCQTHDCCYDHLKTQGCSIYKDYYRYNFSQGNIHCSDKGSWCEQQLCACDKEVAFCLK  120

Qy   121  RNLDTYQKRLRFYWRPHCRGQTPGC  145
          |||||||||||||||||||||||||
Db   121  RNLDTYQKRLRFYWRPHCRGQTPGC  145


RESULT 5
US-09-946-374-378
;  Sequence 378, Application US/09946374
;  Publication No. US2003007312AA1
;  GENERAL INFORMATION:
;  APPLICANT: Baker, Kevin P.
;  APPLICANT: Botstein, David
;  APPLICANT: Desnoyers, Luc
```

APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, Christopher J.
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Smith, Victoria
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2830P1C1
CURRENT APPLICATION NUMBER: US/09/946,374
CURRENT FILING DATE: 2001-09-04
PRIOR APPLICATION NUMBER: 60/098716
PRIOR FILING DATE: 1998-09-01
PRIOR APPLICATION NUMBER: 60/098723
PRIOR FILING DATE: 1998-09-01
PRIOR APPLICATION NUMBER: 60/098749
PRIOR FILING DATE: 1998-09-01
PRIOR APPLICATION NUMBER: 60/098750
PRIOR FILING DATE: 1998-09-01
PRIOR APPLICATION NUMBER: 60/098803
PRIOR FILING DATE: 1998-09-02
PRIOR APPLICATION NUMBER: 60/098821
PRIOR FILING DATE: 1998-09-02
PRIOR APPLICATION NUMBER: 60/098843
PRIOR FILING DATE: 1998-09-02
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PRIOR FILING DATE: 1998-09-09
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PRIOR FILING DATE: 1998-09-16

PRIOR APPLICATION NUMBER: 60/100661
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PRIOR FILING DATE: 1998-09-16
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PRIOR FILING DATE: 1998-09-17
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PRIOR FILING DATE: 1998-09-17
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PRIOR FILING DATE: 1998-09-18
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PRIOR FILING DATE: 1998-09-17
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PRIOR APPLICATION NUMBER: 60/101071
PRIOR FILING DATE: 1998-09-18
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PRIOR FILING DATE: 1998-09-23
PRIOR APPLICATION NUMBER: 60/101479
PRIOR FILING DATE: 1998-09-23
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PRIOR FILING DATE: 1998-09-24
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PRIOR FILING DATE: 1998-09-24
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PRIOR APPLICATION NUMBER: 60/102307
PRIOR FILING DATE: 1998-09-29
PRIOR APPLICATION NUMBER: 60/102330
PRIOR FILING DATE: 1998-09-29
PRIOR APPLICATION NUMBER: 60/102484
PRIOR FILING DATE: 1998-09-30
PRIOR APPLICATION NUMBER: 60/102487
PRIOR FILING DATE: 1998-09-30
PRIOR APPLICATION NUMBER: 60/102570
PRIOR FILING DATE: 1998-09-30
PRIOR APPLICATION NUMBER: 60/102571
PRIOR FILING DATE: 1998-09-30
PRIOR APPLICATION NUMBER: 60/102684

; APPLICANT: Gerritsen,Mary E.
; APPLICANT: Goddard,Audrey
; APPLICANT: Godowski,Paul J.
; APPLICANT: Gurney,Austin L.
; APPLICANT: Sherwood,Steven
; APPLICANT: Smith,Victoria
; APPLICANT: Stewart,Timothy A.
; APPLICANT: Tumas,Daniel
; APPLICANT: Watanabe,Colin K
; APPLICANT: Wood,William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3330R1C345
; CURRENT APPLICATION NUMBER: US/10/147,493
; CURRENT FILING DATE: 2002-05-17
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 534
; LENGTH: 116
; TYPE: PRT
; ORGANISM: Homo Sapien
; US-10-147-493-534

Query Match   58.7%;   Score 500.5;   DB 12;   Length 116;
Best Local Similarity   82.6%;   Pred. No. 1.1e-44;
Matches 90;   Conservative   4;   Mismatches   6;   Indels   9;   Gaps   2;

Qy   1 MELALLCGLVVMAGVIPIQGGIINLNKMVKQVTGKMPILSYWPYGCHCGLGGRGQPKDAT 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 MELALLCGLVVMAGVIPIQGGIINLNKMVKQVTGKMPILSYWPYGCHCGLGGRGQPKDAT 60

Qy   61 DWCCQTHDCCYDHLKTQGCGIYKDYRYNFSQGNIHCSDKGSWCEQQLC 109
          ||||||||||||||||||||| :: |||| |:|
Db   61 DWCCQTHDCCYDHLKTQGCGIYKDN-----NKSSIHCMD----LSQRYC 100

RESULT 7
US-10-145-127-534
; Sequence 534, Application US/10145127
; Publication No. US2004003358A1
; GENERAL INFORMATION:
; APPLICANT: Baker,Kevin P.
; APPLICANT: Beresini,Maureen
; APPLICANT: DeForge,Laura
; APPLICANT: Desnoyers,Luc
; APPLICANT: Filvaroff,Ellen
; APPLICANT: Gao,Wei-Qiang
; APPLICANT: Gerritsen,Mary E.
; APPLICANT: Goddard,Audrey
; APPLICANT: Godowski,Paul J.
; APPLICANT: Gurney,Austin L.
; APPLICANT: Sherwood,Steven
; APPLICANT: Smith,Victoria
; APPLICANT: Stewart,Timothy A.
; APPLICANT: Tumas,Daniel
; APPLICANT: Watanabe,Colin K
; APPLICANT: Wood,William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3330R1C252
; CURRENT APPLICATION NUMBER: US/10/145,127
; CURRENT FILING DATE: 2002-05-13
; Prior Apploication removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 534
; LENGTH: 116
; TYPE: PRT
; ORGANISM: Homo Sapien
; US-10-145-127-534

Query Match   58.7%;   Score 500.5;   DB 12;   Length 116;

; PRIOR FILING DATE: 1998-10-01
; PRIOR APPLICATION NUMBER: 60/102687
; PRIOR FILING DATE: 1998-10-01
; PRIOR APPLICATION NUMBER: 60/102965
; PRIOR FILING DATE: 1998-10-02
; PRIOR APPLICATION NUMBER: 60/103258
; PRIOR FILING DATE: 1998-10-06
; PRIOR APPLICATION NUMBER: 60/103314
; PRIOR FILING DATE: 1998-10-07
; PRIOR APPLICATION NUMBER: 60/103315
; PRIOR FILING DATE: 1998-10-07
; PRIOR APPLICATION NUMBER: 60/103328
; PRIOR FILING DATE: 1998-10-07
; PRIOR APPLICATION NUMBER: 60/103395
; PRIOR FILING DATE: 1998-10-07
; PRIOR APPLICATION NUMBER: 60/103396
; PRIOR FILING DATE: 1998-10-07
; PRIOR APPLICATION NUMBER: 60/103401
; PRIOR FILING DATE: 1998-10-07
; PRIOR APPLICATION NUMBER: 60/103449
; PRIOR FILING DATE: 1998-10-06
; PRIOR APPLICATION NUMBER: 60/103633
; PRIOR FILING DATE: 1998-10-08
; PRIOR APPLICATION NUMBER: 60/103678
; PRIOR FILING DATE: 1998-10-08
; PRIOR APPLICATION NUMBER: 60/103679
; PRIOR FILING DATE: 1998-10-08
; PRIOR APPLICATION NUMBER: 60/103711
; PRIOR FILING DATE: 1998-10-08
; PRIOR APPLICATION NUMBER: 60/104257
; PRIOR FILING DATE: 1998-10-14
; PRIOR APPLICATION NUMBER: 60/104987
; PRIOR FILING DATE: 1998-10-20
; PRIOR APPLICATION NUMBER: 60/105000
; PRIOR FILING DATE: 1998-10-20
; PRIOR APPLICATION NUMBER: 60/105002
; PRIOR FILING DATE: 1998-10-20
; PRIOR APPLICATION NUMBER: 60/105104
; PRIOR FILING DATE: 1998-10-21
; PRIOR APPLICATION NUMBER: 60/105169
; PRIOR FILING DATE: 1998-10-22
; PRIOR APPLICATION NUMBER: 60/105266
; PRIOR FILING DATE: 1998-10-22
; PRIOR APPLICATION NUMBER: 60/105693
; PRIOR FILING DATE: 1998-10-26
; PRIOR APPLICATION NUMBER: 60/105694
; PRIOR FILING DATE: 1998-10-26
; PRIOR APPLICATION NUMBER: 60/105807

Query Match   58.7%;   Score 500.5;   DB 10;   Length 116;
Best Local Similarity   82.6%;   Pred. No. 1.1e-44;
Matches 90;   Conservative   4;   Mismatches   6;   Indels   9;   Gaps   2;

Qy   1 MELALLCGLVVMAGVIPIQGGIINLNKMVKQVTGKMPILSYWPYGCHCGLGGRGQPKDAT 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 MELALLCGLVVMAGVIPIQGGIINLNKMVKQVTGKMPILSYWPYGCHCGLGGRGQPKDAT 60

Qy   61 DWCCQTHDCCYDHLKTQGCGIYKDYRYNFSQGNIHCSDKGSWCEQQLC 109
          ||||||||||||||||||||| :: |||| |:|
Db   61 DWCCQTHDCCYDHLKTQGCGIYKDN-----NKSSIHCMD----LSQRYC 100

RESULT 6
US-10-147-493-534
; Sequence 534, Application US/10147493
; Publication No. US20040029217A1
; GENERAL INFORMATION:
; APPLICANT: Baker,Kevin P.
; APPLICANT: Beresini,Maureen
; APPLICANT: DeForge,Laura
; APPLICANT: Desnoyers,Luc
; APPLICANT: Filvaroff,Ellen
; APPLICANT: Gao,Wei-Qiang

```
Best Local Similarity  82.6%;  Pred. No. 1.1e-44;
Matches  90;  Conservative  4;  Mismatches  6;  Indels  9;  Gaps  2;

Qy    1 MELALLCGLVVMAGVIPIQGGILNLNKMVKQVTGKMPILSYWPYGCHCGLGGRGQPKDAT  60
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1 MELALLCGLVVMAGVIPIQGGILNLNKMVKQVTGKMPILSYWPYGCHCGLGGRGQPKDAT  60

Qy   61 DWCCQTHDCCYDHLKTQGCGIYKDYYRYNFSQGNIHCSDKGSWCEQQLC 109
          :: :||| :|| |||
Db   61 DWCCQTHDCCYDHLKTQGCGIYKDN----NKSSIHCMD----LSQRYC 100
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RESULT 8
US-10-160-503-534
; Sequence 534, Application US/10160503
; Publication No. US20040033559A1
; GENERAL INFORMATION:
;   APPLICANT: Baker,Kevin P.
;   APPLICANT: Beresini,Maureen
;   APPLICANT: DeForge,Laura
;   APPLICANT: Desnoyers,Luc
;   APPLICANT: Filvaroff,Ellen
;   APPLICANT: Gao,Wei-Qiang
;   APPLICANT: Gerritsen,Mary E.
;   APPLICANT: Goddard,Audrey
;   APPLICANT: Godowski,Paul J.
;   APPLICANT: Gurney,Austin L.
;   APPLICANT: Sherwood,Steven
;   APPLICANT: Smith,Victoria
;   APPLICANT: Stewart,Timothy A.
;   APPLICANT: Tumas,Daniel
;   APPLICANT: Watanabe,Colin K
;   APPLICANT: Wood,William
;   APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3330R1C446
; CURRENT APPLICATION NUMBER: US/10/160,503
; CURRENT FILING DATE: 2002-05-30
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 534
;   LENGTH: 116
;   TYPE: PRT
;   ORGANISM: Homo Sapien
US-10-160-503-534

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Query Match             58.7%;  Score 500.5;  DB 12;  Length 116;
Best Local Similarity  82.6%;  Pred. No. 1.1e-44;
Matches  90;  Conservative  4;  Mismatches  6;  Indels  9;  Gaps  2;

Qy    1 MELALLCGLVVMAGVIPIQGGILNLNKMVKQVTGKMPILSYWPYGCHCGLGGRGQPKDAT  60
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1 MELALLCGLVVMAGVIPIQGGILNLNKMVKQVTGKMPILSYWPYGCHCGLGGRGQPKDAT  60

Qy   61 DWCCQTHDCCYDHLKTQGCGIYKDYYRYNFSQGNIHCSDKGSWCEQQLC 109
          :: :||| :|| |||
Db   61 DWCCQTHDCCYDHLKTQGCGIYKDN----NKSSIHCMD----LSQRYC 100
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RESULT 9
US-10-143-118-534
; Sequence 534, Application US/10143118
; Publication No. US20040038335A1
; GENERAL INFORMATION:
;   APPLICANT: Baker,Kevin P.
;   APPLICANT: Beresini,Maureen
;   APPLICANT: DeForge,Laura
;   APPLICANT: Desnoyers,Luc
;   APPLICANT: Filvaroff,Ellen
;   APPLICANT: Gao,Wei-Qiang
;   APPLICANT: Gerritsen,Mary E.
;   APPLICANT: Goddard,Audrey
;   APPLICANT: Godowski,Paul J.
;   APPLICANT: Gurney,Austin L.
;   APPLICANT: Sherwood,Steven
;   APPLICANT: Smith,Victoria
;   APPLICANT: Stewart,Timothy A.
;   APPLICANT: Tumas,Daniel
;   APPLICANT: Watanabe,Colin K
;   APPLICANT: Wood,William
;   APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3330R1C228
; CURRENT APPLICATION NUMBER: US/10/143,118
; CURRENT FILING DATE: 2002-05-09
; Prior Application removed - See Palm or File Wrapper
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 534
;   LENGTH: 116
;   TYPE: PRT
;   ORGANISM: Homo Sapien
US-10-143-118-534

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Query Match             58.7%;  Score 500.5;  DB 12;  Length 116;
Best Local Similarity  82.6%;  Pred. No. 1.1e-44;
Matches  90;  Conservative  4;  Mismatches  6;  Indels  9;  Gaps  2;

Qy    1 MELALLCGLVVMAGVIPIQGGILNLNKMVKQVTGKMPILSYWPYGCHCGLGGRGQPKDAT  60
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1 MELALLCGLVVMAGVIPIQGGILNLNKMVKQVTGKMPILSYWPYGCHCGLGGRGQPKDAT  60

Qy   61 DWCCQTHDCCYDHLKTQGCGIYKDYYRYNFSQGNIHCSDKGSWCEQQLC 109
          :: :||| :|| |||
Db   61 DWCCQTHDCCYDHLKTQGCGIYKDN----NKSSIHCMD----LSQRYC 100
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RESULT 10
US-10-144-993-534
; Sequence 534, Application US/10144993
; Publication No. US20040038336A1
; GENERAL INFORMATION:
;   APPLICANT: Baker,Kevin P.
;   APPLICANT: Beresini,Maureen
;   APPLICANT: DeForge,Laura
;   APPLICANT: Desnoyers,Luc
;   APPLICANT: Filvaroff,Ellen
;   APPLICANT: Gao,Wei-Qiang
;   APPLICANT: Gerritsen,Mary E.
;   APPLICANT: Goddard,Audrey
;   APPLICANT: Godowski,Paul J.
;   APPLICANT: Gurney,Austin L.
;   APPLICANT: Sherwood,Steven
;   APPLICANT: Smith,Victoria
;   APPLICANT: Stewart,Timothy A.
;   APPLICANT: Tumas,Daniel
;   APPLICANT: Watanabe,Colin K
;   APPLICANT: Wood,William
;   APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3330R1C261
; CURRENT APPLICATION NUMBER: US/10/144,993
; CURRENT FILING DATE: 2002-05-13
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 534
;   LENGTH: 116
;   TYPE: PRT
;   ORGANISM: Homo Sapien
US-10-144-993-534

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Query Match             58.7%;  Score 500.5;  DB 12;  Length 116;
Best Local Similarity  82.6%;  Pred. No. 1.1e-44;
Matches  90;  Conservative  4;  Mismatches  6;  Indels  9;  Gaps  2;
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Qy    1 MELALLCGLVVMAGVIPIQGGILNLNKMVKQVTGKMPILSYWPYGCHCGLGGRGQPKDAT 60
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1 MELALLCGLVVMAGVIPIQGGILNLNKMVKQVTGKMPILSYWPYGCHCGLGGRGQPKDAT 60

Qy   61 DWCCQTHDCCYDHLKTQGCGIYKDYRYRNFSQGNIHCSDKGSWCEQQLC 109
        |||||||||||    :: :|||||
Db   61 DWCCQTHDCCYDHLKTQGCGIYKDN----NKSSIHCMD----LSQRYC 100

RESULT 11
US-10-158-787-534
; Sequence 534, Application US/10158787
; Publication No. US2004003916441
; GENERAL INFORMATION:
;   APPLICANT: Baker,Kevin P.
;   APPLICANT: Beresini,Maureen
;   APPLICANT: DeForge,Laura
;   APPLICANT: Desnoyers,Luc
;   APPLICANT: Filvaroff,Ellen
;   APPLICANT: Gao,Wei-Qiang
;   APPLICANT: Gerritsen,Mary E.
;   APPLICANT: Goddard,Audrey
;   APPLICANT: Godowski,Paul J.
;   APPLICANT: Gurney,Austin L.
;   APPLICANT: Sherwood,Steven
;   APPLICANT: Smith,Victoria
;   APPLICANT: Stewart,Timothy A.
;   APPLICANT: Tumas,Daniel
;   APPLICANT: Watanabe,Colin K
;   APPLICANT: Wood,William
;   APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION:  ACIDS ENCODING THE SAME
; FILE REFERENCE: P3330R1C449
; CURRENT APPLICATION NUMBER: US/10/158,787
; CURRENT FILING DATE:  2003-04-03
; PRIOR APPLICATION NUMBER: 60/049911
; PRIOR FILING DATE:  1997-06-18
; PRIOR APPLICATION NUMBER: 60/056974
; PRIOR FILING DATE:  1997-08-26
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE:  1997-09-17
; PRIOR APPLICATION NUMBER: 60/059115
; PRIOR FILING DATE:  1997-09-17
; PRIOR APPLICATION NUMBER: 60/059117
; PRIOR FILING DATE:  1997-09-17
; PRIOR APPLICATION NUMBER: 60/059122
; PRIOR FILING DATE:  1997-09-17
; PRIOR APPLICATION NUMBER: 60/059184
; PRIOR FILING DATE:  1997-09-17
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE:  1997-09-18
; PRIOR APPLICATION NUMBER: 60/059352
; PRIOR FILING DATE:  1997-09-19
; PRIOR APPLICATION NUMBER: 60/059588
; PRIOR FILING DATE:  1997-09-19
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 534
;   LENGTH: 116
;   TYPE: PRT
;   ORGANISM: Homo Sapien
US-10-158-787-534

  Query Match             58.7%;  Score 500.5; DB 12; Length 116;
  Best Local Similarity   82.6%;  Pred. No. 1.1e-44;
  Matches   90;  Conservative    4;  Mismatches    6;  Indels    9;  Gaps    2;

Qy    1 MELALLCGLVVMAGVIPIQGGILNLNKMVKQVTGKMPILSYWPYGCHCGLGGRGQPKDAT 60
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1 MELALLCGLVVMAGVIPIQGGILNLNKMVKQVTGKMPILSYWPYGCHCGLGGRGQPKDAT 60

Qy   61 DWCCQTHDCCYDHLKTQGCGIYKDYRYRNFSQGNIHCSDKGSWCEQQLC 109
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        |||||||||||    :: :|||||
Db   61 DWCCQTHDCCYDHLKTQGCGIYKDN----NKSSIHCMD----LSQRYC 100

RESULT 12
US-10-140-024-534
; Sequence 534, Application US/10140024
; Publication No. US2004005842441
; GENERAL INFORMATION:
;   APPLICANT: Baker,Kevin P.
;   APPLICANT: Beresini,Maureen
;   APPLICANT: DeForge,Laura
;   APPLICANT: Desnoyers,Luc
;   APPLICANT: Filvaroff,Ellen
;   APPLICANT: Gao,Wei-Qiang
;   APPLICANT: Gerritsen,Mary E.
;   APPLICANT: Goddard,Audrey
;   APPLICANT: Godowski,Paul J.
;   APPLICANT: Gurney,Austin L.
;   APPLICANT: Sherwood,Steven
;   APPLICANT: Smith,Victoria
;   APPLICANT: Stewart,Timothy A.
;   APPLICANT: Tumas,Daniel
;   APPLICANT: Watanabe,Colin K
;   APPLICANT: Wood,William
;   APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION:  ACIDS ENCODING THE SAME
; FILE REFERENCE: P3330R1C69
; CURRENT APPLICATION NUMBER: US/10/140,024
; CURRENT FILING DATE:  2002-05-06
; Prior Application removed - See Palm or File Wrapper
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 534
;   LENGTH: 116
;   TYPE: PRT
;   ORGANISM: Homo Sapien
US-10-140-024-534

  Query Match             58.7%;  Score 500.5; DB 12; Length 116;
  Best Local Similarity   82.6%;  Pred. No. 1.1e-44;
  Matches   90;  Conservative    4;  Mismatches    6;  Indels    9;  Gaps    2;

Qy    1 MELALLCGLVVMAGVIPIQGGILNLNKMVKQVTGKMPILSYWPYGCHCGLGGRGQPKDAT 60
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1 MELALLCGLVVMAGVIPIQGGILNLNKMVKQVTGKMPILSYWPYGCHCGLGGRGQPKDAT 60

Qy   61 DWCCQTHDCCYDHLKTQGCGIYKDYRYRNFSQGNIHCSDKGSWCEQQLC 109
        |||||||||||    :: :|||||
Db   61 DWCCQTHDCCYDHLKTQGCGIYKDN----NKSSIHCMD----LSQRYC 100

RESULT 13
US-10-140-808-534
; Sequence 534, Application US/10140808
; Publication No. US20030017563A1
; GENERAL INFORMATION:
;   APPLICANT: Baker,Kevin P.
;   APPLICANT: Beresini,Maureen
;   APPLICANT: DeForge,Laura
;   APPLICANT: Desnoyers,Luc
;   APPLICANT: Filvaroff,Ellen
;   APPLICANT: Gao,Wei-Qiang
;   APPLICANT: Gerritsen,Mary E.
;   APPLICANT: Goddard,Audrey
;   APPLICANT: Godowski,Paul J.
;   APPLICANT: Gurney,Austin L.
;   APPLICANT: Sherwood,Steven
;   APPLICANT: Smith,Victoria
;   APPLICANT: Stewart,Timothy A.
;   APPLICANT: Tumas,Daniel
;   APPLICANT: Watanabe,Colin K
;   APPLICANT: Wood,William
```

```
;   APPLICANT: Zhang, Zemin
;   TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
;   TITLE OF INVENTION: ACIDS ENCODING THE SAME
;   FILE REFERENCE: P3330R1C182
;   CURRENT APPLICATION NUMBER: US/10/140,808
;   CURRENT FILING DATE: 2002-05-07
;   Prior Apploication removed - See File Wrapper or Palm
;   NUMBER OF SEQ ID NOS: 550
;   SEQ ID NO 534
;   LENGTH: 116
;   TYPE: PRT
;   ORGANISM: Homo Sapien
US-10-140-808-534

Query Match           58.7%;   Score 500.5;   DB 12;   Length 116;
Best Local Similarity  82.6%;  Pred. No. 1.1e-44;
Matches  90;  Conservative  4;  Mismatches  6;  Indels  9;  Gaps  2;

Qy    1  MEIALLCGLVVMAGVIPIQGGILNLNKMVKQVTGKMPILSYWPYGCHCGLGGRGQPKDAT  60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1  MEIALLCGLVVMAGVIPIQGGILNLNKMVKQVTGKMPILSYWPYGCHCGLGGRGQPKDAT  60

Qy   61  DWCCQTHDCCYDHLKTQGCGIYKDYYRYNFSQGNIHCSDKGSWCEQQLC 109
            ||||||||||||||||||||      :: :|||    |::|
Db   61  DWCCQTHDCCYDHLKTQGCGIYKDN----NKSSIHCMD----LSQRYC 100


RESULT 14
US-10-006-485A-378
;   Sequence 378, Application US/10006485A
;   Publication No. US20030064062A1
;   GENERAL INFORMATION:
;   APPLICANT: Baker, Kevin P.
;   APPLICANT: Botstein, David
;   APPLICANT: Desnoyers, Luc
;   APPLICANT: Eaton, Dan l.
;   APPLICANT: Ferrara, Napoleone
;   APPLICANT: Fong, Sherman
;   APPLICANT: Gao, Wei-Qiang
;   APPLICANT: Goddard, Audrey
;   APPLICANT: Godowski, Paul J.
;   APPLICANT: Grimaldi, Christopher J.
;   APPLICANT: Gurney, Austin L.
;   APPLICANT: Hillan, Kenneth J.
;   APPLICANT: Pan, James
;   APPLICANT: Paoni, Nicholas F.
;   TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
;   TITLE OF INVENTION:  Acids Encoding the Same
;   FILE REFERENCE: P2830P1C9
;   CURRENT APPLICATION NUMBER: US/10/006,485A
;   CURRENT FILING DATE: 2001-12-06
;   PRIOR APPLICATION NUMBER: 60/098716
;   PRIOR FILING DATE: 1998-09-01
;   PRIOR APPLICATION NUMBER: 60/098723
;   PRIOR FILING DATE: 1998-09-01
;   PRIOR APPLICATION NUMBER: 60/098749
;   PRIOR FILING DATE: 1998-09-01
;   PRIOR APPLICATION NUMBER: 60/098750
;   PRIOR FILING DATE: 1998-09-01
;   PRIOR APPLICATION NUMBER: 60/098803
;   PRIOR FILING DATE: 1998-09-02
;   PRIOR APPLICATION NUMBER: 60/098821
;   PRIOR FILING DATE: 1998-09-02
;   PRIOR APPLICATION NUMBER: 60/098843
;   PRIOR FILING DATE: 1998-09-02
;   PRIOR APPLICATION NUMBER: 60/099536
;   PRIOR FILING DATE: 1998-09-09
;   PRIOR APPLICATION NUMBER: 60/099596
;   PRIOR FILING DATE: 1998-09-09
;   PRIOR APPLICATION NUMBER: 60/099598
;   PRIOR FILING DATE: 1998-09-09
;   PRIOR APPLICATION NUMBER: 60/099602
;   PRIOR FILING DATE: 1998-09-09
;   PRIOR APPLICATION NUMBER: 60/099642
;   PRIOR FILING DATE: 1998-09-09
;   PRIOR APPLICATION NUMBER: 60/099741
;   PRIOR FILING DATE: 1998-09-10
;   PRIOR APPLICATION NUMBER: 60/099754
;   PRIOR FILING DATE: 1998-09-10
;   PRIOR APPLICATION NUMBER: 60/099763
;   PRIOR FILING DATE: 1998-09-10
;   PRIOR APPLICATION NUMBER: 60/099792
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;   PRIOR APPLICATION NUMBER: 60/099815
;   PRIOR FILING DATE: 1998-09-10
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;   PRIOR FILING DATE: 1998-09-18
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;   PRIOR FILING DATE: 1998-09-22
;   PRIOR APPLICATION NUMBER: 60/101471
;   PRIOR FILING DATE: 1998-09-23
;   PRIOR APPLICATION NUMBER: 60/101472
;   PRIOR FILING DATE: 1998-09-23
;   PRIOR APPLICATION NUMBER: 60/101474
;   PRIOR FILING DATE: 1998-09-23
;   PRIOR APPLICATION NUMBER: 60/101475
;   PRIOR FILING DATE: 1998-09-23
;   PRIOR APPLICATION NUMBER: 60/101476
;   PRIOR FILING DATE: 1998-09-23
;   PRIOR APPLICATION NUMBER: 60/101477
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;   PRIOR APPLICATION NUMBER: 60/101479
;   PRIOR FILING DATE: 1998-09-23
;   PRIOR APPLICATION NUMBER: 60/101738
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;     PRIOR FILING DATE: 1998-09-24
;     PRIOR APPLICATION NUMBER: 60/101741
;     PRIOR FILING DATE: 1998-09-24
;     PRIOR APPLICATION NUMBER: 60/101743
;     PRIOR FILING DATE: 1998-09-24
;     PRIOR APPLICATION NUMBER: 60/101915
;     PRIOR FILING DATE: 1998-09-24
;     PRIOR APPLICATION NUMBER: 60/101916
;     PRIOR FILING DATE: 1998-09-24
;     PRIOR APPLICATION NUMBER: 60/102207
;     PRIOR FILING DATE: 1998-09-29
;     PRIOR APPLICATION NUMBER: 60/102240
;     PRIOR FILING DATE: 1998-09-29
;     PRIOR APPLICATION NUMBER: 60/102307
;     PRIOR FILING DATE: 1998-09-29
;     PRIOR APPLICATION NUMBER: 60/102330
;     PRIOR FILING DATE: 1998-09-29
;     PRIOR APPLICATION NUMBER: 60/102331
;     PRIOR FILING DATE: 1998-09-29
;     PRIOR APPLICATION NUMBER: 60/102484
;     PRIOR FILING DATE: 1998-09-30
;     PRIOR APPLICATION NUMBER: 60/102487
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;     PRIOR APPLICATION NUMBER: 60/102570
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;     PRIOR FILING DATE: 1998-10-01
;     PRIOR APPLICATION NUMBER: 60/102687
;     PRIOR FILING DATE: 1998-10-01
;     PRIOR APPLICATION NUMBER: 60/102965
;     PRIOR FILING DATE: 1998-10-02
;     PRIOR APPLICATION NUMBER: 60/103258
;     PRIOR FILING DATE: 1998-10-06
;     PRIOR APPLICATION NUMBER: 60/103314
;     PRIOR FILING DATE: 1998-10-07
;     PRIOR APPLICATION NUMBER: 60/103315
;     PRIOR FILING DATE: 1998-10-07
;     PRIOR APPLICATION NUMBER: 60/103328
;     PRIOR FILING DATE: 1998-10-07
;     PRIOR APPLICATION NUMBER: 60/103395
;     PRIOR FILING DATE: 1998-10-07
;     PRIOR APPLICATION NUMBER: 60/103396
;     PRIOR FILING DATE: 1998-10-07
;     PRIOR APPLICATION NUMBER: 60/103401
;     PRIOR FILING DATE: 1998-10-07
;     PRIOR APPLICATION NUMBER: 60/103449
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;     PRIOR APPLICATION NUMBER: 60/103633
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;     PRIOR FILING DATE: 1998-10-08
;     PRIOR APPLICATION NUMBER: 60/103679
;     PRIOR FILING DATE: 1998-10-08
;     PRIOR APPLICATION NUMBER: 60/103711
;     PRIOR FILING DATE: 1998-10-08
;     PRIOR APPLICATION NUMBER: 60/104257
;     PRIOR FILING DATE: 1998-10-14
;     PRIOR APPLICATION NUMBER: 60/104987
;     PRIOR FILING DATE: 1998-10-20
;     PRIOR APPLICATION NUMBER: 60/105000
;     PRIOR FILING DATE: 1998-10-20
;     PRIOR APPLICATION NUMBER: 60/105002
;     PRIOR FILING DATE: 1998-10-20
;     PRIOR APPLICATION NUMBER: 60/105104
;     PRIOR FILING DATE: 1998-10-21
;     PRIOR APPLICATION NUMBER: 60/105169
;     PRIOR FILING DATE: 1998-10-22
;     PRIOR APPLICATION NUMBER: 60/105266
;     PRIOR FILING DATE: 1998-10-22
;     PRIOR APPLICATION NUMBER: 60/105693
;     PRIOR FILING DATE: 1998-10-26
;     PRIOR APPLICATION NUMBER: 60/105694
;     PRIOR FILING DATE: 1998-10-26
;     PRIOR APPLICATION NUMBER: 60/105807
;     PRIOR FILING DATE: 1998-10-27
;     PRIOR APPLICATION NUMBER: 60/105881
;     PRIOR FILING DATE: 1998-10-27
;     PRIOR APPLICATION NUMBER: 60/105882
;     PRIOR FILING DATE: 1998-10-27
;     PRIOR APPLICATION NUMBER: 60/106023
;     PRIOR FILING DATE: 1998-10-28

  Query Match        58.7%;  Score 500.5;  DB 12;  Length 116;
  Best Local Similarity   82.6%;  Pred. No. 1.1e-44;
  Matches   90;  Conservative   4;  Mismatches   4;  Indels   6;  Gaps   2;

Qy    1 MELALLCGLVMAGVIPIQGGILNLNKMVKQVTGKMPILSYWPYGCHCGLGGRGQPKDAT 60
        |||||||||| |||||||||||||||||||||||||||||||||||||||||||||||
Db    1 MELALLCGLVVMAGVIPIQGGILNLNKMVKQVTGKMPILSYWPYGCHCGLGGRGQPKDAT 60

Qy   61 DWCCQTHDCCYDHLKTQGCGIYKDYRYRNFSQGNIHCSDKGSWCEQQLC 109
        ||||||||||||||||||||||||   :: ::|||        |
Db   61 DWCCQTHDCCYDHLKTQGCGIYKDN----NKSSIHCMD----LSQRYC 100
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RESULT 15
US-10-013-907A-378

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; Sequence 378, Application US/10013907A
; Publication No. US20030064925A1
; GENERAL INFORMATION:
;  APPLICANT: Baker, Kevin P.
;  APPLICANT: Botstein, David
;  APPLICANT: Desnoyers, Luc
;  APPLICANT: Eaton, Dan 1.
;  APPLICANT: Ferrara, Napoleone
;  APPLICANT: Fong, Sherman
;  APPLICANT: Gao, Wei-Qiang
;  APPLICANT: Goddard, Audrey
;  APPLICANT: Godowski, Paul J.
;  APPLICANT: Grimaldi, Christopher J.
;  APPLICANT: Gurney, Austin L.
;  APPLICANT: Hillan, Kenneth J.
;  APPLICANT: Pan, James
;  APPLICANT: Paoni, Nicholas F.
;  TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
;  TITLE OF INVENTION: Acids Encoding the Same
;  FILE REFERENCE: P2830P1C34
;  CURRENT APPLICATION NUMBER: US/10/013,907A
;  CURRENT FILING DATE: 2001-12-10
;  Prior Application removed - See File Wrapper or Palm
;  NUMBER OF SEQ ID NOS: 477
;  SEQ ID NO 378
;  LENGTH: 116
;  TYPE: PRT
;  ORGANISM: Homo sapiens
US-10-013-907A-378

  Query Match        58.7%;  Score 500.5;  DB 12;  Length 116;
  Best Local Similarity   82.6%;  Pred. No. 1.1e-44;
  Matches   90;  Conservative   4;  Mismatches   4;  Indels   6;  Gaps   2;

Qy    1 MELALLCGLVMAGVIPIQGGILNLNKMVKQVTGKMPILSYWPYGCHCGLGGRGQPKDAT 60
        |||||||||| |||||||||||||||||||||||||||||||||||||||||||||||
Db    1 MELALLCGLVVMAGVIPIQGGILNLNKMVKQVTGKMPILSYWPYGCHCGLGGRGQPKDAT 60

Qy   61 DWCCQTHDCCYDHLKTQGCGIYKDYRYRNFSQGNIHCSDKGSWCEQQLC 109
        ||||||||||||||||||||||||   :: ::|||        |
Db   61 DWCCQTHDCCYDHLKTQGCGIYKDN----NKSSIHCMD----LSQRYC 100
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Search completed: October 5, 2004, 19:41:12
Job time : 34.8667 secs

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              GenCore version 5.1.6
         Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on:      October 5, 2004, 19:21:45 ; Search time 9.86 Seconds
                                          (without alignments)
                                          1414.581 Million cell updates/sec

Title:       US-09-830-321A-1
Perfect score: 852
Sequence:    1 MELALLCGLVVMAGVIPIQG.........YQKRLRFYWRPHCRGQTPGC 145

Scoring table: BLOSUM62
             Gapop 10.0 , Gapext 0.5

Searched:    283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters:       283366

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   PIR_78:*
             1: _pir1:*
             2: pir2:*
             3: pir3:*
             4: pir4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

                          SUMMARIES
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Result No.	Score	% Query Match	Length	DB	ID	Description
1	401.5	47.1	146	2	A35493	phospholipase A2
2	399.5	46.9	146	2	A33394	phospholipase A2
3	395.5	46.4	144	1	PSHUYF	phospholipase A2
4	389.5	45.7	146	2	JU0283	phospholipase A2
5	389	45.7	145	2	I48093	phospholipase A2
6	365.5	42.9	146	2	I48342	phospholipase A2
7	347	40.7	138	2	A49959	phospholipase A2
8	335.5	39.4	138	1	PSRSBT	phospholipase A2
9	335.5	39.4	138	1	I51381	phospholipase A2
10	332	39.0	125	2	JX0052	phospholipase A2
11	331.5	38.9	138	1	PSRSB2	phospholipase A2
12	328.5	38.6	138	2	JC1342	phospholipase A2
13	320.5	37.6	122	2	S13000	phospholipase A2
14	319.5	37.5	137	2	S68429	myotoxin precursor
15	316.5	37.1	122	2	PSTVXF	phospholipase A2
16	314.5	36.9	138	2	S10992	ammodytin L precur
17	313.5	36.8	138	2	E48188	phospholipase A2 precur
18	312.5	36.7	121	2	PC4024	phospholipase A2 h
19	312.5	36.7	122	2	PSABA	phospholipase A2
20	311.5	36.6	122	2	JX0063	phospholipase A2
21	311.5	36.6	138	2	D48188	phospholipase A2
22	310	36.4	138	2	F48188	phospholipase A2
23	309.5	36.3	138	2	S59522	phospholipase A2
24	307.5	36.1	121	1	PSSNAM	phospholipase A2 h
25	305.5	35.9	138	2	PSVIAC	phospholipase A2
26	305.5	35.9	138	2	S10333	ammodytoxin B prec
27	305.5	35.9	138	2	I51186	phospholipase A2
28	304.5	35.7	138	1	PSVIAA	phospholipase A2
29	302	35.4	138	2	I50098	phospholipase A2 -
30	298	35.0	123	2	B53872	phospholipase A2 (
31	295.5	34.7	158	2	B54762	phospholipase A2 (
32	295	34.6	138	2	A48188	phospholipase A2 (
33	293	34.4	138	1	PSTVIF	phospholipase A2 (
34	290.5	34.1	122	2	S33267	phospholipase A2 (
35	288.5	33.9	122	2	A25806	phospholipase A2 (
36	288.5	33.9	124	2	I51190	phospholipase A2 -
37	288	33.8	137	2	S22388	phospholipase A2 (
38	287.5	33.7	130	2	A54762	phospholipase A2 (
39	287	33.7	138	2	A46169	phospholipase A2 (
40	285.5	33.5	120	2	S13019	phospholipase A2 (
41	285.5	33.5	122	2	S09314	phospholipase A2 (
42	284.5	33.4	138	2	S29299	phospholipase A2 (
43	283.5	33.3	138	2	S29298	phospholipase A2 (
44	283	33.2	122	2	S15113	phospholipase A2 (
45	282	33.1	122	2	A29290	phospholipase A2 (

```
                          ALIGNMENTS

RESULT 1
A35493
phospholipase A2 (BC 3.1.1.4) II precursor - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 14-Sep-1990 #sequence_revision 18-Nov-1992 #text_change 18-Jun-1999
C;Accession: A35493; S11388; S71310
R;Komada, M.; Kudo, I.; Inoue, K.
Biochem. Biophys. Res. Commun. 168, 1059-1065, 1990
A;Title: Structure of gene coding for rat group II phospholipase A-2.
A;Reference number: A35493; MUID:90267443; PMID:2346480
A;Accession: A35493
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-146 <KOM>
A;Cross-references: GB:M37127; NID:g204318; PIDN:AAA41223.1; PID:g204319
A;Note: the authors translated the codon TAT for residue 42 as Thr
R;Kusunoki, C.; Satoh, S.; Kobayashi, M.; Niwa, M.
Biochim. Biophys. Acta 1087, 95-97, 1990
A;Title: Structure of genomic DNA for rat platelet phospholipase A(2).
A;Reference number: S11388; MUID:90381322; PMID:2400792
A;Accession: S11388
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-146 <KUS>
A;Cross-references: EMBL:X51529; NID:g56930; PIDN:CAA35909.1; PID:g56931
R;Aarsman, A.J.; Schalkwijk, C.G.; Neys, F.W.; Iijima, N.; Wherett, J.R.; van den Bosch,
Arch. Biochem. Biophys. 331, 95-103, 1996
A;Title: Purification and characterization of Ca(2+)-dependent phospholipases A(2) from r
A;Reference number: S71310; MUID:96268465; PMID:8660688
A;Accession: S71310
A;Molecule type: protein
A;Residues: 22-29,'X',31-32,'X',34 <AAR>
C;Superfamily: phospholipase A2
C;Experimental source: kidney
C;Keywords: carboxylic ester hydrolase; lipid degradation
F;68,113/Active site: His, Asp #status predicted

Query Match          47.1%;  Score 401.5;  DB 2;  Length 146;
Best Local Similarity 47.9%; Pred. No. 1.1e-29;
Matches  70;  Conservative  23;  Mismatches  52;  Indels  1;  Gaps  1;

Qy     1 MELALLCGLVVMA-GVIPIQGGILNLNKMVKQVTGKMPILSYWPYGCHCGLGGRGQPKDA  59
           |: :| || ||   : :.   :| | .|:    ::||||:||||:||||||
Db     1 MKVLLLAVVIMAFGSIQVQGSLLEFGQMILFKTGKRADVSYGYGFYGHCGVGGRGSPKDA  60

Qy    60 TDWCCQTHDCCYDHLKTQGCGIYKDYRYNFSQGNIHCSDKGSWCEQQLCACDKEVAFCL  119
          ||||| |||||| | : :||||||| : : : :: :||||::: |||| |:|:|| :|
Db    61 TDWCCVTHDCCYNRLEKRGCGTKFLTYKFSYRGQISCSTNQDSCRKQLCQCDKAAAECF  120

Qy   120 KRNLDTYQKRLRFYWRPHCRGQTPGC  145
         :|| .:| : | : :.:|| |.| |
Db   121 ARNKKSYSLKYQFYLNKFCKGKTPSC  146
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RESULT 2
A33394
phospholipase A2 (EC 3.1.1.4) precursor (version 1) - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 29-Jan-1990 #sequence_revision 29-Jan-1990 #text_change 20-Jun-2000
C;Accession: A33394; JU0131
R;Ishizaki, J.; Ohara, O.; Nakamura, E.; Tamaki, M.; Ono, T.; Kanda, A.; Yoshida, N.; Te
Biochem. Biophys. Res. Commun. 162, 1030-1036, 1989
A;Title: cDNA cloning and sequence determination of rat membrane-associated phospholipas
A;Reference number: A33394; MUID:89350908; PMID:2764915
A;Accession: A33394
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-146 <ISH>
A;Cross-references: GB:M25148
R;Komada, M.; Kudo, I.; Mizushima, H.; Kitamura, N.; Inoue, K.
J. Biochem. 106, 545-547, 1989
A;Title: Structure of cDNA coding for rat platelet phospholipase A2.
A;Reference number: JU0131; MUID:90111043; PMID:2606907
A;Accession: JU0131
A;Molecule type: mRNA
A;Residues: 1-146 <KOM>
A;Cross-references: GB:D00523; NID:g220857; PIDN:BAA00410.1; PID:g220858
C;Superfamily: phospholipase A2
C;Keywords: carboxylic ester hydrolase
F;1-21/Domain: signal sequence #status predicted <SIG>
F;22-146/Product: phospholipase A2 #status predicted <MAT>
F;68,113/Active site: His, Asp #status predicted

Query Match   46.9%; Score 399.5; DB 2; Length 146;
Best Local Similarity   47.9%;   Pred. No. 1.7e-29;
Matches   70; Conservative   23; Mismatches   52; Indels   1; Gaps   1;

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Qy    1 MELALLCLGLVVMA-GVIPIQGGILNLRMVKQVTGKMPILSYWPYGCHCGLGGRGQPKDA 59
          |::||  :||:||| :|::||| |  :|:  ||||  |||||||||||||||||||||||
Db    1 MKVLLLLAVVIMAFGSIQVQGSLLEFGQMILFKTGKRADVSYGFYGCHCGVGGRGSPKDA 60

Qy   60 TDWCCQTHDCCYDHLKTGCGIYKDYRYNFSQGNIHCSDKGSWCEQQICACDKEVAFCL   119
          ||||||||||||| |||:|||  |::::|||   ::|||  :|||||||:|   ||
Db   61 TDWCCVTHDCCYNRLEKRGCGTKFLTYKFSYRGGQISCSTNQDSCRKQLCQCDKAAAECF 120

Qy  120 KRNLDTYQKRLRFYWRPHCRGQTPGC 145
          :||  :| ::|||:|
Db  121 ARNKKSYSLKYQFYPNKFCKGKTPSC 146
```

RESULT 3
PSHUYF
phospholipase A2 (EC 3.1.1.4) IIA precursor [validated] - human
N;Alternate names: phosphatidylcholine 2-acylhydrolase; placental PLA2; platelet-secrete
C;Species: Homo sapiens (man)
C;Date: 31-Mar-1993 #sequence_revision 31-Mar-1993 #text_change 15-Sep-2000
C;Accession: A32862; B32862; A60266; A32847; A60263; A31350; PT0056; A32913; A60265; A61
R;Kramer, R.M.; Hession, C.; Johansen, B.; Hayes, G.; McGray, P.; Chow, E.P.; Tizard, R.
J. Biol. Chem. 264, 5768-5775, 1989
A;Title: Structure and properties of a human non-pancreatic phospholipase A-2.
A;Reference number: A32862; MUID:89174633; PMID:2925633
A;Accession: A32862
A;Status: not compared with conceptual translation
A;Molecule type: DNA
A;Residues: 1-144 <KRA>
A;Accession: B32862
A;Molecule type: protein
A;Residues: 21-39 <KR2>
A;Note: this protein was also detected in platelets
R;Kramer, R.M.; Johansen, B.; Hession, C.; Pepinsky, R.B.
Adv. Exp. Med. Biol. 275, 35-53, 1990
A;Title: Structure and properties of a secretable phospholipase A-2 from human platelets
A;Reference number: A60266; MUID:91050834; PMID:2239446
A;Accession: A60266
A;Status: not compared with conceptual translation

A;Molecule type: DNA
A;Residues: 1-144 <KR3>
R;Seilhamer, J.J.; Pruzanski, W.; Vadas, P.; Plant, S.; Miller, J.A.; Kloss, J.; Johnson
J. Biol. Chem. 264, 5335-5338, 1989
A;Title: Cloning and recombinant expression of phospholipase A-2 present in rheumatoid a
A;Reference number: A32847; MUID:89174566; PMID:2925608
A;Accession: A32847
A;Molecule type: mRNA
A;Residues: 1-144 <SEI>
A;Cross-references: GB:J04704; EMBL:M22430; NID:g190888; PIDN:AAA36550.1; PID:g190889
R;Crowl, R.; Stoner, C.; Stoller, T.; Pan, Y.C.; Conroy, R.
Adv. Exp. Med. Biol. 279, 173-184, 1990
A;Title: Isolation and characterization of cDNA clones from human placenta coding for ph
A;Reference number: A60263; MUID:91263879; PMID:1710870
A;Accession: A60263
A;Status: not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-144 <CRO>
R;Lai, C.Y.; Wada, K.
Biochem. Biophys. Res. Commun. 157, 488-493, 1988
A;Title: Phospholipase A-2 from human synovial fluid: purification and structural homolo
A;Reference number: A31350; MUID:89076274; PMID:3202859
A;Accession: A31350
A;Molecule type: protein
A;Residues: 21-33 <LAI>
R;Hara, S.; Kudo, I.; Matsuta, K.; Miyamoto, T.; Inoue, K.
J. Biochem. 104, 326-328, 1988
A;Title: Amino acid composition and NH2-terminal amino acid sequence of human phospholip
A;Reference number: PT0056; MUID:89197814; PMID:3240982
A;Accession: PT0056
A;Molecule type: protein
A;Residues: 21-46,'X',48-54 <HAR>
R;Kanda, A.; Ono, T.; Yoshida, N.; Tojo, H.; Okamoto, M.
Biochem. Biophys. Res. Commun. 163, 42-48, 1989
A;Title: The primary structure of a membrane-associated phospholipase A-2 from human spl
A;Reference number: A32913; MUID:89374261; PMID:2775276
A;Accession: A32913
A;Molecule type: protein
A;Residues: 21-144 <KAN>
R;Parks, T.P.; Lukas, S.; Hoffman, A.F.
Adv. Exp. Med. Biol. 275, 55-81, 1990
A;Title: Purification and characterization of a phospholipase A-2 from human osteoarthri
A;Reference number: A60265; MUID:91050835; PMID:2146857
A;Accession: A60265
A;Molecule type: protein
A;Residues: 21-45,'X',<PAR>
R;Reckless, A.D.; White, C.
Arthritis Rheum. 34, 1106-1115, 1991
A;Title: Phospholipase A-2 is a major component of the salt-extractable pool of matrix p
A;Reference number: A61201; MUID:92029121; PMID:1930329
A;Accession: A61201
A;Molecule type: protein
A;Residues: 21-40 <REC>
A;Experimental source: adult articular cartilage
R;Green, J.A.; Smith, G.M.; Buchta, R.; Lee, R.; Ho, K.Y.; Rajkovic, I.A.; Scott, K.F.
Inflammation 15, 355-366, 1991
A;Title: Circulating phospholipase A-2 activity associated with sepsis and septic shock
A;Reference number: A61634; MUID:92098137; PMID:1757123
A;Accession: A61634
A;Molecule type: protein
A;Residues: 21-44 <GRE>
R;Wery, J.P.; Schevitz, R.W.; Clawson, D.K.; Bobbitt, J.L.; Dow, E.R.; Gamboa, G.; Goods
Teater, C.; Warrick, M.W.; Jones, N.D.
submitted to the Brookhaven Protein Data Bank, May 1992
A;Reference number: A51043; PDB:1BBC
A;Contents: annotation; X-ray crystallography, 2.2 angstroms, residues 21-144
R;Wery, J.P.; Schevitz, R.W.; Clawson, D.K.; Bobbitt, J.L.; Dow, E.R.; Gamboa, G.; Goods
Teater, C.; Warrick, M.W.; Jones, N.D.
Nature 352, 79-82, 1991
A;Title: Structure of recombinant human rheumatoid arthritic synovial fluid phospholipas
A;Reference number: A58514; MUID:91287826; PMID:2062381
A;Accession: A60266
A;Contents: annotation; X-ray crystallography
C;Genetics:

A;Gene: GDB:PLA2G2A; PLA2B; PLA2L
A;Cross-references: GDB:120296; OMIM:172411
A;Map position: 1p36.1-1p35
A;Introns: 14/1; 62/2; 98/1
C;Function:
A;Description: catalyzes hydrolysis of 1,2-diacyl-sn-glycero-3-phosphocholine to 1-acyl-
A;Note: the reaction is strongly enhanced when the phospholipid is condensed into a mice
C;Superfamily: phospholipase A2
C;Keywords: calcium; carboxylic ester hydrolase; extracellular protein; lipid degradatio
F;1-20/Domain: signal sequence #status predicted <SIG>
F;21-144/Product: phospholipase A2 IIA #status experimental <MAT>
F;46-137,48-64,63-117,69-144,70-110,79-103,97-108/Disulfide bonds: #status experimental
F;47,49,51,68/Binding site: calcium (His, Gly, Gly, Asp) #status predicted
F;67,111/Active site: His, Asp #status predicted

Query Match   46.4%; Score 395.5; DB 1; Length 144;
Best Local Similarity   47.6%; Pred. No. 3.9e-29;
Matches   69; Conservative   23; Mismatches   52; Indels   1; Gaps   1;

Qy   1 MELALLCGLVVMAGVIPIQGGILNLNKMVKQVTGKMPILSYWPYGCHCGLGGRGQPKDAT 60
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Db   1 MKTLLLLAVIMFGLLQAHGNLVNFHRMIKLTTGKEAALSYGFYGCHCGVGGRGSPKDAT 60

Qy   61 DWCCQTHDCCYDHLKTQGCGIYKDYYRYNFSQGNIHCSDKGSWCEQQLCACDKEVAFCLK 120
           ||||||||||| |:|||| : |||||||:||||||||||:|:||| ||:|||||:|| |
Db   61 DRCCVTHDCCYKRLEKRGCGTKFLSYKFSNSGSRITCAKQDS-CRSQLCECDKAAATCFA 119

Qy   121 RNLDTYQKRLRFYWRPHCRGQTPGC 145
           ||||||||:|:|| ||||||
Db   120 RNKTTYNKKYQYYSNKHCRGSTPRC 144

RESULT 4
JU0283
phospholipase A2 (EC 3.1.1.4) precursor (version 2) - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 24-Jul-1997
A;Accession: JU0283
R;Komada, M.; Kudo, I.; Mizushima, H.; Kitamura, N.; Inoue, K.
J. Biochem. 106, 545-547, 1989
A;Title: Structure of cDNA coding for rat platelet phospholipase A2.
A;Reference number: JU0131; MUID:90110043; PMID:2605907
A;Accession: JU0283
A;Molecule type: mRNA
A;Residues: 1-146 <KOM>
C;Superfamily: phospholipase A2
C;Keywords: carboxylic ester hydrolase
F;1-21/Domain: signal sequence #status predicted <SIG>
F;22-146/Product: phospholipase A2 #status predicted <MAT>
F;68,113/Active site: His, Asp #status predicted

Query Match   45.7%; Score 389.5; DB 2; Length 146;
Best Local Similarity   47.3%; Pred. No. 1.4e-28;
Matches   69; Conservative   23; Mismatches   53; Indels   1; Gaps   1;

Qy   1 MELALLCGLVVMA-GVIPIQGGILNLNKMVKQVTGKMPILSYWPYGCHCGLGGRGQPKDA 59
           |:||| |||| : :: :|:||:||:||:||:||||||||||||||| |||||||||
Db   1 MKVLLLLAVVIMAFGSIQVQGSLLEFGQMILFKTGKRADVSYGFYGCHCGVGGRGSPKDA 60

Qy   60 TDWCCQTHDCCYDHLKTQGCGIYKDYYRYNFSQGNIHCSDKGSWCEQQLCACDKEVAFCL 119
           ||||||||||| |:|||| : |||||||:||||||||||:|:||| ||:|||||:|||
Db   61 TDWCCVTHGCCYNLLEKRGCGTKFLTYKFSYRGGQISCSTNQDSCRKQLCQCDKAAAECF 120

Qy   120 KRNLDTYQKRLRFYWRPHCRGQTPGC 145
           :|||||||:|:|| |||||
Db   121 ARNKKSYSLKYQFYPNKFCKGKTPSC 146

RESULT 5
I48093
phospholipase A2 (EC 3.1.1.4) type II - guinea pig
C;Species: Cavia porcellus (guinea pig)
C;Date: 27-Feb-1997 #sequence_revision 27-Feb-1997 #text_change 18-Jun-1999

C;Accession: I48093
R;Vial, D.; Senorale-Pose, M.; Havet, N.; Molio, L.; Vargaftig, B.B.; Touqui, L.
J. Biol. Chem. 270, 17327-17332, 1995
A;Title: Expression of the type-II phospholipase A2 in alveolar macrophages. Down-regulat
A;Reference number: I48093; MUID:95340522; PMID:7615534
A;Accession: I48093
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-145 <RES>
A;Cross-references: EMBL:X82631; NID:g951010; PIDN:CAA57953.1; PID:g951011
C;Superfamily: phospholipase A2
C;Keywords: carboxylic ester hydrolase
F;67,112/Active site: His, Asp #status predicted

Query Match   45.7%; Score 389; DB 2; Length 145;
Best Local Similarity   49.3%; Pred. No. 1.5e-28;
Matches   72; Conservative   20; Mismatches   52; Indels   2; Gaps   2;

Qy   1 MELALLCGLVVMAGVIP-IQGGILNLNKMVKQVTGKMPILSYWPYGCHCGLGGRGQPKDA 59
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Db   1 MKLLLLL-LVVMASDLPQAHGHLKQFTEMIKLTTGKNGLTSYGAYGHCGVGGKGTPKDA 59

Qy   60 TDWCCQTHDCCYDHLKTQGCGIYKDYYRYNFSQGNIHCSDKGSWCEQQLCACDKEVAFCL 119
           ||||| || ||| |: | | |||||:|| ||: ||:|:||: |||:|::||:
Db   60 TDRCCVRHDCCYDRLMKRGCGTKFLNYRFTHKGGSITCSVKQNSCQKQLCECDKAAAYCF 119

Qy   120 KRNLDTYQKRLRFYWRPHCRGQTPGC 145
           :|||||||:|:|| ||| |||
Db   120 AANLKSYSRRYQFYYNGLCRGKTPSC 145

RESULT 6
I48342
phospholipase A2 (EC 3.1.1.4), secretory group II - mouse
C;Species: Mus musculus (house mouse)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 18-Jun-1999
C;Accession: I48342; PC2009; S35948; I49352
R;Mulherkar, R.; Rao, R.S.; Wagle, A.S.; Patki, V.; Deo, M.G.
Biochem. Biophys. Res. Commun. 195, 1254-1263, 1993
A;Title: Enhancing factor, a Paneth cell specific protein from mouse small intestines: pr
A;Reference number: I48342; MUID:94029955; PMID:8267767
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-146 <MUL1>
A;Cross-references: EMBL:X74266; NID:g557247; PIDN:CAA52325.1; PID:g557248
R;Mulherkar, R.; Rao, R.S.; Wagle, A.S.; Patki, V.; Deo, M.G.
Biochem. Biophys. Res. Commun. 197, 351-352, 1993
A;Title: Enhancing factor, a peneth cell specific protein from mouse small intestines: pr
A;Reference number: PC2009; MUID:94071967; PMID:8250944
A;Accession: PC2009
A;Molecule type: mRNA
A;Residues: 22-146 <MUL2>
A;Note: correction of S35948
R;Mulherkar, R.; Rao, R.; Wagle, A.; Patki, V.; Deo, M.
submitted to the EMBL Data Library, July 1993
A;Reference number: S35948
A;Accession: S35948
A;Molecule type: mRNA
A;Residues: 22-115, 'R', 118-146 <MUL3>
A;Cross-references: EMBL:X74266
R;Kennedy, B.P.; Payette, P.; Mudgett, J.; Vadas, P.; Pruzanski, W.; Kwan, M.; Tang, C.;
J. Biol. Chem. 270, 22378-22385, 1995
A;Title: A natural disruption of the secretory group II phospholipase A2 gene in inbred m
A;Reference number: I49352; MUID:95403435; PMID:7673223
A;Accession: I49352
A;Molecule type: DNA
A;Residues: 1-18, 'V', 20-85, 'K', 87-146 <KEN>
A;Cross-references: EMBL:U33358; NID:g984836; PIDN:AAC52252.1; PID:g984837
C;Superfamily: phospholipase A2
C;Keywords: carboxylic ester hydrolase
F;68,113/Active site: His, Asp #status predicted

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Query Match          42.9%;    Score 365.5;  DB 2;   Length 146;
Best Local Similarity 47.3%;   Pred. No. 2.2e-26;
Matches   69;  Conservative   18;  Mismatches  58;   Indels   1;   Gaps   1;

Qy    1  MELALLCGLVVMA-GVIPIQGGILNLNKMVKQVTGKMPILSYWPYGCHCGLGRGQPKDA  59
            |:::||:: ||| ||||||||||||:|:||||||||||:::|:||||
Db    1  MKVLLLAASIMAFGSIQDQGNIAQFGEMIRLKTGKRAELSYAFYGCHCGLGKGSPKDA  60

Qy   60  TDWCCQTHDCCYDHLKTQGCGIYKDYRYRNFSQGNIHCSDKGSWCEQQLCACDKEVAFCL 119
            |||||||||||||     :: |||||| :|:: || |: ||||| |:|||||
Db   61  TDRCCVTHDCCYKSLEKSGCGTKLLTYKYSHQGGQITCSANQNSCQKRLCQCDKAAAECF 120

Qy  120  KRNLDTYQKRLRFYWRPHCRGQTPGC 145
            || ||||||||||  |||||
Db  121  ARNKKTYSLKYQFYPNMFCKGKKPKC 146


RESULT 7
A49959
phospholipase A2 (EC 3.1.1.4) low molecular weight, precursor - human
C;Species: Homo sapiens (man)
C;Date: 10-Feb-1995 #sequence_revision 10-Feb-1995 #text_change 18-Jun-1999
C;Accession: A49959
R;Chen, J.; Engle, S.J.; Seilhamer, J.J.; Tischfield, J.A.
J. Biol. Chem. 269, 2365-2368, 1994
A;Title: Cloning and recombinant expression of a novel human low molecular weight Ca(2+
A;Reference number: A49959; MUID:94131989; PMID:8300559
A;Accession: A49959
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-138 <CHE>
A;Cross-references: GB:U03090; NID:9460914; PIDN:AAC28886.1; PID:g460915
C;Superfamily: phospholipase A2
C;Keywords: carboxylic ester hydrolase
F;67,111/Active site: His, Asp #status predicted

Query Match          40.7%;    Score 347;  DB 2;   Length 138;
Best Local Similarity 43.6%;   Pred. No. 1e-24;
Matches   58;  Conservative   27;  Mismatches  36;   Indels  12;   Gaps   2;

Qy   12  MAGVIP---------IQGGILNLNKMVKQVTGKMPILSYWPYGCHCGLGRGQPKDAT  60
            :::                |||||||||||||||||:|||||||||||||||
Db    1  MKGLLPLAWFLACSVPAVQGGLLDLKSMIEKVTGKNALTNYGFVGYCYCGWGGRGTPKDGT  60

Qy   61  DWCCQTHDCCYDHLKTQGCGIYKDYRYRNFSQGNIHCSDKGSWCEQQLCACDKEVAFCLK 120
            |||||||||| :: ||||||:|: : |||||:||||||| ::: |||||||:: |||
Db   61  DWCCWAHDHCYGRLEEKGCNIRTQSYKYRFAWGVVTC-EPGPFCHVNLCACDRKLVYCLK 119

Qy  121  RNLDTYQKRLRFY 133
            ||||||||:
Db  120  RNLRSYNPQYQYF 132

RESULT 8
PSRSBT
phospholipase A2 (EC 3.1.1.4) crotoxin basic subunit 1 precursor - tropical rattlesnake
N;Alternate names: CB1; crotoxin B, isoform beta; phosphatidylcholine 2-acylhydrolase
C;Species: Crotalus durissus terrificus (tropical rattlesnake, cascabel)
C;Date: 30-Jun-1988 #sequence_revision 30-Sep-1991 #text_change 11-Jun-1999
C;Accession: S02257; A90078; A94424; A94841; S45646; S46599; A26079; A28045; S46596
R;Bouchier, C.; Ducancel, F.; Guignery-Frelat, G.; Bon, C.; Boulain, J.C.; Menez, A.
Nucleic Acids Res. 16, 9050, 1988
A;Title: Cloning and sequencing of cDNAs encoding the two subunits of crotoxin.
A;Reference number: S01392; MUID:89016587; PMID:3174444
A;Accession: S02257
A;Molecule type: mRNA
A;Residues: 1-138 <BOU>
A;Cross-references: EMBL:X12603; NID:g62692; PIDN:CAA31123.1; PID:g62693
R;Aird, S.D.; Kaiser, I.I.; Lewis, R.V.; Kruggel, W.G.
Arch. Biochem. Biophys. 249, 296-300, 1986
A;Title: A complete amino acid sequence for the basic subunit of crotoxin.
A;Reference number: A90078; MUID:86321988; PMID:3753003
```

```
A;Accession: A90078
A;Molecule type: protein
A;Residues: 17-80,'R',82-138 <AIR>
A;Note: 49-Gln, 53-Arg, and 85-Arg were also found
R;Fraenkel-Conrat, H.; Jeng, T.W.; Hsiang, M.
in Natural Toxins, Baker, D., and Wadstrom, T., eds., Pergamon Press, Oxford, 1980
A;Title: Biological activities of crotoxin and amino acid sequence of crotoxin B.
A;Reference number: A94424
A;Accession: A94424
A;Molecule type: protein
A;Residues: 17-48,'Q',50-76,'Y',77-80,'R',82-85,'K',87-114,'B',116-120,'B',122-138 <FRA>
R;Landucci, E.C.T.; Condino-Neto, A.; Perez, A.C.; Hyslop, S.; Corrado, A.P.; Novello, J
Toxicon 32, 217-226, 1994
A;Title: Crotoxin induces aggregation of human washed platelets.
A;Reference number: A49841; MUID:94205018; PMID:8153961
A;Accession: A49841
A;Molecule type: protein
A;Residues: 17-36 <LAN>
R;Faure, G.; Choumet, V.; Bouchier, C.; Camoin, L.; Guillaume, J.L.; Monegier, B.; Vuilh
Eur. J. Biochem. 223, 161-164, 1994
A;Title: The origin of the diversity of crotoxin isoforms in the venom of Crotalus duris
A;Reference number: S45646; MUID:94307256; PMID:8033889
A;Accession: S45646
A;Status: nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 17-138 <FA2>
A;Cross-references: EMBL:X12603
A;Accession: S46599
A;Molecule type: protein
A;Residues: 17-45 <FAU>
C;Comment: Crotoxin is a beta-neurotoxin.
C;Complex: heterodimer of acidic and basic subunits
C;Function:
A;Description: catalyzes hydrolysis of 1,2-diacyl-sn-glycero-3-phosphocholine to 1-acyl-
C;Note: the reaction is strongly enhanced when the phospholipid is condensed into a mice
C;Superfamily: phospholipase A2
C;Keywords: calcium; carboxylic ester hydrolase; heterodimer; lipid degradation; metallo
F;1-16/Domain: signal sequence #status predicted <SIG>
F;17-138/Product: phospholipase A2 basic subunit 1 precursor #status predicted
F;20,80/Binding site: micellar substrate (Gln, Tyr) #status predicted
F;42-131,44-60,59-111,65-138,66-104,73-97,91-102/Disulfide bonds: #status predicted
F;43,45,47,64/Binding site: calcium (Tyr, Gly, Gly, Asp) #status predicted
F;63,105/Active site: His, Asp #status predicted

Query Match          39.4%;    Score 335.5;  DB 1;   Length 138;
Best Local Similarity 46.3%;   Pred. No. 1.1e-23;
Matches   63;  Conservative   18;  Mismatches  52;   Indels   3;   Gaps   2;

Qy   10  VVMAGVIPIQGGILNLNKMVKQVTGKMPILSYWPYGCHCGLGGRGQPKDATDWCCQTHDC  69
            | ||: :||||:  |:| |||||:||| :||||||:: |||||||
Db    6  IVAVLLVGVBGHLLQPNKMIKFETRKNAIPFYAFYGCYCGWGGRGRPKDATDRCCFVHDC  65

Qy   70  CYDHLKTQGCGIYKDYRYRNFSQGNIHCSDKGSWCEQQLCACDKEVAFCLKRNLDTYQKR 129
            |:|| |:||:|||||||||||:||||||| || |||||||:: |||||||
Db   66  CYG--KLAKCNTKWDIYPYSLKSGYITCG-KGTWCEEQICECDRVAAECLRRSLSTYKYG 122

Qy  130  LRFYWRPHCRGQTPGC 145
            |: :| |||:||
Db  123  YMFYPDSRCRGPSETC 138

RESULT 9
I51381
phospholipase A2 (EC 3.1.1.4) Mojave toxin basic subunit precursor - Mojave rattlesnake
N;Alternate names: Mtx-B; phosphatidylcholine 2-acylhydrolase
C;Species: Crotalus scutulatus scutulatus (Mojave rattlesnake)
C;Date: 13-Sep-1996 #sequence_revision 14-Feb-1997 #text_change 11-Jun-1999
A;Accession: I51381; A35951
R;John, T.R.; Smith, L.A.; Kaiser, I.I.
Gene 139, 229-234, 1994
A;Title: Genomic sequences encoding the acidic and basic subunits of Mojave toxin: unusu
A;Reference number: I51380; MUID:94156205; PMID:812610
A;Accession: I51381
```

A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-138 <JOH>
A;Cross-references: EMBL:U01027; NID:g451317; PIDN:AAC59674.1; PID:g451318
R;Aird, S.D.; Kruggel, W.G.; Kaiser, I.I.
Toxicon 28, 669-673, 1990
A;Title: Amino acid sequence of the basic subunit of Mojave toxin from the venom of the
A;Reference number: A35951; MUID:90385490; PMID:2402763
A;Accession: A35951
A;Molecule type: protein
A;Residues: 17-138 <AIR>
C;Genetics:
A;Introns: 14/1; 58/2; 92/1
C;Complex: heterodimer of acidic and basic subunits
C;Function:
A;Description: catalyzes hydrolysis of 1,2-diacyl-sn-glycero-3-phosphocholine to 1-acyl-
A;Note: the reaction is strongly enhanced when the phospholipid is condensed into a mice
C;Superfamily: phospholipase A2
C;Keywords: calcium; carboxylic ester hydrolase; heterodimer; lipid degradation; metallc
F;1-16/Domain: signal sequence #status predicted <SIG>
F;17-138/Product: phospholipase A2 basic chain #status experimental <MAT>
F;20,80/Binding site: micellar substrate (Gln, Tyr) #status predicted
F;42-131,44-60,59-111,65-138,66-104,73-97,91-102/Disulfide bonds: #status predicted
F;43,45,47,64/Binding site: calcium (Tyr, Gly, Gly, Asp) #status predicted
F;63,105/Active site: His, Asp #status predicted

Query Match   39.4%; Score 335.5; DB 1; Length 138;
Best Local Similarity   46.3%; Pred. No. 1.1e-23;
Matches   63; Conservative   18; Mismatches   52; Indels   3; Gaps   2;

Qy   10 VVMAGVIPIQGGILNLNKMVKQVTGKMPILSYWPYGCHCGLGGRGQPKDATDWCCQTHDC 69
              | : :.||: ||:||||:||||||||||||||||| || ||||
Db   6 IVAVLLVGEGHLLQFNKMIKFETRKNAIPFYAFYGCYCGWGGRGRPKDATDRCCFVHDC 65

Qy   70 CYDHLKTGCGIYKDYRYRNFSQGNIHCSDKGSWCEQQLCACDKEVAFCLKRNLDTYQKR 129
              | || | ||| ||:| ::|| :|||||||| ||||| | ::|| |||:|||
Db   66 CYG--KLAKCNTKWDIYPYSLKSGYITCG-KGTWCEEQICECDRVAAELCRRSLSTYKYG 122

Qy   130 LRFYWRPHCRGQTPGC 145
               ||||||| | |
Db   123 YMFYPDSRCRGPSETC 138

RESULT 10
JX0052
phospholipase A2 (EC 3.1.1.4) - rat
N;Alternate names: phosphatidylcholine 2-acylhydrolase
C;Species: Rattus norvegicus (Norway rat)
C;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 24-Jul-1997
A;Accession: JX0052; A41438; A26924; A38247; A28618; A33506
R;Hayakawa, M.; Kudo, I.; Tomita, M.; Nojima, S.; Inoue, K.
J. Biochem. 104, 767-772, 1988
A;Title: The primary structure of rat platelet phospholipase A2.
A;Reference number: JX0052; MUID:89174508; PMID:3235451
A;Accession: JX0052
A;Molecule type: protein
A;Residues: 1-125 <HAY>
A;Experimental source: Wistar
R;Hayakawa, M.; Kudo, I.; Tomita, M.; Inoue, K.
J. Biochem. 103, 263-266, 1988
A;Title: Purification and characterization of membrane-bound phospholipase A-2 from rat
A;Reference number: A41438; MUID:88227898; PMID:3372490
A;Accession: A41438
A;Status: preliminary
A;Molecule type: protein
A;Residues: 'X',2-19 <HA2>
R;Hayakawa, M.; Horigome, K.; Kudo, I.; Tomita, M.; Nojima, S.; Inoue, K.
J. Biochem. 101, 1311-1314, 1987
A;Title: Amino acid composition and NH-2-terminal amino acid sequence of rat platelet se
A;Reference number: A26924; MUID:88007474; PMID:3654593
A;Accession: A26924
A;Molecule type: protein
A;Residues: 'X',2-25 <HA3>

R;Schalkwijk, C.; Pfeilschifter, J.; Maerki, F.; van den Bosch, H.
J. Biol. Chem. 267, 8846-8851, 1992
A;Title: Interleukin-1beta- and forskolin-induced synthesis and secretion of group II phc
A;Reference number: A38247; MUID:92250468; PMID:1577722
A;Accession: A38247
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-25, 'X',27,'X',29-33,'X',35-36,'X',38-40 <SCH>
R;Ono, T.; Tojo, H.; Kuramitsu, S.; Kagamiyama, H.; Okamoto, M.
J. Biol. Chem. 263, 5732-5738, 1988
A;Title: Purification and characterization of a membrane-associated phospholipase A2 from
A;Reference number: A28618; MUID:88186890; PMID:3356705
A;Accession: A28618
A;Molecule type: protein
A;Experimental source: spleen
A;Residues: 'X',2-26,'X',28-36 <ONO>
R;Aarsman, A.J.; de Jong, J.G.N.; Arnoldussen, E.; Neys, F.W.; van Wassenaar, P.D.; Van c
J. Biol. Chem. 264, 10008-10014, 1989
A;Title: Immunoaffinity purification, partial sequence, and subcellular localization of r
A;Reference number: A33506; MUID:89255484; PMID:2722857
A;Accession: A33506
A;Status: preliminary
A;Molecule type: protein
A;Residues: 'D',2-24 <AAR>
A;Experimental source: hepatic
C;Superfamily: phospholipase A2
C;Keywords: carboxylic ester hydrolase
F;47,92/Active site: His, Asp #status predicted

Query Match   39.0%; Score 332; DB 2; Length 125;
Best Local Similarity   46.0%; Pred. No. 2.2e-23;
Matches   57; Conservative   17; Mismatches   50; Indels   0; Gaps   0;

Qy   22 ILNLNKMVKQVTGKMPILSYWPYGCHCGLGGRGQPKDATDWCCQTHDCCYDHLKTGCGGI 81
              | ||||| || ||||||||||||||||||||||||||| ||||:||: |
Db   2 LLEFGQMILFKTGKRADVSYGFYGCHCGVGGRGSPKDATDECCVTHECCYNRLEKSGCGT 61

Qy   82 YKDYYRYRNFSQGNIHCSDKGSWCEQQLCACDKEVAFCLKRNLDTYQKRLRFYWRPHCRGQ 141
              | :| || | || | :::| ||:| | | | | |: |::| :.|:
Db   62 KFLTYKFSYRGGQISCSTNQDSCRKQLCQCDKAAAECFSRNKKSYSLKYQFYPNKFCKXX 121

Qy   142 TPGC 145
              | |
Db   122 TPSC 125

RESULT 11
PSRSB2
phospholipase A2 (EC 3.1.1.4) crotoxin basic chain 2 precursor - tropical rattlesnake
N;Alternate names: crotoxin B isoform alpha; phosphatidylcholine 2-acylhydrolase
C;Species: Crotalus durissus terrificus (tropical rattlesnake, cascabel)
C;Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 21-Jan-2000
A;Accession: S15068; B60265; S45647; S46598; S46597
R;Bouchier, C.; Boulain, J.C.; Bon, C.; Menez, A.
Biochim. Biophys. Acta 1088, 401-408, 1991
A;Title: Analysis of cDNAs encoding the two subunits of crotoxin, a phospholipase A(2) ne
rsor.
A;Reference number: S15068; MUID:91198145; PMID:2015302
A;Accession: S15068
A;Molecule type: mRNA
A;Residues: 1-138 <BOU>
A;Cross-references: EMBL:X16100; NID:g62696; NID:g62696; PIDN:CAA34227.1; PID:g62697
R;Parks, T.P.; Lukas, S.; Hoffman, A.F.
Adv. Exp. Med. Biol. 275, 55-81, 1990
A;Title: Purification and characterization of a phospholipase A-2 from human osteoarthrit
A;Reference number: A60265; MUID:91050835; PMID:2146857
A;Accession: B60265
A;Molecule type: protein
A;Residues: 17-41,'X' <PAR>
R;Faure, G.; Choumet, V.; Bouchier, C.; Camoin, L.; Guillaume, J.L.; Monegier, B.; Vuilhc
Eur. J. Biochem. 223, 161-164, 1994
A;Title: The origin of the diversity of crotoxin isoforms in the venom of Crotalus durisg
A;Reference number: S45646; MUID:94307256; PMID:8033889

A;Accession: S45647
A;Status: nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 17-138 <FAU>
A;Cross-references: EMBL:X16100
A;Accession: S46598
A;Molecule type: protein
A;Residues: 17-51 <FA2>
C;Comment: Crotoxin is a beta-neurotoxin.
C;Complex: heterodimer of acidic and basic chains
C;Function:
C;Description: catalyzes hydrolysis of 1,2-diacyl-sn-glycero-3-phosphocholine to 1-acyl-
A;Note: the reaction is strongly enhanced when the phospholipid is condensed into a micer
C;Superfamily: phospholipase A2
C;Keywords: calcium; carboxylic ester hydrolase; heterodimer; lipid degradation; metallo
F;17-138/Product: crotoxin basic chain 2 #status experimental <MAT>
F;20,80/Binding site: micellar substrate (Gln, Tyr) #status predicted
F;42-131,44-60,59-111,65-138,66-104,73-97,91-102/Disulfide bonds: #status predicted
F;43,45,47,64/Binding site: calcium (Tyr, Gly, Gly, Asp) #status predicted
F;63,105/Active site: His, Asp #status predicted

Query Match   38.9%; Score 331.5; DB 1; Length 138;
Best Local Similarity   44.1%; Pred. No. 2.7e-23;
Matches   60; Conservative   21; Mismatches   52; Indels   3; Gaps   2;

Qy   10 VVMAGVIPIQGGILNLNKMVKQVTGKMPILSYWPYGHCGLGGRGQPKDATDWCCQTHDC 69
             ::|:.:.||||||| |||:|| |||||||||||||||||||||||||||||||||||||
Db   6 IVAVLLVGEGSLLQFNKMIKFETRKNAVPFYAFYGCYCGWGQGRPKDATDRCCFVHDC 65

Qy   70 CYDHLKTQGCGIYKDYYRYNFSQGNIHCSDKGSWCEQQLCACDKEVAFCLKRNLDTYQKR 129
             |||||||:||||||| ||.| |: |:|||| ::|:::|| |:
Db   66 CYG--KLAKCNTKWDIYRYSLKSGYITCG-KGIWCKEQICECDRVAAECLRRSLSTYKNE 122

Qy   130 LRFYWRPHCRGQTPGC 145
             ||||||||||| ||||
Db   123 YMFYPDSRCREPSETC 138

RESULT 12
JC1342
phospholipase A2 (EC 3.1.1.4) precursor - halys viper
C;Species: Agkistrodon halys (halys viper)
C;Date: 09-Oct-1997 #sequence_revision 07-Nov-1997 #text_change 13-Nov-1998
C;Accession: JC1342
R;Pan, H.; Ou-Yang, L.L.; Yang, G.Z.; Zhou, Y.C.; Wu, X.F.
Acta Biochim. Biophys. Sin. 28, 579-582, 1996
A;Title: Cloning of the BPLA2 gene from Agkistrodon halys Pallas.
A;Reference number: JC1342
A;Contents: Snake venom
A;Accession: JC1342
A;Molecule type: mRNA
A;Residues: 1-138 <PAN>
A;Note: the authors translated the codon GAC for residue 54 as Asn
C;Comment: This protein catalyzes specifically the hydrolysis of the C-2 ester bond of 3
C;Superfamily: phospholipase A2
C;Keywords: carboxylic ester hydrolase
F;1-16/Domain: signal sequence #status predicted <SIG>
F;17-138/Product: phospholipase A2 #status predicted <MAT>

Query Match   38.6%; Score 328.5; DB 2; Length 138;
Best Local Similarity   43.4%; Pred. No. 5e-23;
Matches   59; Conservative   24; Mismatches   50; Indels   3; Gaps   2;

Qy   10 VVMAGVIPIQGGILNLNKMVKQVTGKMPILSYWPYGHCGLGGRGQPKDATDWCCQTHDC 69
             ::|:.:.||||||| |||:|| |||||||||||||||||||||||||||||||||||||
Db   6 IVAVLLVGEGSLLQFNKMIKKMTGKEPVVSYAFYGCYCGSSGRGKPKDATDRCCFVHDC 65

Qy   70 CYDHLKTQGCGIYKDYYRYNFSQGNIHCSDKGSWCEQQLCACDKEVAFCLKRNLDTYQKR 129
             |||||||:||||||| ||.| |: |:|||| ::|:::|| |:
Db   66 CYE--KLTGCDPKWDDYTYSWKNGTIVCGGDDP-CKKEVCECDKAAAICFRDNLKTYKKR 122

Qy   130 LRFYWRPHCRGQTPGC 145

Db   123 YMTYPNILCSSKSEKC 138

RESULT 13
S13900
phospholipase A2 (EC 3.1.1.4) - Bothrops asper
C;Species: Bothrops asper
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 31-Oct-1997
C;Accession: S13900
R;Francis, B.; Gutierrez, J.M.; Lomonte, B.; Kaiser, I.I.
Arch. Biochem. Biophys. 284, 352-359, 1991
A;Title: Myotoxin II from Bothrops asper (Terciopelo) venom is a lysine-49 phospholipase
A;Reference number: S13900; MUID:91112832; PMID:1899180
A;Accession: S13900
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-122 <FRA>
C;Superfamily: phospholipase A2
C;Keywords: carboxylic ester hydrolase

Query Match   37.6%; Score 320.5; DB 2; Length 122;
Best Local Similarity   50.4%; Pred. No. 2.4e-22;
Matches   58; Conservative   15; Mismatches   39; Indels   3; Gaps   2;

Qy   22 ILNLNKMVKQVTGKMPILSYWPYGHCGLGGRGQPKDATDWCCQTHDCCYDHLKTQGCGI 81
             :|.|||:|:||.||:||:|||||||||||||||||||||||||||||||||:. :||||
Db   2 LFELGKMILQETGKNPAKSYGAYGCNCGVLGRGKPKDATDRCCYVHKCCYK--KLTGCNP 59

Qy   82 YKDYYRYNFSQGNIHCSDKGSWCEQQLCACDKEVAFCLKRNLDTYQKRLRFYWRP 136
             | || | |.::|| :| || :|: |::||: :..| ||.| |::||:|||||:|
Db   60 KKDRYSYSWKDKTIVCGENNS-CLKELCECDKAVAICLRENLNTYNKKYRYYLKP 113

RESULT 14
S68429
myotoxin precursor - southern copperhead
C;Species: Agkistrodon contortrix contortrix (southern copperhead)
C;Date: 15-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 18-Jun-1999
C;Accession: S68429; S74296
R;de Araujo, H.S.S.; White, S.P.; Ownby, C.L.
Arch. Biochem. Biophys. 326, 21-30, 1996
A;Title: cDNA cloning and sequence analysis of a lysine-49 phospholipase A2 (2) myotoxin f
A;Reference number: S68429; MUID:96154243; PMID:8579368
A;Accession: S68429
A;Molecule type: mRNA
A;Residues: 1-137 <DEA>
A;Cross-references: EMBL:U21335; NID:g809484; PIDN:AAC59887.1; PID:g809485
A;Accession: S74296
A;Molecule type: protein
A;Residues: 17-36 <DER>
C;Superfamily: phospholipase A2
F;1-16/Domain: signal sequence #status predicted <SIG>
F;17-137/Product: myotoxin #status experimental <MAT>

Query Match   37.5%; Score 319.5; DB 2; Length 137;
Best Local Similarity   45.4%; Pred. No. 3.3e-22;
Matches   59; Conservative   20; Mismatches   48; Indels   3; Gaps   2;

Qy   10 VVMAGVIPIQGGILNLNKMVKQVTGKMPILSYWPYGHCGLGGRGQPKDATDWCCQTHDC 69
             :|:.:|:.||||||| |||:|||||.||:|||.:|||||:||.:|||||||||||||:||
Db   6 IVALLLGVEGSLLELGKMILQETGKNAITSYGSYGCNCGWGHRGQPKDATDRCCFVHKC 65

Qy   70 CYDHLKTQGCGIYKDYYRYNFSQGNIHCSDKGSWCEQQLCACDKEVAFCLKRNLDTYQKR 129
             |||||||:||||| | ||:| | | |||:|| |:|| |:|: |::::|| |||.| |:||
Db   66 CYK--KLTDCNHKTDRYSYSWKNKAIICEEKNP-CLKEMCECDKAVAICLRENLDTYNKK 122

Qy   130 LRFYWRPHCR 139
             ||||:|||||
Db   123 YKAYFKFKCK 132

RESULT 15

PSTVXF
phospholipase A2 (EC 3.1.1.4) X - habu
N;Alternate names: phosphatidylcholine 2-acylhydrolase
C;Species: Trimeresurus flavoviridis (habu)
C;Date: 30-Sep-1987 #sequence_revision 30-Sep-1987 #text_change 24-Apr-1998
C;Accession: A25500
R;Kini, R.M.; Kawabata, S.I.; Iwanaga, S.
Toxicon 24, 1117-1129, 1986
A;Title: Comparison of amino terminal region of three isoenzymes of phospholipases A2 (T
quence of the basic phospholipase, TFV PL-X.
A;Reference number: A94320; MUID:87179112; PMID:3564060
A;Accession: A25500
A;Molecule type: protein
A;Residues: 1-122 <KIN>
C;Function:
A;Description: catalyzes hydrolysis of 1,2-diacyl-sn-glycero-3-phosphocholine to 1-acyl-
A;Note: the reaction is strongly enhanced when the phospholipid is condensed into a mice
C;Superfamily: phospholipase A2
C;Keywords: calcium; carboxylic ester hydrolase; homodimer; lipid degradation; metallopr
F;26-122,28-44,43-95,49-115,50-88,57-81,75-86/Disulfide bonds: #status predicted
F;27,29,31,48/Binding site: calcium (Tyr, Gly, Asp) #status predicted
F;47,89/Active site: His, Asp #status predicted

Query Match   37.1%;   Score 316.5;   DB 1;   Length 122;
Best Local Similarity   46.8%;   Pred. No. 5.6e-22;
Matches   58;   Conservative 16;   Mismatches 47;   Indels   3;   Gaps   2;

Qy   22 ILNLNKMVKQVTGKMPILSYWPYGCHCGLGGRGQPKDATDWCCQTHDCCYDHLKTQGCGGI 81
                |:||:::||| |||:||| |||:||:|| |||||:|||||: |||
Db   2 LLQFRKMIKKMTGKEPIVSYAFYGCYCGKGGRGKPKDATDRCCFVHDCCYE--KVTGCDP 59

Qy   82 YKDYYRYNFSQGNIHCSDKGSWCEQQLCACDKEVAFCLKRNLDTYQKRLRFYWRPHCRGQ 141
                |||: |:|| :| ||| :| :: |||||: : |||||:
Db   60 KWSYYTYSLENGDIVCGG-DPYCTKVKCECDKKAAICFRDNLKTYKNRYMTFPDIFCTDP 118

Qy   142 TPGC 145
                ||||
Db   119 TEGC 122

Search completed: October 5, 2004, 19:36:26
Job time : 10.86 secs

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                 GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on:   October  5, 2004, 19:13:29  ; Search time 5.8 Seconds
                                         (without alignments)
                              1301.754 Million cell updates/sec

Title:        US-09-830-321A-1
Perfect score: 852
Sequence:     1 MELALLCGLVVMAGVIPIQG.........YQKRLRFYWRPHCRGQTPGC 145

Scoring table: BLOSUM62
               Gapop 10.0 , Gapext 0.5

Searched:      141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters:    141681

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

                         SUMMARIES

Database :    SwissProt_42:*

     Pred. No. is the number of results predicted by chance to have a
     score greater than or equal to the score of the result being printed,
     and is derived by analysis of the total score distribution.
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Result No.	Score	% Match	Query Length	DB	ID	Description
1	846	99.3	145	1	PA2D_HUMAN	Q9unk4 homo sapien
2	624.5	73.1	144	1	PA2D_MOUSE	Q9wvf6 mus musculu
3	399.5	46.9	146	1	PA2A_RAT	P14423 rattus norv
4	395.5	46.4	144	1	PA2A_HUMAN	P14555 homo sapien
5	389	45.7	145	1	PA2M_CAVPO	P47711 cavia porce
6	371.5	43.6	146	1	PA2A_MOUSE	P31482 mus musculu
7	352	41.3	168	1	PA2F_HUMAN	Q9bzm2 homo sapien
8	347	40.7	138	1	PA2M_HUMAN	P39877 homo sapien
9	340.5	40.0	138	1	PA23_BOTAS	Q9pve3 bothrops as
10	336	39.4	122	1	PA22_BOTMO	Q9i834 bothrops mo
11	336	39.4	168	1	PA2F_MOUSE	Q9qzt4 mus musculu
12	335.5	39.4	138	1	PA2B_CRODU	P07517 crotalus du
13	332	39.0	138	1	PA2C_CRODU	P24027 crotalus du
14	331.5	38.9	138	1	PA2W_TRIFL	Q02517 trimeresuru
15	330.5	38.8	138	1	PA2H_AGKAC	O57385 agkistrodon
16	330	38.7	137	1	PA25_MOUSE	P97391 mus musculu
17	330	38.7	138	1	PA2Y_TRIFL	Q90y77 trimeresuru
18	329	38.6	138	1	PA2Q_TRIFL	Q8jig0 trimeresuru
19	328.5	38.6	121	1	PA22_BOTAS	P24605 bothrops as
20	328.5	38.6	138	1	PA24_AGKHP	O42187 agkistrodon
21	328.5	38.6	142	1	PA2E_MOUSE	Q9qul3 mus musculu
22	320.5	37.6	119	1	PA2H_BOTNE	Q9iat9 bothrops ne
23	319.5	37.5	137	1	PA2M_AGKCL	P49121 agkistrodon
24	318.5	37.4	121	1	PA22_BOTPI	P82287 bothrops pi
25	317.5	37.3	122	1	PA2A_TRIFL	P59264 trimeresuru
26	317.5	37.3	122	1	PA2B_TRIFL	P59265 trimeresuru
27	317.5	37.3	138	1	PA21_ECHCO	Q90zz9 echis color
28	316.5	37.1	122	1	PA2X_TRIFL	P06860 trimeresuru
29	315.5	37.0	137	1	PA25_RAT	P51433 rattus norv
30	314.5	36.9	121	1	PA21_BOTPI	P58399 bothrops pi
31	313.5	36.8	138	1	PA21_VIPAA	P17935 vipera ammo
32	312.5	36.7	121	1	PA2H_BOTJR	Q90249 bothrops ja
33	312.5	36.7	122	1	PA21_AGKHA	P04417 agkistrodon
34	311.5	36.6	122	1	PA23_AGKHP	P14421 agkistrodon
35	311.5	36.6	138	1	PA2F_AGKRH	Q9pvf3 agkistrodon
36	311.5	36.6	138	1	PA2J_TRIFL	P20381 trimeresuru
37	310	36.4	138	1	PA2P_TRIFL	Q92147 trimeresuru
38	309.5	36.3	138	1	PA2A_TRIMU	Q90w39 trimeresuru
39	308.5	36.2	122	1	PA29_AGKHP	O42188 agkistrodon
40	308.5	36.2	142	1	PA2E_HUMAN	Q9nzk7 homo sapien
41	308	36.2	138	1	PA2_TRIJE	Q8jiy9 trimeresuru
42	307.5	36.1	121	1	PA28_DABRR	P59071 daboia russ
43	307.5	36.1	121	1	PA2H_AGKPI	P04361 agkistrodon
44	307.5	36.1	137	1	PA2H_CERGO	Q8uvu7 cerrophidio
45	306.5	36.0	137	1	PA2H_CROAT	Q8uvz7 crotalus at

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                         ALIGNMENTS

RESULT 1
PA2D_HUMAN
ID   PA2D_HUMAN     STANDARD;      PRT;    145 AA.
AC   Q9UNK4; Q9UK01;
DT   28-FEB-2003 (Rel. 41, Created)
DT   28-FEB-2003 (Rel. 41, Last sequence update)
DT   10-OCT-2003 (Rel. 42, Last annotation update)
DE   Group IID secretory phospholipase A2 precursor (EC 3.1.1.4)
DE   (Phosphatidylcholine 2-acylhydrolase GIID) (GIID sPLA2) (PLA2IID)
DE   (sPLA(2)-IID) (Secretory-type PLA, stroma-associated homolog).
GN   PLA2G2D OR SPLASH.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A., VARIANT GLY-80, AND CHARACTERIZATION.
RX   MEDLINE=99386983; PubMed=10455175;
RA   Ishizaki J., Suzuki N., Higashino K.-I., Yokota Y., Ono T.,
RA   Kawamoto K., Fujii N., Arita H., Hanasaki K.;
RT   "Cloning and characterization of novel mouse and human secretory
RT   phospholipase A2s.";
RL   J. Biol. Chem. 274:24973-24979(1999).
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=21040292; PubMed=11196711;
RA   Shakhov A.N., Rubtsov A.V., Lyakhov I.G., Tumanov A.V.,
RA   Nedospasov S.A.;
RT   "SPLASH (PLA(2)IID), a novel member of phospholipase A2 family, is
RT   associated with lymphotoxin-deficiency.";
RL   Genes Immun. 1:191-199(2000).
RN   [3]
RP   SEQUENCE FROM N.A.
RA   Wallis J.;
RL   Submitted (OCT-2000) to the EMBL/GenBank/DDBJ databases.
RN   [4]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Pancreas, and Spleen;
RX   MEDLINE=22388257; PubMed=12477932;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
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Qy    61 DWCCQTHDCCYDHLKTQGCGIYKDYYRYNFSQGNIHCSDKGSWCEQQLCACDKEVAFCLK 120
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    61 DWCCQTHDCCYDHLKTQGCGIYKDYYRYNFSQGNIHCSDKGSWCEQQLCACDKEVAFCLK 120

Qy   121 RNLDTYQKRLRFYWRPHCRGQTPGC 145
         |||||||||||||||||||||||||
Db   121 RNLDTYQKRLRFYWRPHCRGQTPGC 145
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RESULT 2
PA2D_MOUSE

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ID   PA2D_MOUSE    STANDARD;    PRT;    144 AA.
AC   Q9WVF6; Q9JLK0;
DT   28-FEB-2003 (Rel. 41, Created)
DT   28-FEB-2003 (Rel. 41, Last sequence update)
DT   10-OCT-2003 (Rel. 42, Last annotation update)
DE   Group IID secretory phospholipase A2 precursor (EC 3.1.1.4)
DE   (Phosphatidylcholine 2-acylhydrolase GIID) (GIID sPLA2) (PLA2IID)
DE   (sPLA(2)-IID) (Secretory-type PLA, stroma-associated homolog).
GN   PLA2G2D OR PLA2A2 OR SPLASH.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A. (ISOFORM 1), AND CHARACTERIZATION.
RC   STRAIN=BALB/c;
RX   MEDLINE=99386983; PubMed=10455175;
RA   Ishizaki J., Suzuki N., Higashino K.-I., Yokota Y., Ono T.,
RA   Kawamoto K., Fujii N., Arita H., Hanasaki K.;
RT   "Cloning and characterization of novel mouse and human secretory
RT   phospholipase A2s.";
RL   J. Biol. Chem. 274:24973-24979(1999).
RN   [2]
RP   SEQUENCE FROM N.A. (ISOFORM 1).
RX   MEDLINE=99315857; PubMed=10383420;
RA   Valentin E., Koduri R.S., Scimeca J.-C., Carle G., Gelb M.H.,
RA   Lazdunski M., Lambeau G.;
RT   "Cloning and recombinant expression of a novel mouse-secreted
RT   phospholipase A2.";
RL   J. Biol. Chem. 274:19152-19160(1999).
RN   [3]
RP   SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
RC   STRAIN=C57BL/6 X 129;
RX   MEDLINE=21040292; PubMed=11196711;
RA   Shakhov A.N., Rubtsov A.V., Lyakhov I.G., Tumanov A.V.,
RA   Nedospasov S.A.;
RT   "SPLASH (PLA(2)IID), a novel member of phospholipase A2 family, is
RT   associated with lymphotoxin-deficiency.";
RL   Genes Immun. 1:191-199(2000).
RN   [4]
RP   SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
RC   STRAIN=C57BL/6J; TISSUE=Thymus;
RX   MEDLINE=21085660; PubMed=11217851;
RA   Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA   Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA   Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA   Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA   Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA   Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA   Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA   Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA   Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA   Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA   Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA   Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA   Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA   Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA   Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA   Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA   Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA   Hayashizaki Y.;
RT   "Generation and initial analysis of more than 15,000 full-length
RT   human and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
CC   -!- FUNCTION: PA2 catalyzes the calcium-dependent hydrolysis of the 2-
CC       acyl groups in 3-sn-phosphoglycerides. L-alpha-1-palmitoyl-2-
CC       linoleoyl phosphatidylethanolamine is more efficiently hydrolyzed
CC       than the other phospholipids examined.
CC   -!- CATALYTIC ACTIVITY: Phosphatidylcholine + H(2)O = 1-
CC       acylglycerophosphocholine + a fatty acid anion.
CC   -!- COFACTOR: Binds 1 calcium ion per subunit.
CC   -!- SUBCELLULAR LOCATION: Secreted (Potential).
CC   -!- TISSUE SPECIFICITY: Broadly expressed.
CC   -!- MISCELLANEOUS: Maximally active at neutral to alkaline pH and with
CC       2 mM Ca(2+).
CC   -!- SIMILARITY: Belongs to the phospholipase A2 family.
CC   -------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   -------------------------------------------------------------------
DR   EMBL; AF112982; AAD51390.1; -.
DR   EMBL; AF188625; AAF09020.1; -.
DR   EMBL; AL158172; CAC13159.1; -.
DR   EMBL; BC025706; AAH25706.1; -.
DR   HSSP; P14555; 1POD.
DR   Genew; HGNC:9033; PLA2G2D.
DR   MIM; 605630; -.
DR   GO; GO:0005576; C:extracellular; TAS.
DR   GO; GO:0004624; F:secreted phospholipase A2 activity; TAS.
DR   GO; GO:0006954; P:inflammatory response; TAS.
DR   GO; GO:0006644; P:phospholipid metabolism; TAS.
DR   InterPro; IPR001211; Phospholipase A2.
DR   Pfam; PF00068; phoslip; 1.
DR   PRINTS; PR00389; PHPHLIPASEA2.
DR   ProDom; PD000303; Phospholipase_A2; 1.
DR   SMART; SM00085; PA2c; 1.
DR   PROSITE; PS00119; PA2_ASP; 1.
DR   PROSITE; PS00118; PA2_HIS; 1.
KW   Hydrolase; Lipid degradation; Signal; Calcium; Polymorphism.
FT   SIGNAL        1     20       POTENTIAL.
FT   CHAIN        21    145       GROUP IID SECRETORY PHOSPHOLIPASE A2.
FT   ACT_SITE     67     67       BY SIMILARITY.
FT   ACT_SITE    112    112       BY SIMILARITY.
FT   DISULFID     46    138       BY SIMILARITY.
FT   DISULFID     48     64       BY SIMILARITY.
FT   DISULFID     63    118       BY SIMILARITY.
FT   DISULFID     69    145       BY SIMILARITY.
FT   DISULFID     70    111       BY SIMILARITY.
FT   DISULFID     79    104       BY SIMILARITY.
FT   DISULFID     97    109       BY SIMILARITY.
FT   CARBOHYD     89     89       N-LINKED (GLCNAC...) (POTENTIAL).
FT   METAL        47     47       CALCIUM (VIA CARBONYL OXYGEN)
FT                                (BY SIMILARITY).
FT   METAL        49     49       CALCIUM (VIA CARBONYL OXYGEN)
FT                                (BY SIMILARITY).
FT   METAL        51     51       CALCIUM (VIA CARBONYL OXYGEN)
FT                                (BY SIMILARITY).
FT   METAL        68     68       CALCIUM (BY SIMILARITY).
FT   VARIANT      80     80       S -> G.
FT                                /FTId=VAR_012741.
SQ   SEQUENCE   145 AA;  16546 MW;  CF3A49D516BD1EF CRC64;  Length 145;

Query Match     99.3%;  Score 846;  DB 1;  Length 145;
Best Local Similarity  99.3%;
Matches  144;  Conservative  0;  Mismatches  1;  Indels  0;  Gaps  0;
                                           Pred. No. 1.7e-78;

Qy    1 MELALLCGLVVMAGVIPIQGGILNLNKMVKQVTGKMPILSYWPYGCHCGLGGRGQPKDAT 60
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1 MELALLCGLVVMAGVIPIQGGILNLNKMVKQVTGKMPILSYWPYGCHCGLGGRGQPKDAT 60
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Qy    1 MELALLCGLVVMAGVIPIQGGILNLNKMVKQVTGKMPILSYWPYGCHGCLGGRGOPKDAT 60
        ||||||| |  || :||:. ||||||||||| :.| :||:||||||||| |||| |||||
Db    1 MRLALLCGL-LLAGITATQGGLLNLNKMVTHMTGKKAFFSYWPYGCHCGLGGKGQPKDAT 59

Qy   61 DWCCQTHDCCYDHLKTQGGGIYKDYYRYNFSQGNIHCSDKGSWCBQQLCACDKEVAFCLK 120
        ||||| |||| ||| :. | ::|| :|| |||  | |||:|||| :||||||||||| ||
Db   60 DWCCQKHDCCYAHLKIDGCKSLTDNYKYSISQGTIQCSDNGSWCERQLCACDKEVALCLK 119

Qy  121 RNLDTYQKRLRFYWRPHCRGQTPGC 145
        :||| |:|||| ||||.|  | || 
Db  120 QNLDSYNKRLRYYWRPRCKGKTPAC 144
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RESULT 3
PA2A_RAT
ID   PA2A_RAT   STANDARD;   PRT;   146 AA.
AC   P14423;
DT   01-JAN-1990 (Rel. 13, Created)
DT   01-FEB-1991 (Rel. 17, Last sequence update)
DT   15-MAR-2004 (Rel. 43, Last annotation update)
DE   Phospholipase A2, membrane associated precursor (EC 3.1.1.4)
DE   (Phosphatidylcholine 2-acylhydrolase) (Group IIA phospholipase A2)
DE   (GIIC sPLA2).
GN   PLA2G2A.
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Sprague-Dawley; TISSUE=Platelet;
RX   MEDLINE=90110043; PubMed=2606907;
RA   Komada M., Kudo I., Mizushima H., Kitamura N., Inoue K.;
RT   "Structure of cDNA coding for rat platelet phospholipase A2.";
RL   J. Biochem. 106:545-547(1989).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Spleen;
RX   MEDLINE=90267443; PubMed=2346480;
RA   Komada M., Kudo I., Inoue K.;
RT   "Structure of gene coding for rat group II phospholipase A2.";
RL   Biochem. Biophys. Res. Commun. 168:1059-1065(1990).
RN   [3]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=89350908; PubMed=2764915;
RA   Ishizaki J., Ohara O., Nakamura E., Tamaki M., Ono T., Kanda A.,
RA   Yoshida N., Teraoka H., Tojo H., Okamoto M.;
RT   "cDNA cloning and sequence determination of rat membrane-associated
RT   phospholipase A2.";
RL   Biochem. Biophys. Res. Commun. 162:1030-1036(1989).
RN   [4]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Sprague-Dawley; TISSUE=Liver;
RX   MEDLINE=90381322; PubMed=2400792;
RA   Kusunoki C., Satoh S., Kobayashi M., Niwa M.;
RT   "Structure of genomic DNA for rat platelet phospholipase A2.";
RL   Biochim. Biophys. Acta 1087:95-97(1990).
RN   [5]
RP   SEQUENCE OF 22-146.
RC   STRAIN=Wistar; TISSUE=Platelet;
RX   MEDLINE=89174508; PubMed=3235451;
RA   Hayakawa M., Kudo I., Tomita M., Nojima S., Inoue K.;
RT   "The primary structure of rat platelet phospholipase A2.";
RL   J. Biochem. 104:767-772(1988).
RN   [6]
RP   SEQUENCE OF 22-57.
RC   TISSUE=Spleen;
RX   MEDLINE=88186890; PubMed=3356705;
RA   Ono T., Tojo H., Kuramitsu S., Kagamiyama H., Okamoto M.;
RT   "Purification and characterization of a membrane-associated
RT   phospholipase A2 from rat spleen. Its comparison with a cytosolic
RT   phospholipase A2 S-1.";
RL   J. Biol. Chem. 263:5732-5738(1988).
RT   "Functional annotation of a full-length mouse cDNA collection.";
RL   Nature 409:685-690(2001).
CC   -!- FUNCTION: PA2 catalyzes the calcium-dependent hydrolysis of the 2-
CC   acyl groups in 3-sn-phosphoglycerides. L-alpha-1-palmitoyl-2-
CC   linoleoyl phosphatidylethanolamine is more efficiently hydrolyzed
CC   than the other phospholipids examined.
CC   -!- CATALYTIC ACTIVITY: Phosphatidylcholine + H(2)O = 1-
CC   acylglycerophosphocholine + a fatty acid anion.
CC   -!- COFACTOR: Binds 1 calcium ion per subunit.
CC   -!- SUBCELLULAR LOCATION: Secreted (isoform 1) and Cytoplasmic
CC   (isoform 2) (Potential).
CC   -!- ALTERNATIVE PRODUCTS:
CC   Event=Alternative splicing; Named isoforms=2;
CC   Name=1;
CC   IsoId=Q9WVF6-1; Sequence=Displayed;
CC   Name=2;
CC   IsoId=Q9WVF6-2; Sequence=VSP_004508;
CC   -!- TISSUE SPECIFICITY: Expressed in several tissues including
CC   pancreas, spleen, thymus, skin, lung, and ovary.
CC   -!- SIMILARITY: Belongs to the phospholipase A2 family.
CC   --
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CC   or send an email to license@isb-sib.ch).
CC   --
DR   EMBL; AF112983; AAD51391.1; -.
DR   EMBL; AF124374; AAD42773.1; -.
DR   EMBL; AF188624; AAF09019.1; -.
DR   EMBL; AF169407; AAF42987.1; -.
DR   EMBL; AF169408; AAF42988.1; -.
DR   EMBL; AK018005; BAB31033.1; -.
DR   EMBL; AK004232; -; NOT_ANNOTATED_CDS.
DR   HSSP; P24605; 1CLP.
DR   MGD; MGI:1341796; Pla2g2d.
DR   InterPro; IPR001211; PhospholipaseA2.
DR   Pfam; PF00068; phoslip; 1.
DR   PRINTS; PR00389; PHPHLIPASEA2.
DR   ProDom; PD000303; PhospholipaseA2; 1.
DR   SMART; SM00085; PA2c; 1.
DR   PROSITE; PS00119; PA2_ASP; 1.
DR   PROSITE; PS00118; PA2_HIS; 1.
KW   Hydrolase; Lipid degradation; Signal; Calcium; Alternative splicing.
FT   SIGNAL   1   19   POTENTIAL.
FT   CHAIN   20   144   GROUP IID SECRETORY PHOSPHOLIPASE A2.
FT   ACT_SITE   66   BY SIMILARITY.
FT   ACT_SITE   111   BY SIMILARITY.
FT   DISULFID   45   137   BY SIMILARITY.
FT   DISULFID   47   63   BY SIMILARITY.
FT   DISULFID   62   117   BY SIMILARITY.
FT   DISULFID   68   144   BY SIMILARITY.
FT   DISULFID   69   110   BY SIMILARITY.
FT   DISULFID   78   103   BY SIMILARITY.
FT   DISULFID   96   108   BY SIMILARITY.
FT   CARBOHYD   99   99   N-LINKED (GLCNAC...) (POTENTIAL).
FT   METAL   46   46   CALCIUM (VIA CARBONYL OXYGEN)
FT   (BY SIMILARITY).
FT   METAL   48   48   CALCIUM (VIA CARBONYL OXYGEN)
FT   (BY SIMILARITY).
FT   METAL   50   50   CALCIUM (VIA CARBONYL OXYGEN)
FT   (BY SIMILARITY).
FT   METAL   67   67   CALCIUM (BY SIMILARITY).
FT   VARSPLIC   1   26   Missing (in isoform 2).
FT   /FTId=VSP_004508.
SQ   SEQUENCE 144 AA; 16164 MW; 7697ADA07F8D270A CRC64;

Query Match 73.3%; Score 624.5; DB 1; Length 144;
Best Local Similarity 71.0%; Pred. No. 3.8e-56;
Matches 103; Conservative 14; Mismatches 27; Indels 1; Gaps 1;

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FT   CONFLICT      69     69       D -> E (IN REF. 5).
FT   CONFLICT      78     78       R -> V (IN REF. 5).
FT   CONFLICT      85     85       L -> V (IN REF. 3).
FT   CONFLICT     121    121       A -> S (IN REF. 5).
SQ   SEQUENCE     146 AA;   16294 MW;   60DDC9E79BF109F7 CRC64;

     Query Match             46.9%;  Score 399.5;  DB 1;  Length 146;
     Best Local Similarity   47.9%;  Pred. No. 2e-33;
     Matches   70;  Conservative  23;  Mismatches  52;  Indels  1;  Gaps   1;

Qy      1 MELALLCGLVWMA-GVIPIQGGILNLNKMVKQVTGKMPILSWPYGHCGLGRGQPKDA  59
          |:|:|||  :| :| |  :||:: ||| |:|| ||:||||||:|| ||||||| :|||
Db      1 MKVLLLLAVVIMAFGSIQVQGSLLEFQMILFKTGKADVSYGFYGHCGVGGRGSPKDA  60

Qy     60 TDWCCQTHDCCYDHLKTQGCGIYKDYRYRYNFSQGNIHCSDKGSWCEQQLCACDKEVAFCL 119
          |||||||||| |||: : ||||:: |:: :||
Db     61 TDWCCVTHDCCYNRLEKRGCGTKFLTYKFSYRGGQISCSTNQDSCRKQLCQCDKAAAECF 120

Qy    120 KRNLDTYQKRLRFYWRPHICRGQTPGC 145
          |   :| :|||:|:|| || |
Db    121 ARNKKSYSLKYQFYPNKFCKGKTPSC 146


RESULT 4
PA2A_HUMAN
ID   PA2A_HUMAN     STANDARD;       PRT;    144 AA.
AC   P14555; Q9UCD2;
DT   01-JAN-1990 (Rel. 13, Created)
DT   01-APR-1990 (Rel. 14, Last sequence update)
DT   15-MAR-2004 (Rel. 43, Last annotation update)
DE   Phospholipase A2, membrane associated precursor (EC 3.1.1.4)
DE   (Phosphatidylcholine 2-acylhydrolase) (Group IIA phospholipase A2)
DE   (GIIC sPLA2) (Non-pancreatic secretory phospholipase A2) (NPS-PLA2).
GN   PLA2G2A OR PLA2B OR RASF-A OR PLA2L.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Rheumatoid arthritic synovial fluid;
RX   MEDLINE=89174566; PubMed=2925608;
RA   Seilhamer J.J., Pruzanski W., Vadas P., Plant S., Miller J.A.,
RA   Kloss J., Johnson L.K.;
RT   "Cloning and recombinant expression of phospholipase A2 present in
RT   rheumatoid arthritic synovial fluid.";
RL   J. Biol. Chem. 264:5335-5338(1989).
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=89174633; PubMed=2925633;
RA   Kramer R.M., Hession C., Johansen B., Hayes G., McGray P., Chow E.P.,
RA   Tizard R., Pepinsky R.B.;
RT   "Structure and properties of a human non-pancreatic phospholipase
RT   A2.";
RL   J. Biol. Chem. 264:5768-5775(1989).
RN   [3]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=91050834; PubMed=2239446;
RA   Kramer R.M., Johansen B., Hession C., Pepinsky R.B.;
RT   "Structure and properties of a secretable phospholipase A2 from human
RT   platelets.";
RL   Adv. Exp. Med. Biol. 275:35-53(1990).
RN   [4]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Prostate;
RX   MEDLINE=22388257; PubMed=12477932;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
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RN   [7]
RP   SEQUENCE OF 22-46.
RC   TISSUE=Platelet;
RX   MEDLINE=88007474; PubMed=3654593;
RA   Hayakawa M., Horigome K., Kudo I., Tomita M., Nojima S., Inoue K.;
RT   "Amino acid composition and NH2-terminal amino acid sequence of rat
RT   platelet secretory phospholipase A2.";
RL   J. Biochem. 101:1311-1314(1987).
RN   [8]
RP   SEQUENCE OF 22-45.
RC   TISSUE=Liver;
RX   MEDLINE=89255484; PubMed=2722857;
RA   Aarsman A.J., de Jong J.G.N., Arnoldussen E., Neys F.W.,
RA   van Wassenaar P.D., van den Bosch H.;
RT   "Immunoaffinity purification, partial sequence, and subcellular
RT   localization of rat liver phospholipase A2.";
RL   J. Biol. Chem. 264:10008-10014(1989).
CC   -!- FUNCTION: Thought to participate in the regulation of the
CC       phospholipid metabolism in biomembranes including eicosanoid
CC       biosynthesis. Catalyzes the calcium-dependent hydrolysis of the 2-
CC       acyl groups in 3-sn-phosphoglycerides.
CC   -!- CATALYTIC ACTIVITY: Phosphatidylcholine + H(2)O = 1-
CC       acylglycerophosphocholine + a fatty acid anion.
CC   -!- COFACTOR: Binds 1 calcium ion per subunit (By similarity).
CC   -!- SUBCELLULAR LOCATION: Membrane-associated.
CC   -!- MISCELLANEOUS: Group II phospholipase A2 is found in many cells
CC       and also extracellularly. The membrane-bound and secreted forms
CC       are identical and are encoded by a single gene.
CC   -!- SIMILARITY: Belongs to the phospholipase A2 family.
CC   --------------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute.  There are no restrictions on its
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   --------------------------------------------------------------------------
DR   EMBL; D00523; BAA00410.1; -.
DR   EMBL; M37127; AAA41223.1; -.
DR   EMBL; M25148; AAA41920.1; -.
DR   EMBL; X51529; CAA35909.1; -.
DR   PIR; A33394; A33394.
DR   HSSP; P14555; 1POD.
DR   InterPro; IPR001211; PhospholipaseA2.
DR   Pfam; PF00068; phoslip; 1.
DR   PRINTS; PR00389; PHPHLIPASEA2.
DR   ProDom; PD000303; PhospholipaseA2; 1.
DR   SMART; SM00085; PA2c; 1.
DR   PROSITE; PS00118; PA2_HIS; 1.
DR   PROSITE; PS00119; PA2_ASP; 1.
KW   Hydrolase; Lipid degradation; Membrane; Signal; Calcium.
FT   SIGNAL        1     21
FT   CHAIN        22    146       PHOSPHOLIPASE A2, MEMBRANE ASSOCIATED.
FT   ACT_SITE     68     68       BY SIMILARITY.
FT   ACT_SITE    113    113       BY SIMILARITY.
FT   DISULFID     47    139       BY SIMILARITY.
FT   DISULFID     49     65       BY SIMILARITY.
FT   DISULFID     64    119       BY SIMILARITY.
FT   DISULFID     70    146       BY SIMILARITY.
FT   DISULFID     71    112       BY SIMILARITY.
FT   DISULFID     80    105       BY SIMILARITY.
FT   DISULFID     98    110       BY SIMILARITY.
FT   METAL        48     48       CALCIUM (VIA CARBONYL OXYGEN)
FT                                (BY SIMILARITY).
FT   METAL        50     50       CALCIUM (VIA CARBONYL OXYGEN)
FT                                (BY SIMILARITY).
FT   METAL        52     52       CALCIUM (VIA CARBONYL OXYGEN)
FT                                (BY SIMILARITY).
FT   METAL        69     69       CALCIUM (BY SIMILARITY).
FT   VARIANT     135    135       P -> L (POLYMORPHISM).
FT   CONFLICT     22     22       S -> D (IN REF. 8).
FT   CONFLICT     63     63       W -> E (IN REF. 5).
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RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length
RT   human and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [5]
RP   SEQUENCE OF 21-144.
RC   TISSUE=Spleen;
RX   MEDLINE=89374261; PubMed=2775276;
RA   Kanda A., Ono T., Yoshida N., Tojo H., Okamoto M.;
RT   "The primary structure of a membrane-associated phospholipase A2 from
RT   human spleen.";
RL   Biochem. Biophys. Res. Commun. 163:42-48(1989).
RN   [6]
RP   SEQUENCE OF 21-54.
RC   TISSUE=Synovial fluid;
RX   MEDLINE=89197814; PubMed=3240982;
RA   Hara S., Kudo I., Matsuta K., Miyamoto T., Inoue K.;
RT   "Amino acid composition and NH2-terminal amino acid sequence of human
RT   phospholipase A2 purified from rheumatoid synovial fluid.";
RL   J. Biochem. 104:326-328(1988).
RN   [7]
RP   SEQUENCE OF 21-33.
RC   TISSUE=Synovial fluid;
RX   MEDLINE=89076274; PubMed=3202859;
RA   Lai C.Y., Wada K.;
RT   "Phospholipase A2 from human synovial fluid: purification and
RT   structural homology to the placental enzyme.";
RL   Biochem. Biophys. Res. Commun. 157:488-493(1988).
RN   [8]
RP   SEQUENCE OF 21-75.
RC   TISSUE=Ileal mucosa;
RX   MEDLINE=94002200; PubMed=8399335;
RA   Minami T., Tojo H., Shinomura Y., Matsuzawa Y., Okamoto M.;
RT   "Purification and characterization of a phospholipase A2 from human
RT   ileal mucosa.";
RL   Biochim. Biophys. Acta 1170:125-130(1993).
RN   [9]
RP   X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS).
RX   MEDLINE=91287826; PubMed=2062381;
RA   Wery J.-P., Schevitz R.W., Clawson D.K., Bobbitt J.L., Dow E.R.,
RA   Gamboa G., Goodson T. Jr., Hermann R.B., Kramer R.M., McClure D.B.,
RA   Mihelich E.D., Putnam J.E., Sharp J.D., Stark D.H., Teater C.,
RA   Warrick M.W., Jones N.D.;
RT   "Structure of recombinant human rheumatoid arthritic synovial fluid
RT   phospholipase A2 at 2.2-A resolution.";
RL   Nature 352:79-82(1991).
RN   [10]
RP   X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS).
RX   MEDLINE=92054586; PubMed=1948070;
RA   Scott D.L., White S.P., Browning J.L., Rosa J.J., Gelb M.H.,
RA   Sigler P.B.;
RT   "Structures of free and inhibited human secretory phospholipase A2
RT   from inflammatory exudate.";
RL   Science 254:1007-1010(1991).
RN   [11]
RP   X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS).
RX   MEDLINE=95393225; PubMed=7664108;
RA   Schevitz R.W., Bach N.J., Carlson D.G., Chirgadze N.Y., Clawson D.K.,
RA   Dillard R.D., Draheim S.E., Hartley L.W., Jones N.D., Mihelich E.D.,
RA   Olkowski J.L., Snyder D.W., Dand S.C., Wery J.-P.;
RT   "Structure-based design of the first potent and selective inhibitor
RT   of human non-pancreatic secretory phospholipase A2.";
RL   Nat. Struct. Biol. 2:458-465(1995).
RN   [12]
RP   X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS).
RX   MEDLINE=9207049; PubMed=9538252;
RA   Kitadokoro K., Hagishita S., Sato T., Ohtan M., Miki K.;
RT   "Crystal structure of human secretory phospholipase A2-IIA complex
RT   with the potent indolizine inhibitor 120-1032.";
RL   J. Biochem. 123:619-623(1998).
CC   -!- FUNCTION: Thought to participate in the regulation of the
CC       phospholipid metabolism in biomembranes including eicosanoid
CC       biosynthesis. Catalyzes the calcium-dependent hydrolysis of the 2-
CC       acyl groups in 3-sn-phosphoglycerides.
CC   -!- CATALYTIC ACTIVITY: Phosphatidylcholine + H(2)O = 1-
CC       acylglycerophosphocholine + a fatty acid anion.
CC   -!- COFACTOR: Binds 1 calcium ion per subunit.
CC   -!- SUBCELLULAR LOCATION: Membrane-associated.
CC   -!- MISCELLANEOUS: Group II phospholipase A2 is found in many cells
CC       and also extracellularly. The membrane-bound and secreted forms
CC       are identical and are encoded by a single gene.
CC   -!- SIMILARITY: Belongs to the phospholipase A2 family.
CC   -----------------------------------------------------------------------
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
DR   EMBL; M22430; AAA36550.1; -.
DR   EMBL; M22431; AAA36549.1; -.
DR   EMBL; BC005919; AAH05919.1; -.
DR   PIR; A32862; PSHUYF.
DR   PDB; 1AYP; 31-JUL-95.
DR   PDB; 1BSC; 31-OCT-93.
DR   PDB; 1POD; 31-OCT-93.
DR   PDB; 1POE; 31-OCT-93.
DR   PDB; 1KVO; 07-JUL-97.
DR   PDB; 1DB4; 12-NOV-99.
DR   PDB; 1DB5; 12-NOV-99.
DR   PDB; 1DCY; 12-NOV-99.
DR   Genew; HGNC:9031; PLA2G2A.
DR   MIM; 172411; -.
DR   GO; GO:0004623; F:phospholipase A2 activity; TAS.
DR   InterPro; IPR001211; PhospholipaseA2.
DR   Pfam; PF00068; phoslip; 1.
DR   PRINTS; PR00389; PHPHLIPASA2.
DR   ProDom; PD000303; PhospholipaseA2; 1.
DR   SMART; SM00085; PA2c; 1.
DR   PROSITE; PS00118; PA2_HIS; 1.
DR   PROSITE; PS00119; PA2_ASP; 1.
KW   Hydrolase; Lipid degradation; Membrane; Signal; Calcium;
KW   3D-structure.
FT   SIGNAL        1     20
FT   CHAIN        21    144       PHOSPHOLIPASE A2, MEMBRANE ASSOCIATED.
FT   ACT_SITE     67     67       BY SIMILARITY.
FT   ACT_SITE    111    111       BY SIMILARITY.
FT   DISULFID     46    137
FT   DISULFID     48     64
FT   DISULFID     63    117
FT   DISULFID     69    144
FT   DISULFID     70    110
FT   DISULFID     79    103
FT   DISULFID     97    108
FT   METAL        47     47       CALCIUM (VIA CARBONYL OXYGEN).
FT   METAL        49     49       CALCIUM (VIA CARBONYL OXYGEN).
FT   METAL        51     51       CALCIUM (VIA CARBONYL OXYGEN).
FT   METAL        68     68       CALCIUM.
FT   HELIX        22     33
FT   HELIX        37     40
FT   TURN         41     41
FT   TURN         45     47
FT   HELIX        59     75
FT   TURN         76     78
FT   STRAND       88     91
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FT   TURN             92     93
FT   STRAND           94     97
FT   HELIX           102    120
FT   TURN            121    121
FT   HELIX           122    124
FT   TURN            127    128

Query Match             46.4%;  Score 395.5; DB 1; Length 144;
Best Local Similarity   47.6%;  Pred. No. 4.9e-33;
Matches   69;  Conservative   23;  Mismatches   52;  Indels   1;  Gaps   1;

Qy      1 MELALLCGLVVMAGVIPIQGGILNLNKMVKQVTGKMPILSYWPYGCHCGLGGRGQPKDAT 60
            |.:    :::|:|    |: :.:|    | ::|| |||||:|:|||||
Db      1 MKTLLLLAVIMIFGLLQAHGNLVNFHRMIKLTTGKBAALSYGFYGCHCGVGGRGSPKDAT 60

Qy     61 DWCCQTHDCCYDHLKTQGGIYKDYRYRNFSQGNIHCSDKGSWCEQLCACDKEVAFCLK 120
            ||| |||||||      |: :|||        |: :: :|| | ::|||| |:
Db     61 DRCCVTHDCCYKRLEKRGCGTKFLSYKFSNSGSRITCAKQDS-CRSQLCECDKAAATCFA 119

Qy    121 RNLDTYQKRLRFYWRPHCRGQTPGC 145
            ||| ||: :.:|||      ||||| |
Db    120 RNKTTYNKKYQYYSNKHCRGSTPRC 144
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RESULT 5
PA2M_CAVPO
ID   PA2M_CAVPO    STANDARD;       PRT;  145 AA.
AC   P47711;
DT   01-FEB-1996 (Rel. 33, Created)
DT   01-FEB-1996 (Rel. 33, Last sequence update)
DT   15-MAR-2004 (Rel. 43, Last annotation update)
DE   Phospholipase A2, membrane associated precursor (EC 3.1.1.4)
DE   (Phosphatidylcholine 2-acylhydrolase) (Group IIA phospholipase A2)
DE   (GIIC sPLA2).
GN   PLA2G2A.
OS   Cavia porcellus (Guinea pig).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.
OX   NCBI_TaxID=10141;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Hartley; TISSUE=Macrophage;
RX   MEDLINE=95340522; PubMed=7615534;
RA   Vial D., Senorale-Pose M., Havet N., Molio L., Vargaftig B.B.,
RA   Touqui L.;
RT   "Expression of the type-II phospholipase A2 in alveolar macrophages.
RT   Down-regulation by an inflammatory signal.";
RL   J. Biol. Chem. 270:17327-17332(1995).
CC   -!- FUNCTION: Thought to participate in the regulation of the
CC       phospholipid metabolism in biomembranes including eicosanoid
CC       biosynthesis (By similarity). Catalyzes the calcium-dependent
CC       hydrolysis of the 2-acyl groups in 3-sn-phosphoglycerides.
CC   -!- CATALYTIC ACTIVITY: Phosphatidylcholine + H(2)O = 1-
CC       acylglycerophosphocholine + a fatty acid anion.
CC   -!- COFACTOR: Binds 1 calcium ion per subunit (By similarity).
CC   -!- SUBCELLULAR LOCATION: Membrane-associated.
CC   -!- TISSUE SPECIFICITY: Alveolar macrophages, and at much lower levels
CC       in peripheral blood monocytes and peritoneal macrophages.
CC   -!- SIMILARITY: Belongs to the phospholipase A2 family.
CC   --------------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   --------------------------------------------------------------------------
DR   EMBL; X82631; CAA57953.1; -.
DR   PIR; I48093; I48093.
DR   HSSP; P14555; 1POD.
DR   InterPro; IPR001211; PhospholipaseA2.
DR   Pfam; PF00068; phoslip; 1.
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DR   PRINTS; PR00389; PHPHLIPASEA2.
DR   ProDom; PD000303; PhospholipaseA2; 1.
DR   SMART; SM00085; PA2c; 1.
DR   PROSITE; PS00118; PA2_HIS; 1.
DR   PROSITE; PS00119; PA2_ASP; 1.
KW   Hydrolase; Lipid degradation; Membrane; Signal; Calcium.
FT   SIGNAL        1     20       POTENTIAL.
FT   CHAIN        21    145       PHOSPHOLIPASE A2, MEMBRANE ASSOCIATED.
FT   ACT_SITE     67     67       BY SIMILARITY.
FT   ACT_SITE    112    112       BY SIMILARITY.
FT   DISULFID     46    138       BY SIMILARITY.
FT   DISULFID     48     64       BY SIMILARITY.
FT   DISULFID     63    118       BY SIMILARITY.
FT   DISULFID     69    145       BY SIMILARITY.
FT   DISULFID     70    111       BY SIMILARITY.
FT   DISULFID     79    104       BY SIMILARITY.
FT   DISULFID     97    109       BY SIMILARITY.
FT   METAL        47     47       CALCIUM (VIA CARBONYL OXYGEN)
FT                                (BY SIMILARITY).
FT   METAL        49     49       CALCIUM (VIA CARBONYL OXYGEN)
FT                                (BY SIMILARITY).
FT   METAL        51     51       CALCIUM (VIA CARBONYL OXYGEN)
FT                                (BY SIMILARITY).
FT   METAL        68     68       CALCIUM (BY SIMILARITY).
SQ   SEQUENCE   145 AA;  16153 MW;  13F22C96594D304D CRC64;
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Query Match             45.7%;  Score 389; DB 1; Length 145;
Best Local Similarity   49.3%;  Pred. No. 2.2e-32;
Matches   72;  Conservative   20;  Mismatches   52;  Indels   2;  Gaps   2;

Qy      1 MELALLCGLVVMAGVIP-IQGGILNLNKMVKQVTGKMPILSYWPYGCHCGLGGRGQPKDA 59
            | :    :::|:|    |  |: :.:|    | ::|| |||||:|:|||||
Db      1 MKILLLL-LVVMASDLPQAHGHLKQFTEMIKLTTGKNGLTSYGAYGCHCGVGGKGTPKDA 59

Qy     60 TDWCCQTHDCCYDHLKTQGGIYKDYRYRNFSQGNIHCSDKGSWCEQLCACDKEVAFCL 119
            ||| |||||||      |: :|||        |: :: :|| | ::|||| |:
Db     60 TDRCCVRHDCCYDRLMKRGCGTKFLNYRFTHKGSSITCSVKQNSCQKQLCECDKAAAYCF 119

Qy    120 KRNLDTYQKRLRFYWRPHCRGQTPGC 145
            | ||| ||: :.:|||      ||||| |
Db    120 AANLKSYSRRYQFYNGLCRGKTPSC 145
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RESULT 6
PA2A_MOUSE
ID   PA2A_MOUSE    STANDARD;       PRT;  146 AA.
AC   P31482; Q60871;
DT   01-JUL-1993 (Rel. 26, Created)
DT   10-OCT-2003 (Rel. 42, Last sequence update)
DT   15-MAR-2004 (Rel. 43, Last annotation update)
DE   Phospholipase A2, membrane associated precursor (EC 3.1.1.4)
DE   (Phosphatidylcholine 2-acylhydrolase) (Group IIA phospholipase A2)
DE   (GIIC sPLA2) (Enhancing factor) (EF).
GN   PLA2G2A.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=BALB/c;
RA   Mulherkar R.;
RL   Submitted (OCT-1994) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   SEQUENCE FROM N.A., AND POLYMORPHISM.
RC   STRAIN=BALB/c, and CD-1; TISSUE=Intestine;
RX   MEDLINE=95403435; PubMed=7673223;
RA   Kennedy B.P., Payette P., Mudgett J., Vadas P., Pruzanski W.,
RA   Ywan M., Tang C., Rancourt D.E., Cromlish W.;
RT   "A natural disruption of the secretory group II phospholipase A2 gene
RT   in inbred mouse strains.";
RL   J. Biol. Chem. 270:22378-22385(1995).
RN   [3]
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RP   SEQUENCE FROM N.A.
RC   STRAIN=C3H;
RX   MEDLINE=95300227; PubMed=7781071;
RA   MacPhee M., Chepenik K.P., Liddell R.A., Nelson K.K., Siracusa L.D.,
RA   Buchberg A.M.;
RT   "The secretory phospholipase A2 gene is a candidate for the Mom1
RT   locus, a major modifier of ApcMin-induced intestinal neoplasia.";
RL   Cell 81:957-966(1995).
RN   [4]
RP   SEQUENCE FROM N.A.
RC   STRAIN=FVB/N; TISSUE=Colon;
RX   MEDLINE=22888257; PubMed=12477932;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [5]
RP   SEQUENCE OF 22-146 FROM N.A.
RC   STRAIN=BALB/c; TISSUE=Small intestine;
RX   MEDLINE=94029955; PubMed=8267767;
RA   Mulherkar R., Rao R.S., Wagle A.S., Patki V., Deo M.G.;
RT   "Enhancing factor, a Paneth cell specific protein from mouse small
RT   intestines: predicted amino acid sequence from RT-PCR amplified cDNA
RT   and its expression.";
RL   Biochem. Biophys. Res. Commun. 195:1254-1263(1993).
RN   [6]
RP   ERRATUM.
RX   MEDLINE=94071967; PubMed=8250944;
RA   Mulherkar R., Rao R.S., Wagle A.S., Patki V., Deo M.G.;
RL   Biochem. Biophys. Res. Commun. 197:351-352(1993).
RN   [7]
RP   PRELIMINARY SEQUENCE OF 22-41.
RC   TISSUE=Small intestine;
RX   MEDLINE=93146172; PubMed=8425615;
RA   Mulherkar R., Rao R., Rao L., Patki V., Chauhan V.S., Deo M.G.;
RT   "Enhancing factor protein from mouse small intestines belongs to the
RT   phospholipase A2 family.";
RL   FEBS Lett. 317:263-266(1993).
CC   -!- FUNCTION: May play a role in cell proliferation, by increasing the
CC       binding of EGF to the cells and thereby modulating its action. In
CC       doing so, this isozyme binds to a membrane-associated receptor
CC       distinct from the EGF receptor and which could be a heparan-
CC       sulfate proteoglycan located on the cell membrane.
CC   -!- FUNCTION: PA2 catalyzes the calcium-dependent hydrolysis of the 2-
CC       acyl groups in 3-sn-phosphoglycerides.
CC   -!- CATALYTIC ACTIVITY: Phosphatidylcholine + H(2)O = 1-
CC       acylglycerophosphocholine + a fatty acid anion.
CC   -!- COFACTOR: Binds 1 calcium ion per subunit (By similarity).
CC   -!- SUBCELLULAR LOCATION: Membrane-associated.
CC   -!- TISSUE SPECIFICITY: Mainly in the Paneth cells adjacent to the
CC       stem population in the small intestines. Also expressed in
CC       regenerating liver and hyperplastic esophageal epithelium.
CC   -!- POLYMORPHISM: In strains 129/Sv, B10.RIII and C57BL/6, a
CC       polymorphism causes a frameshift and premature truncation of the
CC       protein, rendering it inactive. Strains BALB/c, C3H/He, DBA/1,
CC       DBA/2, MRL and NZB/BlN contain the normal protein while strain CD-
CC       1 is heterozygous for the mutation.
CC   -!- SIMILARITY: Belongs to the phospholipase A2 family.
CC
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CC   the European Bioinformatics Institute.  There are no restrictions on its
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CC   modified and this statement is not removed.  Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC
DR   EMBL; X74266; CAA52325.1; -.
DR   EMBL; U32358; AAC52252.1; -.
DR   EMBL; U28244; AAB06315.1; ALT_INIT.
DR   EMBL; BC045156; AAH45156.1; -.
DR   PIR; I48342; I48342.
DR   PIR; S29495; S29495.
DR   HSSP; P14555; 1POD.
DR   MGD; MGI:104642; Pla2g2a.
DR   InterPro; IPR001211; Phospholipase A2.
DR   Pfam; PF00068; phoslip; 1.
DR   PRINTS; PR00389; PHPHLIPASA2.
DR   ProDom; PD000303; Phospholipase A2; 1.
DR   SMART; SM00085; PA2c; 1.
DR   PROSITE; PS00118; PA2_HIS; 1.
DR   PROSITE; PS00119; PA2_ASP; 1.
KW   Hydrolase; Lipid degradation; Calcium; Growth regulation; Signal;
KW   Membrane; Polymorphism.
FT   SIGNAL        1     21
FT   CHAIN        22    146       PHOSPHOLIPASE A2, MEMBRANE ASSOCIATED.
FT   ACT_SITE     68     68       BY SIMILARITY.
FT   ACT_SITE    113    113       BY SIMILARITY.
FT   DISULFID     47    139       BY SIMILARITY.
FT   DISULFID     49     65       BY SIMILARITY.
FT   DISULFID     64    119       BY SIMILARITY.
FT   DISULFID     70    146       BY SIMILARITY.
FT   DISULFID     71    112       BY SIMILARITY.
FT   DISULFID     80    105       BY SIMILARITY.
FT   DISULFID     98    110       BY SIMILARITY.
FT   METAL        48     48       CALCIUM (VIA CARBONYL OXYGEN)
FT                                (BY SIMILARITY).
FT   METAL        50     50       CALCIUM (VIA CARBONYL OXYGEN)
FT                                (BY SIMILARITY).
FT   METAL        52     52       CALCIUM (VIA CARBONYL OXYGEN)
FT                                (BY SIMILARITY).
FT   METAL        69     69       CALCIUM (BY SIMILARITY).
FT   CONFLICT     19     19       V -> D (IN REF. 1).
FT   CONFLICT     86     86       K -> T (IN REF. 1).
SQ   SEQUENCE   146 AA;  16145 MW;  AB904F6B3B1BA5C7 CRC64;

Query Match             43.6%;  Score 371.5;  DB 1;  Length 146;
Best Local Similarity   47.3%;  Pred. No. 1.3e-30;
Matches   69;  Conservative   19;  Mismatches   57;  Indels    1;  Gaps    1;

Qy      1 MELALLCGLVVMA-GVIPIQGGILNLNKMVKQVTGKMPILSYWPYGCHCGLGGRGQPKDA 59
            ::   ||||| | ||||||||| |||||||| ||||::|| |:||||||||||| | ||
Db      1 MKVLLLAASIMAFGSIQVQGNIAQFGEMIRLKTGKRAELSYAFYGCHCGLGGKGSPKDA 60

Qy     60 TDWCCQTHDCCYDHLKTQGCGIYKDYRYNFSQGNIHCSDKGSWCEQQLCACDKEVAFCL 119
            || || |||||| |  | ||   |: || ::  || |:: | |:| |||:  :  : |
Db     61 TDRCCVTHDCCYKSLEKSGCGTKLLKFKYSHQGGGITCSANQNSCQKRLCQCDKAAAECF 120

Qy    120 KRNLDTYQKRLRFYWRPHCRGQTPGC 145
            :||  || | |: ||| : : || |
Db    121 ARNKKTYSLKYQFYPNMFCKGKKPKC 146


RESULT 7
PA2F_HUMAN
ID   PA2F_HUMAN     STANDARD;      PRT;    168 AA.
AC   Q9BZM2; Q9H506;
DT   28-FEB-2003 (Rel. 41, Created)
DT   28-FEB-2003 (Rel. 41, Last sequence update)
DT   10-OCT-2003 (Rel. 42, Last annotation update)
```

```
DE   Group IIF secretory phospholipase A2 precursor (EC 3.1.1.4)
DE   (Phosphatidylcholine 2-acylhydrolase GIIF) (GIIF sPLA2) (sPLA(2)-IIF).
GN   PLA2G2F.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A., AND CHARACTERIZATION.
RX   MEDLINE=20563887; PubMed=11112443;
RA   Valentin E., Singer A.G., Ghomashchi F., Lazdunski M., Gelb M.H.,
RA   Lambeau G.;
RT   "Cloning and recombinant expression of human group IIF-secreted
RT   phospholipase A(2).";
RL   Biochem. Biophys. Res. Commun. 279:223-228(2000).
RN   [2]
RP   SEQUENCE OF 1-98 FROM N.A.
RA   Wallis J.;
RL   Submitted (OCT-2000) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: PA2 catalyzes the calcium-dependent hydrolysis of the 2-
CC       acyl groups in 3-sn-phosphoglycerides. Hydrolyzes
CC       phosphatidylglycerol versus phosphatidylcholine with a 15-fold
CC       preference.
CC   -!- CATALYTIC ACTIVITY: Phosphatidylcholine + H(2)O = 1-
CC       acylglycerophosphocholine + a fatty acid anion.
CC   -!- COFACTOR: Binds 1 calcium ion per subunit.
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- TISSUE SPECIFICITY: Expressed at high levels in placenta, testis,
CC       thymus and at lower levels in heart, kidney, liver and prostate.
CC   -!- SIMILARITY: Belongs to the phospholipase A2 family.
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```
DR   EMBL; AF306566; AAG50242.1; -.
DR   EMBL; AL158172; CAC13160.1; ALT_INIT.
DR   HSSP; P82287; 1QLL.
DR   GO; GO:0005576; C:extracellular; NAS.
DR   GO; GO:0004623; F:phospholipase A2 activity; NAS.
DR   InterPro; IPR001211; Phospholipase_A2.
DR   Pfam; PF00068; phoslip; 1.
DR   PRINTS; PR00389; PHPHLIPASEA2.
DR   ProDom; PD000303; Phospholipase_A2; 1.
DR   SMART; SM00085; PA2c; 1.
DR   PROSITE; PS00119; PA2_ASP; FALSE_NEG.
DR   PROSITE; PS00118; PA2_HIS; 1.
KW   Hydrolase; Lipid degradation; Signal; Calcium.
FT   SIGNAL        1     20       POTENTIAL.
FT   CHAIN        21    168       GROUP IIF SECRETORY PHOSPHOLIPASE A2.
FT   ACT_SITE     67     67       BY SIMILARITY.
FT   ACT_SITE    114    114       BY SIMILARITY.
FT   DISULFID     46    138       BY SIMILARITY.
FT   DISULFID     48     64       BY SIMILARITY.
FT   DISULFID     63    120       BY SIMILARITY.
FT   DISULFID     69    145       BY SIMILARITY.
FT   DISULFID     70    113       BY SIMILARITY.
FT   DISULFID     79    106       BY SIMILARITY.
FT   DISULFID     98    111       BY SIMILARITY.
FT   CARBOHYD     92     92       N-LINKED (GLCNAC...)  (POTENTIAL).
FT   CARBOHYD    102    102       N-LINKED (GLCNAC...)  (POTENTIAL).
FT   CARBOHYD    123    123       N-LINKED (GLCNAC...)  (POTENTIAL).
FT   CARBOHYD    144    144       N-LINKED (GLCNAC...)  (POTENTIAL).
FT   METAL        47     47       CALCIUM (VIA CARBONYL OXYGEN)
FT                                (BY SIMILARITY).
FT   METAL        49     49       CALCIUM (VIA CARBONYL OXYGEN)
FT                                (BY SIMILARITY).
FT   METAL        51     51       CALCIUM (VIA CARBONYL OXYGEN)
FT                                (BY SIMILARITY).
FT   METAL        68     68       CALCIUM (BY SIMILARITY).
SQ   SEQUENCE   168 AA;  18658 MW;  35B15929B246A762 CRC64;  Length 168;

Query Match                     41.3%;  Score 352;  DB 1;
Best Local Similarity           45.5%;  Pred. No. 1.4e-28;
Matches    66;  Conservative   19;  Mismatches   52;  Indels    8;  Gaps    4;

Qy     3  LALLCGLVVMAGVIPIQGGILNLNKMVKQVTGKMPILSYWPYGCHCGLGGRGQPKDATDW   62
          |:|:|||  |||||||||||||||||  ||  ||||||||||||||||||||||
Db     7  VAILAGSVLSTA---HGSLLNLKAMVEAVTGRSAILSFVGYGCYGLGGRGQPKDVDW     62

Qy    63  CCGTHDCCYDHLKTQGGCGIYKDYYRYNFSQG-NIHCSD-KGSWCEQQ:CACDKEVAFCLK 120
          ||||||||  |::  |||||        |:||  |  || |||||||| : : ||
Db    63  CCHAHDCCYQELFDQGCHPYVDHYDHTIENNTEIVCSDLNKTECDKQTCMCDKNMVLCLM  122

Qy   121  RNLDTYQKRLRFYWRPHCRGQTPGC  145
          ||:  :||||  ::|||  ||
Db   123  N--QTYREYRGFLNVVCQGPTPNC   145

RESULT 8
PA25_HUMAN
ID   PA25_HUMAN     STANDARD;     PRT;   138 AA.
AC   P39877;
DT   01-FEB-1995 (Rel. 31, Created)
DT   01-FEB-1995 (Rel. 31, Last sequence update)
DT   15-MAR-2004 (Rel. 43, Last annotation update)
DE   Calcium-dependent phospholipase A2 precursor (EC 3.1.1.4)
DE   (Phosphatidylcholine 2-acylhydrolase) (PLA2-10) (Group V phospholipase
DE   A2).
GN   PLA2G5.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Stomach;
RX   MEDLINE=94131989; PubMed=8300559;
RA   Chen J., Engle S.J., Seilhamer J.J., Tischfield J.A.;
RT   "Cloning and recombinant expression of a novel human low molecular
RT   weight Ca(2+)-dependent phospholipase A2.";
RL   J. Biol. Chem. 269:2365-2368(1994).
RN   [2]
RP   SEQUENCE FROM N.A.
RA   Wallis J.;
RL   Submitted (OCT-2000) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: PA2 catalyzes the calcium-dependent hydrolysis of the 2-
CC       acyl groups in 3-sn-phosphoglycerides. This isozyme hydrolyzes
CC       more efficiently L-alpha-1-palmitoyl-2-oleoyl phosphatidylcholine
CC       than L-alpha-1-palmitoyl-2-arachidonyl phosphatidylcholine, L-
CC       alpha-1-palmitoyl-2-arachidonyl phosphatidylethanolamine, or L-
CC       alpha-1-stearoyl-2-arachidonyl phosphatidylinositol. May be
CC       involved in the production of lung surfactant, the remodeling or
CC       regulation of cardiac muscle.
CC   -!- CATALYTIC ACTIVITY: Phosphatidylcholine + H(2)O = 1-
CC       acylglycerophosphocholine + a fatty acid anion.
CC   -!- COFACTOR: Binds 1 calcium ion per subunit (By similarity).
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- TISSUE SPECIFICITY: Heart, placenta and less abundantly, in lung.
CC   -!- PTM: This enzyme lacks one of the seven disulfide bonds found in
CC       similar PA2 proteins.
CC   -!- MISCELLANEOUS: Maximal activity is found at pH 6.5 and remains
CC       high up to pH 9.0.
CC   -!- SIMILARITY: Belongs to the phospholipase A2 family.
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CC   --------
DR   EMBL; U03090; AAC28886.1; -.
DR   EMBL; AL158172; CAC13158.1; -.
DR   PIR; A49959; A49959.
DR   Genew; HGNC:9038; PLA2G5.
DR   HSSP; P14421; 1A2A.
DR   MIM; 601192; -.
DR   GO; GO:0005576; C:extracellular; TAS.
DR   GO; GO:0004625; F:calcium-dependent secreted phospholipase A2. . .; TAS.
DR   GO; GO:0006644; P:phospholipid metabolism; TAS.
DR   InterPro; IPR001211; PhospholipaseA2.
DR   Pfam; PF00068; phoslip; 1.
DR   PRINTS; PR00389; PHPHLIPASEA2.
DR   ProDom; PD000303; PhospholipaseA2; 1.
DR   SMART; SM00085; PA2c; 1.
DR   PROSITE; PS00118; PA2_HIS; 1.
DR   PROSITE; PS00119; PA2_ASP; 1.
KW   Hydrolase; Lipid degradation; Calcium; Signal.
FT   SIGNAL         1     20       POTENTIAL.
FT   CHAIN         21    138       CALCIUM-DEPENDENT PHOSPHOLIPASE A2.
FT   ACT_SITE      67     67       BY SIMILARITY.
FT   ACT_SITE     111    111       BY SIMILARITY.
FT   DISULFID      46    137       BY SIMILARITY.
FT   DISULFID      48     64       BY SIMILARITY.
FT   DISULFID      63    117       BY SIMILARITY.
FT   DISULFID      70    110       BY SIMILARITY.
FT   DISULFID      79    103       BY SIMILARITY.
FT   DISULFID      97    108       BY SIMILARITY.
FT   METAL         47     47       CALCIUM (VIA CARBONYL OXYGEN)
FT                                 (BY SIMILARITY).
FT   METAL         49     49       CALCIUM (VIA CARBONYL OXYGEN)
FT                                 (BY SIMILARITY).
FT   METAL         51     51       CALCIUM (VIA CARBONYL OXYGEN)
FT                                 (BY SIMILARITY).
FT   METAL         68     68       CALCIUM (BY SIMILARITY).
SQ   SEQUENCE     138 AA;  15674 MW;  0D17DC76E55F42BC CRC64;

Query Match      40.7%;   Score 347;   DB 1;   Length 138;
Best Local Similarity 43.6%;   Pred. No. 3.7e-28;
Matches   58;   Conservative   27;   Mismatches   36;   Indels   12;   Gaps   2;

Qy    12 MAGVIP----------IQGGILNLNKMVKQVTGKMPILSYWPYGHCGLGGRGQPKDAT 60
            |||:|    |::||:|:| :::||||| :|:|||||||||||| |||:|| ||||
Db     1 MKGLLPLAWFLACSVPAVQGGLLDLKSMIEKVTGKNALTNYGFYGYCYGWGRGTPKDGT 60

Qy    61 DWCCQTHDCCYDHLKTQGCGIYKDYYRYNFSQGNIHCSDKGSWCEQLCACDKEVAFCLK 120
            |::::| :|:|||:: |:: ||:|:: :|| :|| |:|:  |:|:: ::  :|||
Db    61 DWCCWAHDHCYGRLEEKGCNIRTQSYKYRFAWGVVTC-EPGPFCHVNLCACDRKLVYCLK 119

Qy   121 RNLDTYQKRLRFY 133
            ||| ||| | :
Db   120 RNLRSYNPQYQYF 132

RESULT 9
PA23_BOTAS
ID   PA23_BOTAS   STANDARD;   PRT;   138 AA.
AC   Q9PVE3;
DT   28-FEB-2003 (Rel. 41, Created)
DT   28-FEB-2003 (Rel. 41, Last sequence update)
DT   28-FEB-2003 (Rel. 41, Last annotation update)
DE   Phospholipase A2 homolog 3 precursor (Myotoxin III) (M1-3-3).
OS   Bothrops asper (Terciopelo).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC   Viperidae; Crotalinae; Bothrops.
OX   NCBI_TaxID=8722;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Venom gland;
RA   Pescatori M., Grasso A., Rufini S.;
RT   "Molecular cloning of a K-49 PLA2-like myotoxin from the snake
RT   Bothrops asper.";
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RL   Submitted (NOV-1998) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: Myotoxic protein that lacks enzymatic activity (By
CC       similarity).
CC   -!- SUBCELLULAR LOCATION: Secreted (By similarity).
CC   -!- MISCELLANEOUS: Does not bind calcium as one of the calcium binding
CC       ligands is lost (Asp->Lys in position 64) (Probable).
CC   -!- SIMILARITY: Belongs to the phospholipase A2 family. Group II
CC       subfamily.
CC   --------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   --------
DR   EMBL; AF109911; AAF14241.1; -.
DR   HSSP; P24605; 1CLP.
DR   InterPro; IPR001211; PhospholipaseA2.
DR   Pfam; PF00068; phoslip; 1.
DR   PRINTS; PR00389; PHPHLIPASEA2.
DR   ProDom; PD000303; PhospholipaseA2; 1.
DR   SMART; SM00085; PA2c; 1.
DR   PROSITE; PS00119; PA2_ASP; 1.
DR   PROSITE; PS00118; PA2_HIS; 1.
KW   Toxin; Signal; Multigene family.
FT   SIGNAL         1     16       BY SIMILARITY.
FT   CHAIN         17    138       PHOSPHOLIPASE A2 HOMOLOG 3.
FT   ACT_SITE      63     63       BY SIMILARITY.
FT   ACT_SITE     105    105       BY SIMILARITY.
FT   DISULFID      42    132       BY SIMILARITY.
FT   DISULFID      44     60       BY SIMILARITY.
FT   DISULFID      59    111       BY SIMILARITY.
FT   DISULFID      65    138       BY SIMILARITY.
FT   DISULFID      66    104       BY SIMILARITY.
FT   DISULFID      73     97       BY SIMILARITY.
FT   DISULFID      91    102       BY SIMILARITY.
SQ   SEQUENCE     138 AA;  15559 MW;  AF7491F7E3049BF2 CRC64;

Query Match      40.0%;   Score 340.5;   DB 1;   Length 138;
Best Local Similarity 47.4%;   Pred. No. 1.7e-27;
Matches   64;   Conservative   21;   Mismatches   43;   Indels   7;   Gaps   4;

Qy    10 VVMAGVIPIQGGILNLNKMVKQVTGKMPILSYWPYGHCGLGGRGQPKDATDWCCQTHDC 69
            |::| ||: ||||||||||||||||||||||||||||||||||||| |||||||||
Db     9 VLLVGV--EGSLVELGKMILQETGKNPVTSYGAYGCNCGVLJGRGKPKDATDRCCYVHKC 65

Qy    70 CYDHLKTQGCGIYKDYYRYNFSQGNIHCSDKGSWCEQLCACDKEVAFCLKRNLDTYQKR 129
            ||:::|||::|::||:: :| ::: :|:  |:::: ::    :|:: :::|||:|:
Db    66 CYK--KLTGCNPKKDRYSYSWKDKTIVCGENNS-CLKELCECDKAVAICLRKNLDTYNKK 122

Qy   130 LR-FYWRPHCRGQTP 143
            || ::|:
Db   123 YKNNYLKPFCKKADP 137

RESULT 10
PA22_BOTMO
ID   PA22_BOTMO   STANDARD;   PRT;   122 AA.
AC   Q9I834;
DT   28-FEB-2003 (Rel. 41, Created)
DT   28-FEB-2003 (Rel. 41, Last sequence update)
DT   28-FEB-2003 (Rel. 41, Last annotation update)
DE   Phospholipase A2 homolog 2 (Myotoxin II) (MjTX-II) (M-VI).
OS   Bothrops moojeni (Lance-headed viper) (Caissaca).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC   Viperidae; Crotalinae; Bothrops.
OX   NCBI_TaxID=98334;
RN   [1]
RP   SEQUENCE OF 1-52, AND CHARACTERIZATION.
RC   TISSUE=Venom;
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```
RX   MEDLINE=98299483; PubMed=9637370;
RA   Soares A.M., Rodrigues V.M., Homsi-Brandeburgo M.I., Toyama M.H.,
RA   Lombardi F.R., Arni R.K., Giglio J.R.;
RT   "A rapid procedure for the isolation of the Lys-49 myotoxin II from
RT   Bothrops moojeni (caissaca) venom: biochemical characterization,
RT   crystallization, myotoxic and edematogenic activity.";
RL   Toxicon 36:503-514(1998).
RN   [2]
RP   SEQUENCE OF 15-122 FROM N.A.
RC   TISSUE=Venom gland;
RA   Soares A.M., Ward R.J., Rodrigues-Simioni L., Lomonte B.,
RA   Gutierrez J.M., Guerra-Sa R., Rodrigues V., Fontes M.R.M., Arni R.K.,
RA   Giglio J.R.;
RL   Submitted (APR-1999) to the EMBL/GenBank/DDBJ databases.
RN   [3]
RP   X-RAY CRYSTALLOGRAPHY.
RC   TISSUE=Venom;
RA   de Azevedo W.F., Ward R.J., Lombardi F.R., Giglio J.R., Soares A.M.,
RA   Fontes M.R.M., Arni R.K.;
RT   "Crystal structure of myotoxin-II: a myotoxic phospholipase A2
RT   homologue from Bothrops moojeni venom.";
RL   Protein Pept. Lett. 4:329-334(1997).
CC   -!- FUNCTION: Displays myotoxin and edema-inducing activities. Lacks
CC       PA2 enzymatic activities as well as of hemorrhagic, anticoagulant
CC       and coagulant activities.
CC   -!- SUBUNIT: Homodimer.
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- MISCELLANEOUS: Does not bind calcium as one of the calcium binding
CC       ligands is lost (Asp->Lys in position 48).
CC   -!- SIMILARITY: Belongs to the phospholipase A2 family. Group II
CC       subfamily.
CC   --------------------------------------------------------------------------
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CC   used by and for commercial
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   --------------------------------------------------------------------------
DR   EMBL; AF145759; AAF66702.1; -.
DR   HSSP; P82287; 1QLL.
DR   InterPro; IPR001211; Phospholipase A2.
DR   Pfam; PF00068; phoslip; 1.
DR   PRINTS; PD000303; Phospholipase A2.
DR   ProDom; PD000303; Phospholipase A2; 1.
DR   SMART; SM00085; PA2c; 1.
DR   PROSITE; PS00119; PA2_ASP; 1.
DR   PROSITE; PS00118; PA2_HIS; 1.
KW   Toxin; Multigene family.
FT   ACT_SITE      47     47       BY SIMILARITY.
FT   ACT_SITE      89     89       BY SIMILARITY.
FT   DISULFID      26    116       BY SIMILARITY.
FT   DISULFID      28     44       BY SIMILARITY.
FT   DISULFID      43     95       BY SIMILARITY.
FT   DISULFID      49    122       BY SIMILARITY.
FT   DISULFID      50     88       BY SIMILARITY.
FT   DISULFID      57     81       BY SIMILARITY.
FT   DISULFID      75     86       BY SIMILARITY.
FT   CONFLICT      18     18       A -> V (IN REF. 2).
SQ   SEQUENCE    122 AA;  13887 MW;  120AA53FAB3009CB CRC64;
```

Query Match   39.4%; Score 336; DB 1; Length 122;
Best Local Similarity   50.4%; Pred. No. 4.1e-27;
Matches   62; Conservative 15; Mismatches 42; Indels 4; Gaps 3;

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Qy   22 ILNLNKMVKQVTGKMPILSYWPYGCHCGLGGRGQPKDATDWCCQTHDCCYDHLKTQGCGI 81
         | ||: |:  |  || : ||:  |||| ||||:|||:||| |:||||  ||  | | |||
Db    2 LFELGKMIIQETGKNPAKSYGYGCNCGVGGRGKPKDATDRCCYVHKCCYK--KLTGCDP 59

Qy   82 YKDYRYRYNFSQGNIHCSDKGSWCEOQLCACDKEVAFCLKRNLDTYQKRLRF-YWRPHCRG 140
         |:||  |  :|||  |||  |   ||| || | : :|| |||| | :|: || |  ||| |
Db   60 KKDRYISYSWKDKTIVCGENNS-CLKELCECDKAVAICLRENLDTYNKKYRNYLKPFCKK 118
```

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RESULT 11
PA2F MOUSE
ID   PA2F_MOUSE     STANDARD;     PRT;   168 AA.
AC   Q9QZT4;
DT   28-FEB-2003 (Rel. 41, Created)
DT   28-FEB-2003 (Rel. 41, Last sequence update)
DT   10-OCT-2003 (Rel. 42, Last annotation update)
DE   Group IIF secretory phospholipase A2 precursor (EC 3.1.1.4)
DE   (Phosphatidylcholine 2-acylhydrolase GIIF) (GIIF sPLA2) (sPLA(2)-IIF).
GN   PLA2G2F.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=20002639; PubMed=10531313;
RA   Valentin E., Ghomashchi F., Gelb M.H., Lazdunski M., Lambeau G.;
RT   "On the diversity of secreted phospholipases A2. Cloning, tissue
RT   distribution, and functional expression of two novel mouse group II
RT   enzymes.";
RL   J. Biol. Chem. 274:31195-31202(1999).
CC   -!- FUNCTION: PA2 catalyzes the calcium-dependent hydrolysis of the 2-
CC       acyl groups in 3-sn-phosphoglycerides. Hydrolyzes
CC       phosphatidylglycerol versus phosphatidylcholine with a 15-fold
CC       preference (By similarity).
CC   -!- CATALYTIC ACTIVITY: Phosphatidylcholine + H(2)O = 1-
CC       acylglycerophosphocholine + a fatty acid anion.
CC   -!- COFACTOR: Binds 1 calcium ion per subunit.
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- SIMILARITY: Belongs to the phospholipase A2 family.
CC   --------------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   --------------------------------------------------------------------------
DR   EMBL; AF166099; AAF04500.2; -.
DR   HSSP; P00593; 4BP2.
DR   MGD; MGI:1349661; Pla2g2f.
DR   InterPro; IPR001211; Phospholipase A2.
DR   Pfam; PF00068; phoslip; 1.
DR   PRINTS; PR00389; PHPHLIPASEA2.
DR   ProDom; PD000303; Phospholipase A2; 1.
DR   SMART; SM00085; PA2c; 1.
DR   PROSITE; PS00119; PA2_ASP; FALSE_NEG.
DR   PROSITE; PS00118; PA2_HIS; 1.
KW   Hydrolase; Lipid degradation; Signal; Calcium.
FT   SIGNAL        1     20       POTENTIAL.
FT   CHAIN        21    168       GROUP IIF SECRETORY PHOSPHOLIPASE A2.
FT   ACT_SITE     67     67       BY SIMILARITY.
FT   ACT_SITE    114    114       BY SIMILARITY.
FT   DISULFID     46    138       BY SIMILARITY.
FT   DISULFID     48     64       BY SIMILARITY.
FT   DISULFID     63    145       BY SIMILARITY.
FT   DISULFID     69    113       BY SIMILARITY.
FT   DISULFID     70    106       BY SIMILARITY.
FT   DISULFID     79    111       BY SIMILARITY.
FT   DISULFID     98    111       BY SIMILARITY.
FT   CARBOHYD     92     92       N-LINKED (GLCNAC...)  (POTENTIAL).
FT   CARBOHYD    102    102       N-LINKED (GLCNAC...)  (POTENTIAL).
FT   CARBOHYD    144    144       N-LINKED (GLCNAC...)  (POTENTIAL).
FT   METAL        47     47       CALCIUM (VIA CARBONYL OXYGEN)
FT                                (BY SIMILARITY).
```

FT   METAL   49   49   CALCIUM (VIA CARBONYL OXYGEN)
FT   (BY SIMILARITY).
FT   METAL   51   51   CALCIUM (VIA CARBONYL OXYGEN)
FT   (BY SIMILARITY).
FT   METAL   68   68   CALCIUM (BY SIMILARITY).
SQ   SEQUENCE   168 AA;   18880 MW;   9E15FB6AC0F5450C CRC64;

Query Match   39.4%;   Score 336;   DB 1;   Length 168;
Best Local Similarity   42.8%;   Pred. No. 5.8e-27;
Matches   62;   Conservative   23;   Mismatches   52;   Indels   8;   Gaps   4;

Qy   3 LALICGLVVMAGVIPIQGGILNLNKMVKQVTGKMPILSYWPYGCHCGLGGRGQPKDATDW 62
         :|:|:|| ||:| :||| || || ||:||||||||
Db   7 IAVLAGSVVTTA---HSSLLNLKSMVEAITHRNSILSPVGYGCYCGLGGRGHPMDEVDW 62

Qy   63 CCQTHDCCYDHLKTQGCGIYKDYRYRNFSQGN-IHCSD-KGSWCEQQLCACDKEVAFCLK 120
         ||||||||||| || |:|: | |:: | ||| || ||||
Db   63 CCHAHDCCYEKLFEQGCRPYVDHYDHRIRENGTMVCTELNETECDKQTCBCDKSLTLCLK 122

Qy   121 RNLDTYQKRLRFYWRPHCRGQTPGC 145
         : :| : | :|:| :|:| ||:|
Db   123 DH--PYRNKYRGYFNVYCQGPTPNC 145

RESULT 12
PA2B_CRODU
ID   PA2B_CRODU   STANDARD;   PRT;   138 AA.
AC   P07517, P23559;
DT   01-APR-1988 (Rel. 07, Created)
DT   01-NOV-1988 (Rel. 09, Last sequence update)
DT   10-OCT-2003 (Rel. 42, Last annotation update)
DE   Phospholipase A2 CB1 precursor (EC 3.1.1.4) (Crotoxin basic chain 1)
DE   (Mojave toxin basic chain) (Mtx-b) (Phosphatidylcholine 2-
DE   acylhydrolase).
OS   Crotalus durissus terrificus (South American rattlesnake), and
OS   Crotalus scutulatus scutulatus (Mojave rattlesnake).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC   Viperidae; Crotalinae; Crotalus.
OX   NCBI_TaxID=8732, 8738;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   SPECIES=C.s.scutulatus; TISSUE=Venom gland;
RX   MEDLINE=89016587; PubMed=3174444;
RA   Ducancel F., Guignery Frelat G., Menez A., Boulain J.-C., Bouchier C.,
RA   Bon C.;
RT   "Cloning and sequencing of cDNAs encoding the two subunits of
RT   Crotoxin.";
RL   Nucleic Acids Res. 16:9050-9050(1988).
RN   [2]
RP   SEQUENCE OF 17-138.
RC   SPECIES=C.d.terrificus;
RX   MEDLINE=86321988; PubMed=3753003;
RA   Aird S.D., Kaiser I.I. Lewis R.V., Kruggel W.G.;
RT   "A complete amino acid sequence for the basic subunit of crotoxin.";
RL   Arch. Biochem. Biophys. 249:296-300(1986).
RN   [3]
RP   SEQUENCE FROM N.A.
RC   SPECIES=C.s.scutulatus; TISSUE=Liver;
RX   MEDLINE=94156205; PubMed=8112610;
RA   John T.R., Smith L.A., Kaiser I.I.;
RT   "Genomic sequences encoding the acidic and basic subunits of Mojave
RT   toxin: unusually high sequence identity of non-coding regions.";
RL   Gene 139:229-234(1994).
RN   [4]
RP   SEQUENCE OF 17-138.
RC   SPECIES=C.s.scutulatus; TISSUE=Venom;
RX   MEDLINE=90385490; PubMed=2402763;
RA   Aird S.D., Kruggel W.G., Kaiser I.I.;
RT   "Amino acid sequence of the basic subunit of Mojave toxin from the
RT   venom of the Mojave rattlesnake (Crotalus s. scutulatus).";
RL   Toxicon 28:669-673(1990).
RN   [5]

RP   SEQUENCE OF 17-49.
RC   SPECIES=C.d.terrificus; TISSUE=Venom;
RX   MEDLINE=94307256; PubMed=8033889;
RA   Faure G., Choumet V., Bouchier C., Camoin L., Guillaume J.-L.,
RA   Monegier B., Vuilhorgne M., Bon C.;
RT   "The origin of the diversity of crotoxin isoforms in the venom of
RT   Crotalus durissus terrificus.";
RL   Eur. J. Biochem. 223:161-164(1994).
CC   -!- FUNCTION: PA2 catalyzes the calcium-dependent hydrolysis of the 2-
CC   acyl groups in 3-sn-phosphoglycerides. Inhibits neuromuscular
CC   transmission by blocking acetylcholine release from the nerve
CC   termini. Acts presynaptically.
CC   -!- CATALYTIC ACTIVITY: Phosphatidylcholine + H(2)O = 1-
CC   acylglycerophosphocholine + a fatty acid anion.
CC   -!- COFACTOR: Binds 1 calcium ion per subunit (By similarity).
CC   -!- SUBUNIT: This toxin consists of 2 subunits: acidic and basic.
CC   The acidic subunit is nontoxic, without enzymatic activity and
CC   comprises 3 peptides that are crosslinked by 7 disulfide bridges.
CC   The basic subunit is toxic, has phospholipase A2 activity and is
CC   composed of a single chain.
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- TISSUE SPECIFICITY: Expressed by the venom gland.
CC   -!- SIMILARITY: Belongs to the phospholipase A2 family. Group II
CC   subfamily.
CC   ---
DR   EMBL; X12603; CAA31123.1; -.
DR   EMBL; U01027; AAC59674.1; -.
DR   PIR; I51381; I51381.
DR   PIR; S02257; PSRSBT.
DR   HSSP; P14421; 1A2A.
DR   InterPro; IPR001211; PhospholipaseA2.
DR   Pfam; PF00068; phoslip; 1.
DR   PRINTS; PR00389; PHPHLIPASEA2.
DR   ProDom; PD000303; PhospholipaseA2; 1.
DR   SMART; SM00085; PA2c; 1.
DR   PROSITE; PS00119; PA2_ASP; 1.
DR   PROSITE; PS00118; PA2_HIS; 1.
KW   Lipid degradation; Hydrolase; Toxin; Neurotoxin;
KW   Presynaptic neurotoxin; Calcium; Signal; Multigene family.
FT   SIGNAL   1   16
FT   CHAIN   17   138   PHOSPHOLIPASE A2 CB1.
FT   ACT_SITE   63   63   BY SIMILARITY.
FT   ACT_SITE   105   105   BY SIMILARITY.
FT   DISULFID   42   131   BY SIMILARITY.
FT   DISULFID   44   60   BY SIMILARITY.
FT   DISULFID   59   111   BY SIMILARITY.
FT   DISULFID   65   138   BY SIMILARITY.
FT   DISULFID   66   104   BY SIMILARITY.
FT   DISULFID   73   97   BY SIMILARITY.
FT   DISULFID   91   102   BY SIMILARITY.
FT   METAL   43   43   CALCIUM (VIA CARBONYL OXYGEN)
FT   (BY SIMILARITY).
FT   METAL   45   45   CALCIUM (VIA CARBONYL OXYGEN)
FT   (BY SIMILARITY).
FT   METAL   47   47   CALCIUM (VIA CARBONYL OXYGEN)
FT   (BY SIMILARITY).
FT   METAL   64   64   CALCIUM (BY SIMILARITY).
FT   CONFLICT   81   81   P -> R (IN REF. 3).
SQ   SEQUENCE   138 AA;   15907 MW;   84A11891DFFE2E3 CRC64;

Query Match   39.4%;   Score 335.5;   DB 1;   Length 138;
Best Local Similarity   46.3%;   Pred No. 5.3e-27;
Matches   63;   Conservative   18;   Mismatches   52;   Indels   3;   Gaps   2;

Qy   10 VVMAGVIPIQGGILNLNKMVKQVTGKMPILSYWPYGCHCGLGGRGQPKDATDWCCQTHDC 69

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              :| .||  ..::|  .:|     |||:|||:||||    |||     |||    |||
Db     6  IVAVLLVGVEGHLLQFNKMIKFETRKNAIPFYAFYGCYCGWGRGRPKDATDRCCFVHDC  65

Qy    70  CYDHLKTQGCGIYKDYYRYNFSQGNIHCSDKGSWCEQQLCACDKEVAFCLKRNLDTYQKR 129

Db    70  KLAKCNTKWDIYPYSLKSGYITCG-KGTWCEEQICECDRVAAECLRRSLSTYKYG 122

Qy   130  LRFYWRPHCRGQTPGC 145

Db   123  YMFYPDSRCRGPSETC 138


RESULT 13
PA2W_TRIFL      STANDARD;      PRT;    138 AA.
ID   PA2W_TRIFL
AC   Q02517;
DT   01-FEB-1994 (Rel. 28, Created)
DT   01-FEB-1994 (Rel. 28, Last sequence update)
DT   10-OCT-2003 (Rel. 42, Last annotation update)
DE   Phospholipase A2 isozyme PL-X' precursor (EC 3.1.1.4)
DE   (Phosphatidylcholine 2-acylhydrolase).
OS   Trimeresurus flavoviridis (Habu).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC   Viperidae; Crotalinae; Trimeresurus.
OX   NCBI_TaxID=88087;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Venom gland;
RX   MEDLINE=92409555; PubMed=1528861;
RA   Ogawa T., Oda N., Nakashima K.-I., Sasaki H., Hattori M., Sakaki Y.,
RA   Kihara H., Ohno M.;
RT   "Unusually high conservation of untranslated sequences in cDNAs for
RT   Trimeresurus flavoviridis phospholipase A2 isozymes.";
RL   Proc. Natl. Acad. Sci. U.S.A. 89:8557-8561(1992).
CC   -!- FUNCTION: PA2 catalyzes the calcium-dependent hydrolysis of the
CC       2-acyl groups in 3-sn-phosphoglycerides.
CC   -!- CATALYTIC ACTIVITY: Phosphatidylcholine + H(2)O = 1-
CC       acylglycerophosphocholine + a fatty acid anion.
CC   -!- COFACTOR: Binds 1 calcium ion per subunit (By similarity).
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- TISSUE SPECIFICITY: Expressed by the venom gland.
CC   -!- SIMILARITY: Belongs to the phospholipase A2 family. Group II
CC       subfamily.
CC   -------------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   -------------------------------------------------------------------------
DR   EMBL; D10721; BAA01564.1; -.
DR   HSSP; P51972; 1VAP.
DR   InterPro; IPR001211; PhospholipaseA2.
DR   Pfam; PF00068; phosLip; 1.
DR   PRINTS; PR00389; PHPHLIPASEA2.
DR   ProDom; PD000303; PhospholipaseA2; 1.
DR   SMART; SM00085; PA2c; 1.
DR   PROSITE; PS00119; PA2_ASP; 1.
DR   PROSITE; PS00118; PA2_HIS; 1.
KW   Hydrolase; Lipid degradation; Calcium; Multigene family; Signal.
FT   SIGNAL        1     16
FT   CHAIN        17    138       PHOSPHOLIPASE A2 ISOZYME PL-X'.
FT   ACT_SITE     63     63       BY SIMILARITY.
FT   ACT_SITE    105    105       BY SIMILARITY.
FT   DISULFID     42    131       BY SIMILARITY.
FT   DISULFID     44     60       BY SIMILARITY.
FT   DISULFID     59    111       BY SIMILARITY.
FT   DISULFID     65    138       BY SIMILARITY.
FT   DISULFID     66    104       BY SIMILARITY.
FT   DISULFID     73     97       BY SIMILARITY.
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FT   DISULFID     91    102       BY SIMILARITY.
FT   METAL        43     43       CALCIUM (VIA CARBONYL OXYGEN)
FT                                (BY SIMILARITY).
FT   METAL        45     45       CALCIUM (VIA CARBONYL OXYGEN)
FT                                (BY SIMILARITY).
FT   METAL        47     47       CALCIUM (VIA CARBONYL OXYGEN)
FT                                (BY SIMILARITY).
FT   METAL        64     64       CALCIUM (BY SIMILARITY).
SQ   SEQUENCE    138 AA;  15733 MW;  471B01878CCA1ED1 CRC64;

Query Match            39.0%;   Score 332; DB 1; Length 138;
Best Local Similarity  46.3%;   Pred. No. 1.2e-26;
Matches   63;  Conservative  19;  Mismatches  48;  Indels  6;  Gaps  3;

Qy    10  VVMAGVIPIQGGILNLNMVKQVTGKMPILSTWPYGCHCGLGGRGQPKDATDWCCQTHDC  69
             |:.||   ||:|||:|||   ||:||| |||||:|||||||||
Db     9  VLLVGV--EGHLLQFRKMIKKMTGKEPIVSYAFYGCYCGKGGRGPKDATDRCCFVHDC  65

Qy    70  CYDHLKTQGCGIYKDYYRYNFSQGNIHCSDKGSWCEQQLCACDKEVAFCLKRNLDTYQKR 129
          |||     ||:|| |:||:|||| |:..|||||  .:|:|.:.|...||...:|:.|
Db    66  CYE--KVTGCDPKWDYYTYSSENGDIVCGGDNP-CTKEVCECDKAAAICFRDNLKTYKKR 122

Qy   130  LRFYWRPHCRGQTPGC 145
          |||:||||||| ||:|
Db   123  YMTFPDIFCTDPTEKC 138


RESULT 14
PA2C_CRODU      STANDARD;      PRT;    138 AA.
ID   PA2C_CRODU
AC   P24027;
DT   01-MAR-1992 (Rel. 21, Created)
DT   01-MAR-1992 (Rel. 21, Last sequence update)
DT   10-OCT-2003 (Rel. 42, Last annotation update)
DE   Phospholipase A2 CB2 precursor (EC 3.1.1.4) (Crotoxin basic chain 2)
DE   (Phosphatidylcholine 2-acylhydrolase).
OS   Crotalus durissus terrificus (South American rattlesnake).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC   Viperidae; Crotalinae; Crotalus.
OX   NCBI_TaxID=8732;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Venom gland;
RX   MEDLINE=91198145; PubMed=2015302;
RA   Bouchier C., Boulain J.-C., Bon C., Menez A.;
RT   "Analysis of cDNAs encoding the two subunits of crotoxin, a
RT   phospholipase A2 neurotoxin from rattlesnake venom: the acidic non
RT   enzymatic subunit derives from a phospholipase A2-like precursor.";
RL   Biochim. Biophys. Acta 1088:401-408(1991).
RN   [2]
RP   SEQUENCE OF 17-49.
RC   TISSUE=Venom;
RX   MEDLINE=94307256; PubMed=8033889;
RA   Faure G., Choumet V., Bouchier C., Camoin L., Guillaume J.-L.,
RA   Monegier B., Vuilhorgne M., Bon C.;
RT   "The origin of the diversity of crotoxin isoforms in the venom of
RT   Crotalus durissus terrificus.";
RL   Eur. J. Biochem. 223:161-164(1994).
CC   -!- FUNCTION: PA2 catalyzes the calcium-dependent hydrolysis of the 2-
CC       acyl groups in 3-sn-phosphoglycerides. Inhibits neuromuscular
CC       transmission by blocking acetylcholine release from the nerve
CC       termini. Acts presynaptically.
CC   -!- CATALYTIC ACTIVITY: Phosphatidylcholine + H(2)O = 1-
CC       acylglycerophosphocholine + a fatty acid anion.
CC   -!- COFACTOR: Binds 1 calcium ion per subunit (By similarity).
CC   -!- SUBUNIT: Crotoxin consists of 2 subunits: CA and CB. CA is acidic,
CC       nontoxic, without enzymatic activity and comprises 3 peptides that
CC       are crosslinked by 7 disulfide bridges. CB is basic, toxic, has
CC       phospholipase A2 activity and is composed of a single chain.
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- SIMILARITY: Belongs to the phospholipase A2 family. Group II
CC       subfamily.
```

```
RX   MEDLINE=99183869; PubMed=10084123;
RA   Fan C.Y., Qian Y.C., Yang S.L., Gong Y.;
RT   "cDNA cloning and sequence analysis of Lys-49 phospholipase A2 from
RT   Agkistrodon acutus.";
RL   Genet. Anal. 15:15-18(1999).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Venom gland;
RX   MEDLINE=22478853; PubMed=11594738;
RA   Tsai I.-H., Chen Y.-H., Wang Y.-M., Tu M.-C., Tu A.T.;
RT   "Purification, sequencing, and phylogenetic analyses of novel Lys-49
RT   phospholipases A(2) from the venoms of rattlesnakes and other pit
RT   vipers.";
RL   Arch. Biochem. Biophys. 394:236-244(2001).
-!-  FUNCTION: Myotoxic protein that lacks PA2 enzymatic activity.
-!-  SUBCELLULAR LOCATION: Secreted (By similarity).
-!-  TISSUE SPECIFICITY: Expressed by the venom gland.
-!-  MISCELLANEOUS: Does not bind calcium as one of the calcium binding
CC       ligands is lost (Asp->Lys in position 64).
-!-  SIMILARITY: Belongs to the phospholipase A2 family. Group II
CC       subfamily.
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DR   EMBL; AJ223188; CAA11159.1; -.
DR   EMBL; AF269132; AAL36975.1; -.
DR   PDB; 1MC2; 21-AUG-02.
DR   PDB; 1MG6; 04-SEP-02.
DR   InterPro; IPR001211; PhospholipaseA2.
DR   Pfam; PF00068; phoslip; 1.
DR   PRINTS; PR00389; PHPHLIPASEA2.
DR   ProDom; PD000303; PhospholipaseA2; 1.
DR   SMART; SM00085; PA2c; 1.
DR   PROSITE; PS00119; PA2_ASP; 1.
DR   PROSITE; PS00118; PA2_HIS; 1.
KW   Toxin; Signal; 3D-structure.
FT   SIGNAL        1     16
FT   CHAIN        17    138       PHOSPHOLIPASE A2 HOMOLOG DAC-K49II.
FT   ACT_SITE     63     63       BY SIMILARITY.
FT   ACT_SITE    105    105       BY SIMILARITY.
FT   DISULFID     42    131       BY SIMILARITY.
FT   DISULFID     44     60       BY SIMILARITY.
FT   DISULFID     59    111       BY SIMILARITY.
FT   DISULFID     65    138       BY SIMILARITY.
FT   DISULFID     66    104       BY SIMILARITY.
FT   DISULFID     73     97       BY SIMILARITY.
FT   DISULFID     91    102       BY SIMILARITY.
FT   CONFLICT    130    130       S -> L (IN REF. 2).
SQ   SEQUENCE   138 AA;  15777 MW;  1353CD8C8F54DA99 CRC64;

Query Match             38.8%;  Score 330.5;  DB 1;  Length 138;
Best Local Similarity   43.4%;  Pred. No. 1.7e-26;
Matches    59;  Conservative   21;  Mismatches   53;  Indels    3;  Gaps    2;

Qy         10 VVMAGVIPIQGGILNLNKMVKQVTGKMPILSYWPYGCHCGLGGRGQPKDATDWCCQTHDC 69
              :|::|:.::|||:||||| ||:::: ||::||:||:||||:|:||||  ||:|||
Db          6 IVAVLLVGVBEGSLFLPGKMIWQETGKNPVKNYGLYGCNCGVGGRGEPLDATDRCCFVHKC 65

Qy         70 CYDHLKTQGCGIYKDYYRYNFSQGNIHCSDKGSWCEQQLCACDKEVAFCLKRNLDTYQKR 129
              ||:|| :|||||||:|| |:||:::|:|:|| ||| : :|.|:|||| |||:||||
Db         66 CYK--KLTDCDSKKDRYSYKWKNKAIVCG-KGTWCKEQICECDRVAAEClRRSLSTYKNE 122

Qy        130 LRFYWRPHCRGQTPGC 145
              |||:|||||:|.:
Db        123 FRYHLKPSCKKTSEQC 138
```

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DR   EMBL; X16100; CAA34227.1; -.
DR   PIR; S15068; PSR8B2.
HSSP; P14421; 1A2A.
DR   InterPro; IPR001211; PhospholipaseA2.
DR   Pfam; PF00068; phoslip; 1.
DR   PRINTS; PR00389; PHPHLIPASEA2.
DR   ProDom; PD000303; PhospholipaseA2; 1.
DR   SMART; SM00085; PA2c; 1.
DR   PROSITE; PS00119; PA2_ASP; 1.
DR   PROSITE; PS00118; PA2_HIS; 1.
KW   Hydrolase; Lipid degradation; Calcium; Signal; Multigene family.
FT   SIGNAL        1     16
FT   CHAIN        17    138       PHOSPHOLIPASE A2 CB2.
FT   ACT_SITE     63     63       BY SIMILARITY.
FT   ACT_SITE    105    105       BY SIMILARITY.
FT   DISULFID     42    131       BY SIMILARITY.
FT   DISULFID     44     60       BY SIMILARITY.
FT   DISULFID     59    111       BY SIMILARITY.
FT   DISULFID     65    138       BY SIMILARITY.
FT   DISULFID     66    104       BY SIMILARITY.
FT   DISULFID     73     97       BY SIMILARITY.
FT   DISULFID     91    102       BY SIMILARITY.
FT   METAL        43     43       CALCIUM (VIA CARBONYL OXYGEN)
FT                                (BY SIMILARITY).
FT   METAL        45     45       CALCIUM (VIA CARBONYL OXYGEN)
FT                                (BY SIMILARITY).
FT   METAL        47     47       CALCIUM (VIA CARBONYL OXYGEN)
FT                                (BY SIMILARITY).
FT   METAL        64     64       CALCIUM (BY SIMILARITY).
SQ   SEQUENCE   138 AA;  15968 MW;  935D12258D47B058 CRC64;

Query Match             38.9%;  Score 331.5;  DB 1;  Length 138;
Best Local Similarity   44.1%;  Pred. No. 1.3e-26;
Matches    60;  Conservative   21;  Mismatches   52;  Indels    3;  Gaps    2;

Qy         10 VVMAGVIPIQGGILNLNKMVKQVTGKMPILSYWPYGCHCGLGGRGQPKDATDWCCQTHDC 69
              :|::|:.::|||:|||||:||:::: ||::||:||:|||| |:||||  ||:|||
Db          6 IVAVLLVGVBEGSLLQFNKMIKFETRKNAVPPYAFYGCYCGWGGQGRPKDATDRCCFVHDC 65

Qy         70 CYDHLKTQGCGIYKDYYRYNFSQGNIHCSDKGSWCEQQLCACDKEVAFCLKRNLDTYQKR 129
              ||:||:|||||||:|| |:||::: |||:|| ||| |: :|.|:|||  |||:||:|
Db         66 CYG--KLAKCNTKWDIYRYSLKSGYITCG-KGTWCKEQICECDRVAAEClRRSLSTYKNE 122

Qy        130 LRFYWRPHCRGQTPGC 145
              |||:|||||:|.:
Db        123 YMFYPDSRCREPSETC 138
```

```
RESULT 15
PA2H_AGKAC
ID   PA2H_AGKAC     STANDARD;       PRT;    138 AA.
AC   O57385; Q8UVZ5;
DT   28-FEB-2003 (Rel. 41, Created)
DT   28-FEB-2003 (Rel. 41, Last sequence update)
DT   10-OCT-2003 (Rel. 42, Last annotation update)
DE   Phospholipase A2 homolog Dac-K49II precursor.
OS   Agkistrodon acutus (Hundred-pace snake) (Deinagkistrodon acutus).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC   Viperidae; Crotalinae; Deinagkistrodon.
OX   NCBI_TaxID=36307;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Venom gland;
```

us-09-830-321a-1.rsp

Fri Oct 8 10:22:31 2004

Search completed: October 5, 2004, 19:25:30
Job time : 6.8 secs

```
               GenCore version 5.1.6
          Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on:    October 5, 2004, 18:51:24 ; Search time 28.8067 Seconds
                                       (without alignments)
                                       1588.179 Million cell updates/sec

Title:        US-09-830-321A-1
Perfect score: 852
Sequence:     1 MEIALLCGLVVMAGVIPIQG........YQKRLRFYWRPHCRGQTPGC 145

Scoring table: BLOSUM62
               Gapop 10.0 , Gapext 0.5

Searched:      1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters:    1017041

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   SPTREMBL 25:*
               1: sp_archea:*
               2: sp_bacteria:*
               3: sp_fungi:*
               4: sp_human:*
               5: sp_invertebrate:*
               6: sp_mammal:*
               7: sp_mhc:*
               8: sp_organelle:*
               9: sp_phage:*
              10: sp_plant:*
              11: sp_rodent:*
              12: sp_virus:*
              13: sp_vertebrate:*
              14: sp_unclassified:*
              15: sp_rvirus:*
              16: sp_bacteriap:*
              17: sp_archeap:*
```

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Match Length	DB	ID	Description
1	400.5	47.0	146	11	Q91Y34	Q91y34 rattus norv
2	389	45.7	154	11	Q9QX68	Q9qx68 mesocricetu
3	352	41.3	168	4	Q8N217	Q8n217 homo sapien
4	347	40.7	187	4	Q8N435	Q8n435 homo sapien
5	336	39.4	210	11	Q8CE14	Q8ce14 mus musculu
6	334	39.2	137	13	Q804D7	Q804d7 bothrops ja
7	330	38.7	202	11	Q8BJ93	Q8bj93 mus musculu
8	314	36.9	138	13	Q805A3	Q805a3 trimeresuru
9	312.5	36.7	136	13	Q7T3S7	Q7t3s7 echis carin
10	309	36.3	138	13	Q805A2	Q805a2 trimeresuru
11	306.5	36.0	138	13	Q7T1D5	Q7t1d5 vipera beru
12	296.5	34.8	150	11	Q8K0Y1	Q8k0y1 mus musculu
13	295.5	34.7	138	13	Q7ZZQ1	Q7zzq1 vipera russ
14	294	34.5	138	13	Q8AXY1	Q8axy1 bothrops ja
15	289.5	34.0	138	13	Q7T1C6	Q7t1c6 vipera aspi
16	283.5	33.3	138	13	Q7T2R1	Q7t2r1 vipera russ
17	274.5	32.2	138	13	Q7T1D1	Q7t1d1 vipera beru
18	269.5	31.6	138	13	Q7T1D4	Q7t1d4 vipera aspi
19	269.5	31.6	138	13	Q7T1D3	Q7t1d3 vipera aspi
20	269.5	31.6	138	13	Q7T1D2	Q7t1d2 vipera aspi
21	261.5	30.7	138	13	Q800C2	Q800c2 crotalus vi
22	260.5	30.6	138	13	Q800C4	Q800c4 crotalus vi
23	260.5	30.6	138	13	Q800C1	Q800c1 crotalus vi
24	259.5	30.5	138	13	Q7ZTA7	Q7zta7 crotalus vi
25	255.5	30.0	138	13	Q800C3	Q800c3 crotalus vi
26	255.5	30.0	141	11	Q8CSY6	Q8csy6 mus musculu
27	251.5	29.5	130	13	Q7T3T5	Q7t3t5 vipera russ
28	246	28.9	138	13	Q7ZTA8	Q7zta8 crotalus vi
29	244	28.6	138	13	Q7ZTA6	Q7zta6 crotalus vi
30	234	27.5	147	13	Q7ZW60	Q7zw60 rana catesb
31	222.5	26.1	147	13	Q7T2Q5	Q7t2q5 bungarus fl
32	221.5	26.0	156	5	Q8WS88	Q8ws88 adamsia car
33	218.5	25.6	147	13	Q7T2Q4	Q7t2q4 bungarus fl
34	210.5	24.7	146	13	Q7T1R0	Q7t1r0 bungarus fl
35	208	24.4	142	13	Q802I1	Q802i1 bungarus ca
36	199	23.4	453	11	Q802M2	Q802m2 mus musculu
37	198.5	23.3	146	13	Q8AXW2	Q8axw2 bungarus mu
38	197.5	23.2	144	11	Q8K130	Q8k130 mus musculu
39	196.5	23.1	145	13	Q8AXW0	Q8axw0 bungarus mu
40	196	23.0	149	13	Q9YH62	Q9yh62 dicentrarch
41	196	23.0	149	13	O57313	O57313 pagrus majo
42	192.5	22.6	167	5	Q86DU7	Q86du7 polyandroca
43	192	22.5	177	5	Q8IML0	Q8iml0 drosophila
44	189.5	22.2	146	13	Q8AXW7	Q8axw7 micrurus co
45	189	22.2	137	13	Q8AY48	Q8ay48 bungarus ca

ALIGNMENTS

```
RESULT 1
Q91Y34
ID   Q91Y34      PRELIMINARY;      PRT;    146 AA.
AC   Q91Y34;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Platelet phospholipase A2 precursor (Fragment).
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Wistar; TISSUE=Blood;
RA   Liu T.T., Liang N.S., Meng Z.Q., Xie Y.A., Kuang Z.P., Li Y.;
RT   "Cloning and sequence determination of rat platelet phospholipase A2
RT   from whole blood.";
RL   Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF365363; AAK52061.1; -.
DR   GO; GO:0005509; F:calcium ion binding; IEA.
DR   GO; GO:0004623; F:phospholipase A2 activity; IEA.
DR   GO; GO:0016042; P:lipid catabolism; IEA.
DR   InterPro; IPR001211; PhospholipaseA2.
DR   Pfam; PF00068; phoslip; 1.
DR   PRINTS; PR00389; PHPHLIPASEA2.
DR   ProDom; PD000303; PhospholipaseA2; 1.
DR   SMART; SM000085; PA2c; 1.
DR   PROSITE; PS00119; PA2_ASP; 1.
DR   PROSITE; PS00118; PA2_HIS; 1.
KW   Signal.
FT   SIGNAL        1     21
FT   CHAIN        22   >146       PLATELET PHOSPHOLIPASE A2.
FT   NON_TER     146    146       POTENTIAL.
SQ   SEQUENCE  146 AA;  16306 MW;  6C1C9EC85DCBD67 CRC64;

Query Match    47.0%;   Score 400.5;   DB 11;  Length 146;
Best Local Similarity   47.9%;   Pred. No. 3e-38;
Matches   70;  Conservative   23;  Mismatches   52;  Indels   1;  Gaps   1;
```

```
Qy        1 MELALLCGLVVMA-GVIPIQGGILNLNKMVKQVTGKMPILSYWPYGCHCGLGGRGQPKDA  59
            |::||::||  ::||| :||| :|: |||
Db        1 MKVLLLLAVVIMAFGSIQVQSLLEFGQMIPFKTGKRADVSYGFYGCHCGVGGRGSPKDA   60

Qy       60 TDWCCQTHDCCYDHLKTQGCGIYKDYYRYNFSQGNIHCSDKGSWCEQQLCACDKEVAFCL  119
            |||||:|||||||||||:||||||||||||||||:||||| |:|||||||:| ::||
Db       61 TDWCCVTHDCCYNRLEKRGCGTKFLTYKFSYRGGRISCSTNQDSCRKQLCQCCDKAAAECF  120

Qy      120 KRNLDTYQKRLRFYWRPHCRGQTPGC  145
            |:||||| |:|| :|:||
Db      121 ARNKKSYSLKYQFYPNKFCKGKTPSC  146

RESULT 2
Q9QX68
ID   Q9QX68;
AC   Q9QX68;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Src-associated phospholipase A2 precursor (EC 3.1.1.4).
GN   SRPLA2.
OS   Mesocricetus auratus (Golden hamster).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
OC   Mesocricetus.
OX   NCBI_TaxID=10036;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Fibroblast;
RA   Mizenina O., Musatkina E., Yanushevich Y., Rodina A., Krasilnikov M.,
RA   De Gunzburg J., Camonis J., Tavitian A., Tatosyan A.;
RT   "A novel group IIA phospholipase A2 interacts with v-Src oncoprotein
RT   from RSV-transformed hamster cells.";
RL   J. Biol. Chem. 27606:34006-34012(2001).
DR   EMBL; AJ251361; CAB62564.1; -.
DR   HSSP; P14555; 1POD.
DR   GO; GO:0005509; F:calcium ion binding; IEA.
DR   GO; GO:0004627; F:calcium-dependent cytosolic phospholipase A. . .; IEA.
DR   GO; GO:0004625; F:calcium-dependent secreted phospholipase A2. . .; IEA.
DR   GO; GO:0004628; F:calcium-independent cytosolic phospholipase. . .; IEA.
DR   GO; GO:0004626; F:cytosolic phospholipase A2 activity; IEA.
DR   GO; GO:0016787; F:hydrolase activity; IEA.
DR   GO; GO:0004623; F:phospholipase A2 activity; IEA.
DR   GO; GO:0004624; F:secreted phospholipase A2 activity; IEA.
DR   GO; GO:0016042; P:lipid catabolism; IEA.
DR   InterPro; IPR001211; PhospholipaseA2.
DR   Pfam; PF00068; phoslip; 1.
DR   PRINTS; PR00389; PHPHLIPASERA2.
DR   ProDom; PD000303; PhospholipaseA2; 1.
DR   SMART; SM00085; PA2c; 1.
DR   PROSITE; PS00119; PA2_ASP; 1.
DR   PROSITE; PS00118; PA2_HIS; 1.
KW   Hydrolase; Signal.
FT   SIGNAL         1     21       POTENTIAL.
FT   CHAIN         22    154       SRC-ASSOCIATED PHOSPHOLIPASE A2.
SQ   SEQUENCE   154 AA;  17217 MW;  F5E0A76CE441772C CRC64;

Query Match             45.7%;  Score 389;  DB 11;  Length 154;
Best Local Similarity   48.3%;  Pred. No. 6.7e-37;
Matches   69;  Conservative   21;  Mismatches   53;  Indels   0;  Gaps   0;

Qy        3 LALLCGLVVMAGVIPIQGGILNLNKMVKQVTGKMPILSYWPYGCHCGLGGRGQPKDATDW   62
            |:| || ::||||||||||||||||||||::|||||:|||||||||||||||||||||||
Db        4 LLLLAALIMVFGPIQIQGSLAELNRMIWQLTGMRAGLSYAFYGCHCGLGGRGSPKDATDW   63

Qy       63 CCQTHDCCYDHLKTQGCGIYKDYYRYNFSQGNIHCSDKGSWCEQQLCACDKEVAFCLKRN  122
            |||||||||||||||||||||:|||||||::|||||||:||||||||||||||||  ||:
Db       64 CCAAHDCCYDRLEDLGCGTKSLDYNFKYSRGEITCSVNQDFCGGQLCHCDRLLAECLAQH  123

Qy      123 LDTYQKRLRFYWRPHCRGQTPGC  145
            :| |||||||||||||||
```

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Db      124 QKSYSWKYLMGIKKSCEGESPSC  146

RESULT 3
Q8N217
ID   Q8N217;                     PRELIMINARY;    PRT;    168 AA.
AC   Q8N217;
DT   01-OCT-2002 (TrEMBLrel. 22, Created)
DT   01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Hypothetical protein FLJ36326.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Thymus;
RA   Oshima A., Takahashi-Fujii A., Tanase T., Imose N., Takeuchi K.,
RA   Arita M., Musashino K., Yuuki H., Hara H., Sugiyama T., Irie R.,
RA   Otsuki T., Sato H., Ota T., Wakamatsu A., Ishii S., Yamamoto J.,
RA   Isono Y., Kawai-Hio Y., Saito K., Nishikawa T., Kimura K.,
RA   Yamashita H., Matsuo K., Nakamura Y., Sekine M., Kikuchi H., Kanda K.,
RA   Wagatsuma M., Murakawa K., Kanehori K., Sugiyama A., Kawakami B.,
RA   Suzuki Y., Sugano S., Nagahari K., Masuho Y., Nagai K., Isogai T.;
RT   "NEDO human cDNA sequencing project.";
RL   Submitted (JUL-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AK093645; BAC04210.1; -.
DR   GO; GO:0005509; F:calcium ion binding; IEA.
DR   GO; GO:0004623; F:phospholipase A2 activity; IEA.
DR   GO; GO:0016042; P:lipid catabolism; IEA.
DR   InterPro; IPR001211; PhospholipaseA2.
DR   Pfam; PF00068; phoslip; 1.
DR   PRINTS; PR00389; PHPHLIPASRA2.
DR   ProDom; PD000303; PhospholipaseA2; 1.
DR   SMART; SM00085; PA2c; 1.
DR   PROSITE; PS00118; PA2_HIS; 1.
KW   Hypothetical protein.
SQ   SEQUENCE   168 AA;  18586 MW;  35B1592A34A6A762 CRC64;

Query Match             41.3%;  Score 352;  DB 4;  Length 168;
Best Local Similarity   45.5%;  Pred. No. 1.4e-32;
Matches   66;  Conservative   19;  Mismatches   52;  Indels   8;  Gaps   4;

Qy        3 LALLCGLVVMAGVIPIQGGILNLNKMVKQVTGKMPILSYWPYGCHCGLGGRGQPKDATDW   62
            :|:|| |  :||||||||||:  ::||||| :|:||||| ||:|||||| :|||:|||||
Db        7 VAILAGSVLSTA---HGSLLNLKAMVEAVTGRSAILSFVGYGYCGLGGRGQPKDEVDW   62

Qy       63 CCQTHDCCYDHLKTQGCGIYKDYYRYNFSQG-NIHCSD-KGSWCEQQLCACDKEVAFCLK  120
            |||||||||:|| |:||||  :|| | |  : ||| || |:|||||||| | ||| ||
Db       63 CCHAHDCCYQELFDQGCHPVDHYDHTIENNTEIVCSDLNKTECDKQTCMCDKNMVLCLM  122

Qy      121 RNLDTYQKRLRFYWRPHCRGQTPGC  145
            ||| ||||||||||||||:||
Db      123 N--QTYREBYRGFLNVYCQGPTPNC  145

RESULT 4
Q8N435
ID   Q8N435;                     PRELIMINARY;    PRT;    187 AA.
AC   Q8N435;
DT   01-OCT-2002 (TrEMBLrel. 22, Created)
DT   01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Hypothetical protein (Fragment).
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Brain;
RA   Strausberg R.;
```

```
Db    49  IAVLAGSVVTTA----HSSLLNLKSMVEAITHRNSILSFVGYGCYGLGGRGHPMDEVDW  104
Qy    63  CCQTHDCCYDHLKTQGCGIYKDYRYNFSQGN-IHCSD-KGSWCEQQLCACDKEVAFCLK  120
Db   105  CCHAHDCCYEKLFEQGCRPVDHYDHRIENGTMIVCTELNETECDKQTCECDKSLTLCLK  164

Qy   121  RNLDTYQKRLRFYWRPHCRGQTPGC  145
Db   165  DH--PYRNKYRGYFNVYCCGPTPNC  187
```

RESULT 6
```
ID    Q804D7         PRELIMINARY;       PRT;    137 AA.
AC    Q804D7;
DT    01-JUN-2003 (TrEMBLrel. 24, Created)
DT    01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT    01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE    Myotoxic phospholipase A2-like (Myotoxic A2-like phospholipase).
OS    Bothrops jararacussu (Jararacussu)
OC    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC    Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC    Viperidae; Crotalinae; Bothrops.
OX    NCBI_TaxID=8726;
RN    [1]
RP    SEQUENCE FROM N.A.
RX    MEDLINE=20472069; PubMed=11018293;
RA    Andriao-Escarso S.H., Soares A.M., Rodrigues V.M., Angulo Y., Diaz C.,
RA    Lomonte B., Gutierrez J.M., Giglio J.R.;
RT    "Myotoxic phospholipases A(2) in bothrops snake venoms: effect of
RT    chemical modifications on the enzymatic and pharmacological properties
RT    of bothropstoxins from Bothrops jararacussu.";
RL    Biochimie 82:755-763 (2000).
RN    [2]
RP    SEQUENCE FROM N.A.
RA    Kashima S., Soares A.M., Roberto P.G., Astolfi-Filho S., Pereira J.O.,
RA    Silva M.X., Giulliati S., Farias M. Jr., Giglio J.R., Franca S.C.;
RT    "Analysis of Bothrops jararacussu Venomous Gland Transcriptome with
RT    structural and Functional Categories: Gene Expression Profile of
RT    Phospholipases A2.";
RL    Submitted (NOV-2002) to the EMBL/GenBank/DDBJ databases.
RN    [3]
RP    SEQUENCE FROM N.A.
RA    Hayashi M.A.F., Queiroz G.P., Radis-Baptista G., Yamane T.,
RA    Camargo A.C.M.;
RT    "Bothrops jararacussu myotoxic phospholipase A2-like mRNA.";
RL    Submitted (MAY-2003) to the EMBL/GenBank/DDBJ databases.
DR    EMBL; AY185200; AAO27453.1; -.
DR    EMBL; AY299391; AAP57527.1; -.
DR    GO; GO:0005509; F:calcium ion binding; IEA.
DR    GO; GO:0004623; F:phospholipase A2 activity; IEA.
DR    GO; GO:0016042; P:lipid catabolism; IEA.
DR    InterPro; IPR001211; PhospholipaseA2.
DR    Pfam; PF00068; phoslip; 1.
DR    PRINTS; PR00389; PHPHLIPASEA2.
DR    ProDom; PD000303; PhospholipaseA2; 1.
DR    SMART; SM00085; PA2c; 1.
DR    PROSITE; PS00119; PA2_ASP; 1.
DR    PROSITE; PS00118; PA2_HIS; 1.
SQ    SEQUENCE   137 AA;   15497 MW;   7BB006BABC4DFC39 CRC64;

Query Match           39.2%;   Score 334;   DB 13;   Length 137;
Best Local Similarity 46.3%;   Pred. No. 1.4e-30;
Matches   62;   Conservative   19;   Mismatches   47;   Indels   6;   Gaps   3;

Qy    10  VVMAGVIPIQGGILNLNKMVKQVTGKMPILSYWPYGHCGLGGRGQPKDATDWCCQTHDC   69
Db     9  VLLVGV--EGSLFELGKMILQETGKNPAKSYGAYGCNCGVLGRGKPKDATDRCCVVHKC   65
Qy    70  CYDHLKTQGCGIYKDYRYNFSQGNIHCSDKGSWCEQQLCACDKEVAFCLKRNLDTYQKR  129
Db    66  CYK--KLTGCDPKKDRYSYSWKDKTIVCGENNP-CLKELCECDKAVAICLRENLGTYNKK 122
```

RL   Submitted (AUG-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC036792; AAH36792.1; -.
DR   GO; GO:0005509; F:calcium ion binding; IEA.
DR   GO; GO:0004623; F:phospholipase A2 activity; IEA.
DR   GO; GO:0016042; P:lipid catabolism; IEA.
DR   InterPro; IPR001211; PhospholipaseA2.
DR   Pfam; PF00068; phoslip; 1.
DR   PRINTS; PR00389; PHPHLIPASEA2.
DR   ProDom; PD000303; PhospholipaseA2; 1.
DR   SMART; SM00085; PA2c; 1.
DR   PROSITE; PS00119; PA2_ASP; 1.
DR   PROSITE; PS00118; PA2_HIS; 1.
KW   Hypothetical protein.
FT   NON_TER   1   1
SQ   SEQUENCE   187 AA;   20811 MW;   2DAA2274359A3A60 CRC64;

```
Query Match           40.7%;   Score 347;   DB 4;   Length 187;
Best Local Similarity 43.6%;   Pred. No. 6e-32;
Matches   58;   Conservative   27;   Mismatches   36;   Indels   12;   Gaps   2;

Qy    12  MAGVIP--------IQGGIILNLNKMVKQVTGKMPILSYWPYGHCGLGGRGQPKDDAT   60
Db    50  MKGLLPLAWFLACSVPAVQGGLLDLKSMIEKVTGKNALTNYGFYGCYCGWGRGRTPKDGT 109
Qy    61  DWCCQTHDCCYDHLKTQGCGIYKDYRYRNFSQGNIHCSDKDKGSWCEQQLCACDKEVAFCLK 120
Db   110  DWCCWAHDHCYGRLEEKGCNIRTQSYXYRFAWGVVTC-EPGPFCHVNLCACDRKLVYCLK  168

Qy   121  RNLDTYQKRLRFY  133
Db   169  RNLRSYNPQYQYF  181
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RESULT 5
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ID    Q8CE14         PRELIMINARY;       PRT;    210 AA.
AC    Q8CE14;
DT    01-MAR-2003 (TrEMBLrel. 23, Created)
DT    01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT    01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE    Phospholipase A2.
GN    PLA2G2E.
OS    Mus musculus (Mouse).
OC    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC    Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX    NCBI_TaxID=10090;
RN    [1]
RP    SEQUENCE FROM N.A.
RC    STRAIN=C57BL/6J; TISSUE=Head;
RX    MEDLINE=22354683; PubMed=12466851;
RA    The FANTOM Consortium,
RA    the RIKEN Genome Exploration Research Group Phase I & II Team;
RT    "Analysis of the mouse transcriptome based on functional annotation of
RT    60,770 full-length cDNAs.";
RL    Nature 420:563-573 (2002).
DR    EMBL; AK029254; BAC26357.1; -.
DR    MGD; MGI:1349660; Pla2g2e.
DR    GO; GO:0005509; F:calcium ion binding; IEA.
DR    GO; GO:0004623; F:phospholipase A2 activity; IEA.
DR    GO; GO:0016042; P:lipid catabolism; IEA.
DR    InterPro; IPR001211; PhospholipaseA2.
DR    Pfam; PF00068; phoslip; 1.
DR    PRINTS; PR00389; PHPHLIPASEA2.
DR    ProDom; PD000303; PhospholipaseA2; 1.
DR    SMART; SM00085; PA2c; 1.
DR    PROSITE; PS00118; PA2_HIS; 1.
SQ    SEQUENCE   210 AA;   23259 MW;   5AC55CD96F68FC28 CRC64;

Query Match           39.4%;   Score 336;   DB 11;   Length 210;
Best Local Similarity 42.8%;   Pred. No. 1.3e-30;
Matches   62;   Conservative   23;   Mismatches   52;   Indels   8;   Gaps   4;

Qy     3  LALLCGLVMAGVIPIQGGILNLNKMVKQVTGKMPILSYWPYGHCGLGGRGQPKDATDW   62
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Qy       130 LRFYWRPHCRGQTP 143
             |::| :||:|:|
Db       123 YRYHLKPFCKKADP 136


RESULT 7
Q8BJ93
ID   Q8BJ93;          PRELIMINARY;          PRT;   202 AA.
AC   Q8BJ93;
DT   01-MAR-2003 (TrEMBLrel. 23, Created)
DT   01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Calcium-dependent phospholipase A2 precursor.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=BALB/C;
RX   MEDLINE=22354683; PubMed=12466851;
RA   The FANTOM Consortium;
RA   the RIKEN Genome Exploration Research Group Phase I & II Team;
RT   "Analysis of the mouse transcriptome based on functional annotation of
RT   60,770 full-length cDNAs.";
RL   Nature 420:563-573 (2002).
DR   EMBL; AK090021; BAC41050.1; -.
DR   GO; GO:0005509; F:calcium ion binding; IEA.
DR   GO; GO:0004623; F:phospholipase A2 activity; IEA.
DR   GO; GO:0016042; P:lipid catabolism; IEA.
DR   InterPro; IPR001211; PhospholipaseA2.
DR   Pfam; PF00068; phoslip; 1
DR   PRINTS; PR00389; PHPHLIPASEA2.
DR   ProDom; PD000303; PhospholipaseA2; 1.
DR   SMART; SM00085; PA2c; 1.
DR   PROSITE; PS00119; PA2_ASP; 1.
DR   PROSITE; PS00118; PA2_HIS; 1.
SQ   SEQUENCE  202 AA;  22770 MW;  BDBA97C09F64F7C4 CRC64;

Query Match             38.7%;  Score 330;  DB 11;  Length 202;
Best Local Similarity   44.3%;  Pred. No. 6.1e-30;
  Matches  58;  Conservative  24;  Mismatches  43;  Indels  6;  Gaps  2;

Qy         8 GLVVMA-----GVIPIQGGILNLNKMVKQVTGKMPILSYWPYGCHCGLGGRGQPKDATDW 62
             |||||      :| |||| ||:||||| ||||: |||||||||||  ||||||
Db         3 GLLTLAWFLACSVPAVPGGLLELKSMIEKVTGKNAFKNYGFYGCYCGWGGRGITPKDGTDW 62

Qy        63 CCQTHDCCYDHLKTQGCGIYKDYYRYNFSQGNIHCSDKGSWCEQLCACDKEVAFCLKRN 122
             |||  |||| ||||||||||||||||||||| |||: |:|||: ||  || ||:|:|
Db        63 CCQMHDRCYGQLEEKDCAIRTQSYDYRYTNGLVIC-EHDSFCPMRLCACDRKLVYCLRRN 121

Qy       123 LDTYQKRLRFY 133
             :|||
Db       122 LWTYNPLYQYY 132


RESULT 8
Q805A3
ID   Q805A3;          PRELIMINARY;          PRT;   138 AA.
AC   Q805A3;
DT   01-JUN-2003 (TrEMBLrel. 24, Created)
DT   01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Phospholipase A2.
GN   PLA-N.
OS   Trimeresurus flavoviridis (Habu).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC   Viperidae; Crotalinae; Trimeresurus.
OX   NCBI_TaxID=88087;
RN   [1]
RP   SEQUENCE FROM N.A.
```

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RA   Chijiwa T., Hamai S., Tsubouchi S., Ogawa T., Deshimaru M.,
RA   Oda-Ueda N., Hattori S., Kihara H., Tsunazawa S., Ohno M.;
RT   "Interisland mutation of a novel phospholipase A2 from Trimeresurus
RT   flavoviridis venom and evolution of crotalinae group II phospholipase
RT   A2.";
RL   Submitted (FEB-2003) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AB102728; BAC56892.1; -.
DR   GO; GO:0005509; F:calcium ion binding; IEA.
DR   GO; GO:0004623; F:phospholipase A2 activity; IEA.
DR   GO; GO:0016042; P:lipid catabolism; IEA.
DR   InterPro; IPR001211; PhospholipaseA2.
DR   Pfam; PF00068; phoslip; 1.
DR   PRINTS; PR00389; PHPHLIPASEA2.
DR   ProDom; PD000303; PhospholipaseA2; 1.
DR   SMART; SM00085; PA2c; 1.
DR   PROSITE; PS00119; PA2_ASP; 1.
DR   PROSITE; PS00118; PA2_HIS; 1.
SQ   SEQUENCE  138 AA;  15817 MW;  A2F7B5A23897ECC5 CRC64;

Query Match             36.9%;  Score 314;  DB 13;  Length 138;
Best Local Similarity   44.9%;  Pred. No. 2.8e-28;
  Matches  61;  Conservative  19;  Mismatches  50;  Indels  6;  Gaps  3;

Qy        10 VVMAGVIPIQGGILNLNKMVKQVTGKMPILSYWPYGCHCGLGGRGQPKDATDWCCQTHDC 69
             |:::||   |||:|||||||||||||  |||||||||| |||| ||||||||||| |||
Db         9 VLLVGV--EGNLLQFNMKIKIWTKKNGFPFYTSYGCYCGWGGRGKPKDATDRCCFVHDC 65

Qy        70 CYDHLKTQGCGIYKDYYRYNFSQGNIHCSDKGSWCEQQLCACDKEVAFCLKRNLDTYQKR 129
             |:| |||  |||||||||||  | ||:| |:|||:|  |: ||:|| ||
Db        66 CYE--KLTDCSPKSDIYSYSWKTGVIICGB-GTECEKQICECDRAAAVCFGQNLRTYKKK 122

Qy       130 LRFYWRPHCRGQTPGC 145
             ||||||||||||
Db       123 YMFYPDFLCTDPTEKC 138


RESULT 9
Q7T3S7
ID   Q7T3S7;          PRELIMINARY;          PRT;   136 AA.
AC   Q7T3S7;
DT   01-OCT-2003 (TrEMBLrel. 25, Created)
DT   01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Phospholipase A2 (EC 3.1.1.4).
OS   Echis carinatus (Saw-scaled viper).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC   Viperidae; Viperinae; Echis.
OX   NCBI_TaxID=40353;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Venom gland;
RA   Jasti J., Murugan P., Alagiri S., Singh T.P.;
RT   "X-ray structure of acidic phospholipase A2 from Indian saw-scaled-
RT   viper (Echis carinatus) with a potent platelet aggregation inhibition
RT   activity.";
RL   Submitted (APR-2003) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AY268946; AAP41217.1; -.
KW   Hydrolase.
SQ   SEQUENCE  136 AA;  15523 MW;  39699DA1D01271BA CRC64;

Query Match             36.7%;  Score 312.5;  DB 13;  Length 136;
Best Local Similarity   41.2%;  Pred. No. 4.2e-28;
  Matches  56;  Conservative  22;  Mismatches  53;  Indels  5;  Gaps  3;

Qy        10 VVMAGVIPIQGGILNLNKMVKQVTGKMPILSYWPYGCHCGLGGRGQPKDATDWCCQTHDC 69
             |:::||   |||:|||||  :| |||||| :|||:||||| |||| ||||||||||| |||
Db         6 IVAVWLIAVEGNLYQFGRMIWNRTGKLPILSYGSYGCYCGWGGQGPPKDATDRCCLVHDC 65

Qy        70 CYDHLKTQGCGIYKDYYRYNFSQGNIHCSDKGSWCEQLCACDKEVAFCLKRNLDTYQKR 129
             |:| |||  |||||||||||  | ||:| |:|||:|  |: ||:|| ||
Db        66 CY--TRVGDCSPKMTLYSYRFENGDIICDNKDP-CKRAVCECDREAAICLGENVNTYDKK 122
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Qy  130 LRFYWRPHCRGQTPGC 145
            |:|:
Db  123 YKSY--EDCTEEVQEC 136

RESULT 10
Q805A2
ID   Q805A2      PRELIMINARY;      PRT;   138 AA.
AC   Q805A2;
DT   01-JUN-2003 (TrEMBLrel. 24, Created)
DT   01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   PLA-N(O).
GN   PLA2.
OS   Trimeresurus flavoviridis (Habu).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC   Viperidae; Crotalinae; Trimeresurus.
OX   NCBI_TaxID=88087;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Chijiwa T., Hamai S., Tsubouchi S., Ogawa T., Deshimaru M.,
RA   Oda-Ueda N., Hattori S., Kihara H., Tsunazawa S., Ohno M.;
RT   "Interisland mutation of a novel phospholipase A2 from Trimeresurus
RT   flavoviridis venom and evolution of crotalinae group II phospholipase
RT   A2.";
RL   Submitted (FEB-2003) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AB102729; BAC56893.1; -.
DR   GO; GO:0005509; F:calcium ion binding; IEA.
DR   GO; GO:0004623; F:phospholipase A2 activity; IEA.
DR   GO; GO:0016042; P:lipid catabolism; IEA.
DR   InterPro; IPR001211; PhospholipaseA2.
DR   Pfam; PF00068; phoslip; 1.
DR   PRINTS; PR00389; PHPHLIPASEA2.
DR   ProDom; PD000303; PhospholipaseA2; 1.
DR   SMART; SM00085; PA2c; 1.
DR   PROSITE; PS00119; PA2_ASP; 1.
DR   PROSITE; PS00118; PA2_HIS; 1.
SQ   SEQUENCE 138 AA; 15803 MW; A2F103123897ECC5 CRC64;

Query Match             36.3%;
Best Local Similarity   44.1%;   Score 309;   DB 13;   Length 138;   Pred. No. 1.1e-27;
Matches   60;   Conservative   19;   Mismatches   51;   Indels   6;   Gaps   3;

Qy   10 VVMAGVIPIQGGILNLNKMVKQVTGKMPILSYWPYGCHCGLGGRGQPKDATDWCCQTHDC 69
         |::|| |||||| ||:||:| |||||||||||||||||||||||
Db    9 VLLVGV--EGNLLQPNKMIKIMTKNGFPFYTSYGCYCGWGGRGKPKDATDRCCFVHDC 65

Qy   70 CYDHLKTQGCGIYKDYRYRNFSQGNIHCSDKGSWCEQQLCACDKEVAFCLKRNLDTYQKR 129
         |:: ||::|  |||:||  ::|||||||||||||:||||||||||||||:|: : :
Db   66 CYE--KLTDCSPKSDYSYSWKTGVIICGE-GTECKQICECDRAAAVCFGQNLRTYKNK 122

Qy  130 LRFYWRPHCRGQTPGC 145
         ||||||||||||||||
Db  123 YMFYPDFLCTDPTEKC 138

RESULT 11
Q7T1D5
ID   Q7T1D5      PRELIMINARY;      PRT;   138 AA.
AC   Q7T1D5;
DT   01-OCT-2003 (TrEMBLrel. 25, Created)
DT   01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Phospholipase A2.
GN   PLA2VB.
OS   Vipera berus berus (Common viper).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC   Viperidae; Viperinae; Vipera.
OX   NCBI_TaxID=31156;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=22707820; PubMed=12823540;
RA   Guillemin I., Bouchier C., Garrigues T., Wisner A., Choumet V.;
RT   "Sequences and structural organization of phospholipase A2 genes from
RT   Vipera aspis aspis, V. aspis zinnikeri and Vipera berus berus venom.
RT   Identification of the origin of a new viper population based on
RT   ammodytin I1 heterogeneity.";
RL   Eur. J. Biochem. 270:2697-2706(2003).
DR   EMBL; AY158636; AAN59982.1; -.
SQ   SEQUENCE 138 AA; 15716 MW; 79B9F9E0D16C9CCB CRC64;

Query Match             36.0%;
Best Local Similarity   37.5%;   Score 306.5;   DB 13;   Length 138;   Pred. No. 2.1e-27;
Matches   51;   Conservative   27;   Mismatches   55;   Indels   3;   Gaps   2;

Qy   10 VVMAGVIPIQGGILNLNKMVKQVTGKMPILSYWPYGCHCGLGGRGQPKDATDWCCQTHDC 69
         :|: ::||: : |:|| ||
Db    6 IVAVWLMGVEGNLFQFGNMINHMVGKHAVWSYLSYGCYCGWGGQGKPQDATDRCCFVHDC 65

Qy   70 CYDHLKTQGCGIYKDYRYRNFSQGNIHCSDKGSWCEQQLCACDKEVAFCLKRNLDTYQKR 129
         |  ::|:|  | : :||||| :|||::|  :|:::::||| |:: : : :|:
Db   66 CYG--RANGCDPKLSTYSYNFQNGNIVCGNKYG-CLRHICECDRVAAICFQKNMNTYNKK 122

Qy  130 LRFYWRPHCRGQTPGC 145
         ||||||||||||||||
Db  123 YKNYSSSNCQENSDKC 138

RESULT 12
Q8KOY1
ID   Q8KOY1      PRELIMINARY;      PRT;   150 AA.
AC   Q8KOY1;
DT   01-OCT-2002 (TrEMBLrel. 22, Created)
DT   01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Similar to phospholipase A2, group IIC.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Murinae; Muridae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Kidney;
RA   Strausberg R.;
RL   Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC023347; AAH29347.1; -.
DR   GO; GO:0005509; F:calcium ion binding; IEA.
DR   GO; GO:0004623; F:phospholipase A2 activity; IEA.
DR   GO; GO:0016042; P:lipid catabolism; IEA.
DR   InterPro; IPR001211; PhospholipaseA2.
DR   Pfam; PF00068; phoslip; 1.
DR   PRINTS; PR00389; PHPHLIPASEA2.
DR   ProDom; PD000303; PhospholipaseA2; 1.
DR   SMART; SM00085; PA2c; 1.
DR   PROSITE; PS00119; PA2_ASP; 1.
DR   PROSITE; PS00118; PA2_HIS; 1.
SQ   SEQUENCE 150 AA; 16985 MW; 6548C632B1C2ECEF CRC64;

Query Match             34.8%;
Best Local Similarity   45.3%;   Score 296.5;   DB 11;   Length 150;   Pred. No. 3.3e-26;
Matches   53;   Conservative   14;   Mismatches   45;   Indels   5;   Gaps   2;

Qy   27 KMVKQVTGKMPILSYWPYGCHCGLGGRGQPKDATDWCCQTHDCCYDHLKTQGCGIYKDYY 86
         |||| |||| ||||||| ||| | |
Db   27 RMVKHVTGRSAFFSYYGYCYCGLGSKGLPVDATDRCCWAHDCCYHKLKEYGCQPILNAY 86

Qy   87 RYNFSQGNIHCS---DKGSWCEQQLCACDKEVAFCLKRNLDTYQKRLR--FYWRPHC 138
         |||||||||||   ||||||||||||||| |||||| | | ||
Db   87 QFTIVNGTVTCGCTVASSCLCGQKACECDKQSVYCFKENLATYEKAFKQLFPTRPQC 143

RESULT 13
Q7ZZQ1
ID   Q7ZZQ1      PRELIMINARY;      PRT;   138 AA.
```

```
AC   Q7ZZQ1;
DT   01-JUN-2003 (TrEMBLrel. 24, Created)
DT   01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Phospholipase A2-I.
OS   Vipera russelli siamensis.
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC   Viperidae; Viperinae; Vipera.
OX   NCBI_TaxID=228341;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Yong-Hong J., Yang J., Run-Qiang C., Dong-Sheng L., Xing-Ding Z.,
RA   Wan-Yu W., Yu-Liang X.;
RT   "A novel phospholipase A2 from Vipera russelli siamensis: isolation,
RT   cloning and sequence comparison.";
RL   Submitted (MAR-2003) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AY256974; AAP13805.1; -.
DR   GO; GO:0005509; F:calcium ion binding; IEA.
DR   GO; GO:0004623; F:phospholipase A2 activity; IEA.
DR   GO; GO:0016042; P:lipid catabolism; IEA.
DR   InterPro; IPR001211; Phospholipase A2.
DR   Pfam; PF00068; phoslip; 1.
DR   PRINTS; PR00389; PHPHLIPASEA2.
DR   ProDom; PD000303; PhospholipaseA2; 1.
DR   SMART; SM00085; PA2c; 1.
DR   PROSITE; PS00119; PA2_ASP; 1.
DR   PROSITE; PS00118; PA2_HIS; 1.
SQ   SEQUENCE 138 AA; 15401 MW; EB86AB8D46430DF3 CRC64;

Query Match             34.7%;  Score 295.5;  DB 13;  Length 138;
Best Local Similarity   39.0%;  Pred. No. 3.9e-26;
Matches   53;  Conservative   23;  Mismatches   57;  Indels   3;  Gaps   2;

Qy   10 VVMAGVIPIQGGILNLNKMVKQVTGKMPILSYWPYGCHCGLGGRGQPKDATDWCCQTHDC 69
          ||||||:|| |||||:||||||||||||||:||||||||||||||:|:||:||||||
Db    6 IVAVCLIGVEGNLYQFGBMINQKTGNFGLLSYVYYGCYCGWGGKGKPQDATDRCCFVHDC 65

Qy   70 CYDHLKTQGCGIYKDYRYNFSQGNIHCSDKGSWCEQQLCACDKEVAFCLKRNLDTYQKR 129
          ||:|||||||||||||||||||  |:::| ||||||||||  |:|||
Db   66 CYG--TVNDCNPKMATYSYSFENGDIVCGD-NNLCLKTVCECDRAAAICLGQNVNTYDKN 122

Qy  130 LRFYWRPHCRGQTPGC 145
          :|:: ||
Db  123 YENYAISHCTERSEQC 138

RESULT 14
Q8AXY1
ID   Q8AXY1       PRELIMINARY;       PRT;   138 AA.
AC   Q8AXY1;
DT   01-MAR-2003 (TrEMBLrel. 23, Created)
DT   01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Hypotensive phospholipase A2.
OS   Bothrops jararacussu (Jararacussu).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC   Viperidae; Crotalinae; Bothrops.
OX   NCBI_TaxID=8726;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Venom gland;
RX   MEDLINE=22157211; PubMed=12167491;
RA   Andriao-Escarso S.H., Soares A.M., Fontes M.R., Fuly A.L.,
RA   Correa F.M., Rosa J.C., Greene L.J., Giglio J.R.;
RT   "Structural and functional characterization of an acidic platelet
RT   aggregation inhibitor and hypotensive phospholipase A(2) from Bothrops
RT   jararacussu snake venom.";
RL   Biochem. Pharmacol. 64:723-732(2002).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Venom gland;
```

```
RA   Roberto P.G., Kashima S., Soares A.M., Astolfi-Filho S., Giglio J.R.,
RA   Franca S.C.;
RT   "Functional and Structural Analysis of Acidic and Basic Phospholipases
RT   A2 from Bothrops jararacussu Snake Venom.";
RL   Submitted (AUG-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AY145836; AAN37410.1; -.
DR   GO; GO:0005509; F:calcium ion binding; IEA.
DR   GO; GO:0004623; F:phospholipase A2 activity; IEA.
DR   GO; GO:0016042; P:lipid catabolism; IEA.
DR   InterPro; IPR001211; Phospholipase A2.
DR   Pfam; PF00068; phoslip; 1.
DR   PRINTS; PR00389; PHPHLIPASEA2.
DR   ProDom; PD000303; PhospholipaseA2; 1.
DR   SMART; SM00085; PA2c; 1.
DR   PROSITE; PS00119; PA2_ASP; 1.
DR   PROSITE; PS00118; PA2_HIS; 1.
SQ   SEQUENCE 138 AA; 15456 MW; 513647907BFD0F4E CRC64;

Query Match             34.5%;  Score 294.;  DB 13;  Length 138;
Best Local Similarity   39.7%;  Pred. No. 5.8e-26;
Matches   54;  Conservative   22;  Mismatches   54;  Indels   6;  Gaps   3;

Qy   10 VVMAGVIPIQGGILNLNKMVKQVTGKMPILSYWPYGCHCGLGGRGQPKDATDWCCQTHDC 69
          ||||||:||  ||||:|||||||||| :|||||:||||||||||:|:||:||||||
Db    9 VLLVGV--EGSLWQFGKMINYVMGESGVLQYLSYGCYCGLGGQPTDATDRCCFVHDC 65

Qy   70 CYDHLKTQGCGIYKDYRYNFSQGNIHCSDKGSWCEQQLCACDKEVAFCLKRNLDTYQKR 129
          ||:|||  |||||||||||||  |:::| ||||||||||  |:|||
Db   66 CYG--KVTGCDPKIDSYTYSKKNGDVVCGGDDP-CKKQICECDRVATTCFRDNKDTYDIK 122

Qy  130 LRFYWRPHCRGQTPGC 145
          :|  :: ||
Db  123 YWFYGAKNCQEKSEPC 138

RESULT 15
Q77IC6
ID   Q77IC6       PRELIMINARY;       PRT;   138 AA.
AC   Q77IC6;
DT   01-OCT-2003 (TrEMBLrel. 25, Created)
DT   01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Vappin B isoform 1.
OS   Vipera aspis aspis (Aspic viper).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC   Viperidae; Viperinae; Vipera.
OX   NCBI_TaxID=194601;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=22707820; PubMed=12823540;
RA   Guillemin I., Bouchier C., Garrigues T., Wisner A., Choumet V.;
RT   "Sequences and structural organization of phospholipase A2 genes from
RT   Vipera aspis aspis, V. aspis zinnikeri and Vipera berus berus venom.
RT   Identification of the origin of a new viper population based on
RT   ammodytin I1 heterogeneity.";
RL   Eur. J. Biochem. 270:2697-2706(2003).
DR   EMBL; AY243575; AAO86503.1; -.
SQ   SEQUENCE 138 AA; 15550 MW; 28C749C004DE408E CRC64;

Query Match             34.0%;  Score 289.5;  DB 13;  Length 138;
Best Local Similarity   39.0%;  Pred. No. 1.9e-25;
Matches   53;  Conservative   21;  Mismatches   59;  Indels   3;  Gaps   2;

Qy   10 VVMAGVIPIQGGILNLNKMVKQVTGKMPILSYWPYGCHCGLGGRGQPKDATDWCCQTHDC 69
          ||||||:||  ||||:||||||||||:|||||||||||||||:|:||:||||||
Db    6 IVAVCLIGVEGNLFQSAKMINGKLGAFSVWNYISYGCYCGWGGQGTPKDATDRCCFVHDC 65

Qy   70 CYDHLKTQGCGIYKDYRYNFSQGNIHCSDKGSWCEQQLCACDKEVAFCLKRNLDTYQKR 129
          ||:|||||||||||||||||||  |:::| |||||||||| |:|||
Db   66 CYG--RVRGCNPKLAIYSYSFKKGNIVCG-KNNGCLRDICECDRVAANCFHQNKNTYNKN 122

Qy  130 LRFYWRPHCRGQTPGC 145
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us-09-830-321a-1.rspt

Db   123 YRFLSSSRCRQTSEQC 138

Search completed: October 5, 2004, 19:24:02
Job time : 30.8067 secs

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              GenCore version 5.1.6
         Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on:    October  5, 2004, 18:50:04 ; Search time 138.747 Seconds
                                       (without alignments)
                                       1232.039 Million cell updates/sec

Title:          US-09-830-321A-2
Perfect score:  3235
Sequence:       1 MIFVELSPTIALCLERVASH.........EQLLEALRQAVQRRRQRRPH 605

Scoring table:  BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched:       1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters:   1586107

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :  A_Geneseq_29Jan04:*
      1: geneseqp1980s:*
      2: geneseqp1990s:*
      3: geneseqp2000s:*
      4: geneseqp2001s:*
      5: geneseqp2002s:*
      6: geneseqp2003as:*
      7: geneseqp2003bs:*
      8: geneseqp2004s:*
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SUMMARIES

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

Result No.	Score	% Query Match	Length	DB	ID	Pred. No.	Description
1	3235	100.0	605	3	AAB03628		Aab03628 Human pho
2	2767.5	85.5	778	4	AAU10696		Aau10696 Human cPL
3	2767.5	85.5	778	6	ABG76482		Abg76482 Human par
4	2767.5	85.5	797	5	AAU10697		Aau10697 cPLA2 N-t
5	2767.5	85.5	797	5	ABG76483		Abg76483 Human cyt
6	2767.5	85.5	913	3	AAY51557		Aay51557 Human PLA
7	2767.5	85.5	913	4	AAB74635		Aab74635 Phospholi
8	2767.5	85.5	913	3	AAB82415		Aab82415 Human pho
9	2765.5	85.5	533	3	AAB21140		Aab21140 Human cyt
10	2700	83.5	1020	4	ABG05871		Abg05871 Novel hum
11	2610.5	80.7	1040	4	ABG20154		Abg20154 Novel hum
12	2509.5	77.6	483	2	AAW75132		Aaw75132 Human sec
13	2509.5	77.6	483	4	AAW75067		Aaw75067 Human sec
14	2509.5	77.6	483	6	ABO01943		Abo01943 Novel hum
15	2509.5	77.6	483	6	ABO02008		Abo02008 Novel hum
16	1492	46.1	802	5	AAE22843		Aae22843 Human pho
17	1492	46.1	818	7	ADB61634		Adb61634 Human 818
18	1492	46.1	1026	5	ABB07497		Abb07497 Human lip
19	1492	46.1	1045	7	ADC10174		Adc10174 Human NOV
20	1455	45.0	1746	4	ABG05869		Abg05869 Novel hum
21	1243.5	38.4	996	5	ABB78290		Abb78290 Amino aci
22	1139.5	35.2	849	5	ABB09144		Abb09144 Human pho
23	1139.5	35.2	849	7	ADE08121		Ade08121 Novel pro
24	1138	35.2	853	3	ABB09149		Abb09149 Mouse pho
25	1127	34.8	854	5	ABB09147		Abb09147 Mouse pho
26	1123.5	34.7	1600	4	AAE05958		Aae05958 Human pho
27	1112	34.4	848	5	ABB07494		Abb07494 Human lip
28	1101.5	34.0	1624	4	AAE05956		Aae05956 Human pho
29	1031.5	31.9	1798	5	AAE22833		Aae22833 Human pho
30	1022	31.6	1497	4	ABG20153		Abg20153 Novel hum
31	886.5	27.4	188	4	ABG20150		Abg20150 Novel hum
32	629.5	19.5	438	4	ABG20151		Abg20151 Novel hum
33	619	19.1	749	2	AAR26501		Aar26501 Cytosolic
34	619	19.1	749	2	AAR54090		Aar54090 PLA2 phos
35	619	19.1	749	2	AAR63757		Aar63757 Human pho
36	619	19.1	749	2	AAR97751		Aar97751 Human pho
37	619	19.1	749	2	AAW11607		Aaw11607 Human pho
38	619	19.1	749	2	AAW14650		Aaw14650 Human pho
39	619	19.1	749	3	AAY59631		Aay59631 Human cyt
40	619	19.1	749	6	AAO15549		Aao15549 Human cyt
41	619	19.1	749	6	ABU03480		Abu03480 Angiogene
42	619	19.1	749	7	ADE62603		Ade62603 Human Pro
43	616.5	19.1	611	3	AAB21142		Aab21142 Human cyt
44	611.5	18.9	748	5	AAE22834		Aae22834 Human pho
45	599.5	18.5	748	5	AAE23054		Aae23054 Human pho

ALIGNMENTS

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RESULT 1
AAB03628
ID   AAB03628 standard; protein;  605 AA.
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AC   AAB03628;
XX
DT   05-OCT-2000  (first entry)
XX
DE   Human phospholipase 2 HPPL2.
XX
KW   Human; phospholipase 2; HPPL2; cancer; autoimmune disorder;
KW   inflammatory disorder; reproductive disorder; infection.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Modified-site   72
FT                   /label= potential_phosphorylation_site
FT   Modified-site   78
FT                   /label= potential_phosphorylation_site
FT   Modified-site   104
FT                   /label= potential_phosphorylation_site
FT   Modified-site   186
FT                   /label= potential_phosphorylation_site
FT   Modified-site   282
FT                   /label= potential_phosphorylation_site
FT   Modified-site   293
FT                   /label= potential_phosphorylation_site
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FT                   /label= potential_phosphorylation_site
FT   Modified-site   426
FT                   /label= potential_phosphorylation_site
FT   Modified-site   430
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FT   Modified-site   440
FT                   /label= potential_phosphorylation_site
FT   Modified-site   456
FT                   /label= potential_glycosylation_site
FT   Modified-site   506
FT                   /label= potential_phosphorylation_site
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FT                   /label= potential_phosphorylation_site
FT   Modified-site   550
FT                   /label= potential_glycosylation_site
FT   Modified-site   552
FT                   /label= potential_phosphorylation_site
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FT   Modified-site   566
FT   /label= potential_phosphorylation_site
XX
PN   WO200024911-A2.
PD   04-MAY-2000.
XX
PF   27-OCT-1999;   99WO-US025021.
PR   27-OCT-1998;   98US-00181317.
PR   21-JAN-1999;   99US-00234726.
XX
PA   (INCY-) INCYTE PHARM INC.
XX
PI   Hillman JL, Bandman O, Guegler KJ, Corley NC, Baughn MR;
PI   Azimzai Y, Lal P, Lu DAM;
XX
DR   WPI; 2000-350750/30.
DR   N-PSDB; AAA53270.
XX
PT   Human phospholipase genes and proteins useful to diagnose, prevent or
PT   treat cancer, autoimmune or inflammatory or reproductive disorders.
XX
PS   Disclosure; Page 71-72; 80pp; English.
XX
CC   The present sequence is human phospholipase 2 (HPPL2). This protein is
CC   involved in the hydrolysis of membrane phospholipids. The protein and its
CC   coding sequence can be used to diagnose and treat the following: cancers
CC   such as prostate, breast and testicular cancers, autoimmune and
CC   inflammatory disorders such as AIDS, allergies, anaemia, asthma,
CC   atherosclerosis, Crohn's disease, diabetes mellitus, emphysema, Graves'
CC   disease, irritable bowel syndrome, multiple sclerosis, myasthenia gravis,
CC   psoriasis, rheumatoid arthritis and systemic lupus erythematosus,
CC   infection caused by viruses, fungi, bacteria, parasites and protozoa, and
CC   reproductive disorders including infertility, disruptions of the
CC   menstrual cycle, polycystic ovary syndrome, ectopic pregnancies,
CC   disruptions of spermatogenesis, cancers within the reproductive tract and
CC   impotence.
XX
SQ   Sequence 605 AA;

Query Match   100.0%; Score 3235; DB 3; Length 605;
Best Local Similarity   100.0%; Pred. No. 4.3e-292;
Matches   605; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   1 MIFVELSPPTLALCLERVASHLTDTGLLVLFCPAPCPFFFFEMESLSVAQAGVQWRDLGS 60
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 MIFVELSPPTLALCLERVASHLTDTGLLVLFCPAPCPFFFFEMESLSVAQAGVQWRDLGS 60

Qy   61 LQPPPLGFKRFSCLSLPSSWDYRLRELAVRLGFGPCAEEQAFLSRRKQVVAAALRQALQL 120
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 LQPPPLGFKRFSCLSLPSSWDYRLRELAVRLGFGPCAEEQAFLSRRKQVVAAALRQALQL 120

Qy   121 DGDLQEDEIPVVAIMATGGGIRAMTSLYGQLAGLKELGLLDCVSYITGASGSTWALANLY 180
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121 DGDLQEDEIPVVAIMATGGGIRAMTSLYGQLAGLKELGLLDCVSYITGASGSTWALANLY 180

Qy   181 EDPEWSQKDLAGPTELLKTQVTKNKLGVILAPSQLQRYRQELAERARLGYPSCFTNLWALI 240
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181 EDPEWSQKDLAGPTELLKTQVTKNKLGVILAPSQLQRYRQELAERARLGYPSCFTNLWALI 240

Qy   241 NEALLHDEPHDHKLSDQRALSHGQNPLPIYCALNTKGQSLTTFEFGEWCEFSPYYEVGFP 300
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241 NEALLHDEPHDHKLSDQRALSHGQNPLPIYCALNTKGQSLTTFEFGEWCEFSPYYEVGFP 300

Qy   301 KYGAFIPSELFGSEFFMGQLMKRLPESRICFLEGIWSNLYAANLQDSLYWASEPSQFWDR 360
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   301 KYGAFIPSELFGSEFFMGQLMKRLPESRICFLEGIWSNLYAANLQDSLYWASEPSQFWDR 360

Qy   361 WVRNQANLDKEQVPLLKIEEPPSTAGRIAEFFTDLLITWRPLAQATHNFLRGLHFHKDYFQ 420
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   361 WVRNQANLDKEQVPLLKIEEPPSTAGRIAEFFTDLLITWRPLAQATHNFLRGLHFHKDYFQ 420

Qy   421 HPHFSTWKATTLDGLPNQLTPSEPHLCLLDVGYLINTSCLPLLQPTRDVDLILSLDYNLH 480
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   421 HPHFSTWKATTLDGLPNQLTPSEPHLCLLDVGYLINTSCLPLLQPTRDVDLILSLDYNLH 480

Qy   481 GAFQOLQLLGRFCQEQGIPPFPISPSPEEQLQPRECHTFSDPTCPGAPAVLHFSSGVRRT 540
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   481 GAFQOLQLLGRFCQEQGIPPFPISPSPEEQLQPRECHTFSDPTCPGAPAVLHFSSGVRRT 540

Qy   541 PEEAAAGEVNLSSSSDSPYHYTKVTYSQEDVDKLLHLTHYNVCNNQEQLLEALRQAVQRRR 600
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   541 PEEAAAGEVNLSSSSDSPYHYTKVTYSQEDVDKLLHLTHYNVCNNQEQLLEALRQAVQRRR 600

Qy   601 QRRPH 605
            |||||
Db   601 QRRPH 605

RESULT 2
AAU10696
ID   AAU10696 standard; protein; 778 AA.
XX
AC   AAU10696;
XX
DT   25-FEB-2002 (first entry)
XX
DE   Human cPLA2-beta enzyme.
XX
KW   Calcium-independent cytosolic phospholipase A2-beta; cPLA2-beta;
KW   U937 cell; membrane phospholipid turnover; intracellular signalling;
KW   arachidonic acid cascade; inflammatory disorder; rheumatoid arthritis;
KW   psoriasis; asthma; inflammatory bowel disease; antiinflammatory.
XX
OS   Homo sapiens.
XX
PN   US6287838-B1.
XX
PD   11-SEP-2001.
XX
PF   13-DEC-1999;   99US-00460145.
XX
PR   24-JAN-1997;   97US-00788975.
XX
PA   (GEMY) GENETICS INST INC.
XX
PI   Kriz R, Song C;
XX
DR   WPI; 2002-054342/07.
DR   N-PSDB; AAS17362.
XX
PT   Novel cytosolic phospholipase A2-beta enzyme encoding polynucleotide,
PT   useful for producing the enzyme for use in assays to discover enzyme
PT   antagonists.
XX
PS   Claim 1; Col 15-19; 19pp; English.
XX
CC   The present invention relates to a novel calcium-independent cytosolic
CC   phospholipase A2 (cPLA2)-beta enzyme and the cDNA sequence encoding it.
CC   The cDNA clone is isolated from U937 cells. The cPLA2 enzyme is active in
CC   membrane phospholipid turnover and in regulation of intracellular
CC   signalling mediated by the arachidonic acid cascade. The invention
CC   describes a method for producing phospholipase enzymes which can be used
CC   to identify inhibitors of their function. The inhibitors can used to
CC   treat inflammatory disorders such as rheumatoid arthritis, psoriasis,
CC   asthma, and inflammatory bowel disease. The present sequence represents
CC   human cPLA2-beta enzyme
XX
SQ   Sequence 778 AA;

Query Match   85.5%; Score 2767.5; DB 5; Length 778;
Best Local Similarity   87.6%; Pred. No. 2.5e-248;
Matches   537; Conservative   5; Mismatches   22; Indels   49; Gaps   6;

Qy   24 TGLLVLFCPAPCPFFFFEMESLSVAQAGVQWRDLGSLVAQGVWRDLGSLQPPPLGFKRFSCLSLPSSWDYR 83

```
DR   WPI; 2003-287361/28.
DR   N-PSDB; ABX11883.
XX
PT   Novel purified calcium-independent cytosolic phospholipase A2-beta
PT   enzyme, useful for screening compounds having antiinflammatory activity
PT   mediated by the arachidonic acid cascade.
XX
PS   Claim 2; Col 13-18; 19pp; English.
XX
CC   The invention relates to a purified phospholipase enzyme (calcium-
CC   independent cytosolic phospholipase A_2-beta enzyme) peptide appearing as
CC   ABG76482 encoded by a polynucleotide appearing as ABX11883. The protein
CC   has an enzymatic activity in a mixed micelle assay (MMA) with 1-palmitoyl
CC   -2- (^1^4C)-arachidonyl- phosphatidylcholine. cPLA2-beta is useful for
CC   assaying chemical agents for antiinflammatory activity mediated by the
CC   various components of the arachidonic acid cascade. cPLA2-beta is also
CC   useful in the development of polyclonal and monoclonal antibodies which
CC   are useful as research or diagnostic tools, and to study phospholipase
CC   A_2 activity and inflammatory conditions. The present sequence represents
CC   a partial cPLA2-beta protein
XX
SQ   Sequence 778 AA;

Query Match             85.5%;  Score 2767.5;  DB 6;  Length 778;
Best Local Similarity   87.6%;  Pred. No. 2.5e-248;
Matches  537;  Conservative   5;  Mismatches  22;  Indels  49;  Gaps   6;

Qy   24 TGLLVLFCPAPCS..FFEMESLSVAQAGVQWRDLGSLQPPPLGFKRFSCLSLPSSWDYR 83
         ||  : |||| :                           :|: |||
Db  184 TGTFRFHCPA-C-----WEQE-LSI-------------RLQDAPEEQLKAPLSALPSGQVVR 225

Qy   84 ------------------LRELAVRLGFGPCAEEQAFLSRRKQVVAAALRQALQLDGD 123
                            |||||||||||||||||||||||||||||||||||||||||
Db  226 LVFPTSQEPLMRVELKKEAGLRELAVRLGFGPCAEEQAFLSRRKQVVAAALRQALQLDGD 285

Qy  124 LQEDEIPVVAIMATGGGIRAMTSLYGQLAGLKELGLLDCVSYITGASGSTWALANLYEDP 183
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  286 LQEDEIPVVAIMATGGGIRAMTSLYGQLAGLKELGLLDCVSYITGASGSTWALANLYEDP 345

Qy  184 EWSQKDLAGPTELLKTQVTKNKLGVLAPSQLQRYRQELAERARLGYPSCFFTNLWALINEA 243
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  346 EWSQKDLAGPTELLKTQVTKNKLGVLAPSQLQRYRQELAERARLGYPSCFFTNLWALINEA 405

Qy  244 LLHDEPHDHKLSDQREALSHGQNPLPIYCALNTKGQSLTTFEFGEWCEFSPYEVGFPPKYG 303
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  406 LLHDEPHDHKLSDQREALSHGQNPLPIYCALNTKGQSLTTFEFGEWCEFSPYEVGFPPKYG 465

Qy  304 AFIPSELFGSEFFMGQLMKRLPESRICFLEGIWSNLYAANLQDSLYWASEPSQFWDRWVR 363
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  466 AFIPSELFGSEFFMGQLMKRLPESRICFLEGIWSNLYAANLQDSLYWASEPSQFWDRWVR 525

Qy  364 NQANLDKEQVPLLKIEPPSTAGRIAEFFTDLLTWRPLAQATHNFLRGLHFHKDYFQHPH 423
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  526 NQANLDKEQVPLLKIEPPSTAGRIAEFFTDLLTWRPLAQATHNFLRGLHFHKDYFQHPH 585

Qy  424 FSTWKATTLDGLPNQLTPSEPHLCLLDVGYLINTSCLPLLQPTRDVDLILSLDYNLHGAF 483
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  586 FSTWKATTLDGLPNQLTPSEPHLCLLDVGYLINTSCLPLLQPTRDVDLILSLDYNLHGAF 645

Qy  484 QQLQLLGRFCQEQGIPFPPPISPSPEEQLQPRECHTFSDPTCPGAPAVLHF--------- 533
         ||||||||||||||||||||||||||||||||||||||||||||||||||
Db  646 QQLQLLGRFCQEQGIPFPPPISPSPEEQLQPRECHTFSDPTCPGAPAVLHF 705

Qy  534 -SSGVRRTPEEAAAGEVNLSSSDSPYHYTKVTYSQEDVDKLLHLTHYNVCNNQEQLLEAL 592
          : ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  706 SAPGVRRTPEEAAAGEVNLSSSDSPYHYTKVTYSQEDVDKLLHLTHYNVCNNQEQLLEAL 765

Qy  593 RQAVQRRRQRRPH 605
         |||||||||||||
Db  766 RQAVQRRRQRRPH 778

RESULT 4
```

```
RESULT 3
ABG76482
ID   ABG76482 standard; protein; 778 AA.
XX
AC   ABG76482;
XX
DT   10-MAY-2003 (first entry)
XX
DE   Human partial cytosolic phospholipase A2-beta, cPLA2-beta.
XX
KW   Human; calcium independent cytosolic phospholipase A2-beta; cPLA2-beta;
KW   antiinflammatory; arachidonic acid cascade; enzyme;
KW   inflammatory condition.
XX
OS   Homo sapiens.
XX
PN   US6482625-B1.
XX
PD   19-NOV-2002.
XX
PF   29-JUN-2001; 2001US-00895547.
XX
PR   24-JAN-1997; 97US-00788975.
PR   13-DEC-1999; 99US-00460145.
XX
PA   (GEMY ) GENETICS INST LLC.
XX
PI   Kriz R, Song C;
XX
```

```
Db  184 TGTFRFHCPA-C-----WEQE-LSI-------------RLQDAPEEQLKAPLSALPSGQVVR 225
Qy   84 ------------------LRELAVRLGFGPCAEEQAFLSRRKQVVAAALRQALQLDGD 123
Db  226 LVFPTSQEPLMRVELKKEAGLRELAVRLGFGPCAEEQAFLSRRKQVVAAALRQALQLDGD 285
Qy  124 LQEDEIPVVAIMATGGGIRAMTSLYGQLAGLKELGLLDCVSYITGASGSTWALANLYEDP 183
Db  286 LQEDEIPVVAIMATGGGIRAMTSLYGQLAGLKELGLLDCVSYITGASGSTWALANLYEDP 345
Qy  184 EWSQKDLAGPTELLKTQVTKNKLGVLAPSQLQRYRQELAERARLGYPSCFFTNLWALINEA 243
Db  346 EWSQKDLAGPTELLKTQVTKNKLGVLAPSQLQRYRQELAERARLGYPSCFFTNLWALINEA 405
Qy  244 LLHDEPHDHKLSDQREALSHGQNPLPIYCALNTKGQSLTTFEFGEWCEFSPYEVGFPPKYG 303
Db  406 LLHDEPHDHKLSDQREALSHGQNPLPIYCALNTKGQSLTTFEFGEWCEFSPYEVGFPPKYG 465
Qy  304 AFIPSELFGSEFFMGQLMKRLPESRICFLEGIWSNLYAANLQDSLYWASEPSQFWDRWVR 363
Db  466 AFIPSELFGSEFFMGQLMKRLPESRICFLEGIWSNLYAANLQDSLYWASEPSQFWDRWVR 525
Qy  364 NQANLDKEQVPLLKIEPPSTAGRIAEFFTDLLTWRPLAQATHNFLRGLHFHKDYFQHPH 423
Db  526 NQANLDKEQVPLLKIEPPSTAGRIAEFFTDLLTWRPLAQATHNFLRGLHFHKDYFQHPH 585
Qy  424 FSTWKATTLDGLPNQLTPSEPHLCLLDVGYLINTSCLPLLQPTRDVDLILSLDYNLHGAF 483
Db  586 FSTWKATTLDGLPNQLTPSEPHLCLLDVGYLINTSCLPLLQPTRDVDLILSLDYNLHGAF 645
Qy  484 QQLQLLGRFCQEQGIPFPPPISPSPEEQLQPRECHTFSDPTCPGAPAVLHF--------- 533
Db  646 QQLQLLGRFCQEQGIPFPPPISPSPEEQLQPRECHTFSDPTCPGAPAVLHF 705
Qy  534 -SSGVRRTPEEAAAGEVNLSSSDSPYHYTKVTYSQEDVDKLLHLTHYNVCNNQEQLLEAL 592
Db  706 SAPGVRRTPEEAAAGEVNLSSSDSPYHYTKVTYSQEDVDKLLHLTHYNVCNNQEQLLEAL 765
Qy  593 RQAVQRRRQRRPH 605
Db  766 RQAVQRRRQRRPH 778
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```
AAU10697
ID   AAU10697 standard; protein; 797 AA.
XX
AC   AAU10697;
XX
DT   25-FEB-2002  (first entry)
XX
DE   cPLA2 N-terminal peptide-cPLA2-beta fusion protein.
XX
KW   Calcium-independent cytosolic phospholipase A2-beta; cPLA2-beta; mutant;
KW   U937 cell; membrane phospholipid turnover; intracellular signalling;
KW   arachidonic acid cascade; inflammatory disorder; rheumatoid arthritis;
KW   psoriasis; asthma; inflammatory bowel disease; antiinflammatory; mutein.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
PN   US6287838-B1.
XX
PD   11-SEP-2001.
XX
PF   13-DEC-1999;  99US-00460145.
XX
PR   24-JAN-1997;  97US-00788975.
XX
PA   (GEMY ) GENETICS INST INC.
XX
PI   Kriz R,  Song C;
XX
DR   WPI; 2002-054342/07.
DR   N-PSDB; AAS17363.
XX
PT   Novel cytosolic phospholipase A2-beta enzyme encoding polynucleotide,
PT   useful for producing the enzyme for use in assays to discover enzyme
PT   antagonists.
XX
PS   Claim 1; Col 21-26; 19pp; English.
XX
CC   The present invention relates to a novel calcium-independent cytosolic
CC   phospholipase A2 (cPLA2)-beta enzyme and the cDNA sequence encoding it.
CC   The cDNA clone is isolated from U937 cells. The cPLA2 enzyme is active in
CC   membrane phospholipid turnover and in regulation of intracellular
CC   signalling mediated by the arachidonic acid cascade. The invention
CC   describes a method for producing phospholipase enzymes which can be used
CC   to identify inhibitors of their function. The inhibitors can be used to
CC   treat inflammatory disorders such as rheumatoid arthritis, psoriasis,
CC   asthma, and inflammatory bowel disease. The present sequence represents
CC   cPLA2 N-terminal peptide-cPLA2-beta fusion protein
XX
SQ   Sequence 797 AA;

Query Match             85.5%;  Score 2767.5;  DB 5;  Length 797;
Best Local Similarity   87.6%;  Pred. No. 2.6e-248;
Matches  537;  Conservative   5;  Mismatches  22;  Indels  49;  Gaps  6;

Qy     24 TGLLVLFCPAPCPFFFFFEMESLSVAQAGVQWRDLGSLQPPPLGFKRFSCLSLPSSWDYR 83
          ||||||||||  ||||||| ::  ||:
Db    203 TGTFRFHCPA-C-----WEQE-LSI----------RLQDAPEEQLKAPLSALPSGQVVR 244

Qy     84 ------------LRELAVRLGFGPCAEEQAFLSRRKQVVAALRQALQLDGD 123
                       |||||||||||||||||||||||||||||||||||||
Db    245 LVFPTSQEPLMRVELKKEAGLRELAVRLGFGPCAEEQAFLSRRKQVVAALRQALQLDGD 304

Qy    124 LQEDEIPVVAIMATGGGIRAMTSLYGQLAGLKELGLLDCVSYITGASGSTWALANLYEDP 183
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    305 LQEDEIPVVAIMATGGGIRAMTSLYGQLAGLKELGLLDCVSYITGASGSTWALANLYEDP 364

Qy    184 EWSQKDLAGPTELLKTQVTKNKLGVLAPSQLQRYRQELAEBRARLGYPSCFTNLWALINEA 243
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    365 EWSQKDLAGPTELLKTQVTKNKLGVLAPSQLQRYRQELAEBRARLGYPSCFTNLWALINEA 424

Qy    244 LLHDEPHDHKLSDQREALSHGQNPLPIYCALNTKGQSLTTFEFGEWCEFSPYEVGFPKYG 303
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
```

```
Db    425 LLHDEPHDHKLSDQREALSHGQNPLPIYCALNTKGQSLTTFEFGEWCEFSPYEVGFPKYG 484

Qy    304 AFIPSELFGSEFFMGQLMKRLPESRICFLEGIWSNLYAANLQDSLYWASEPSQFWDRWVR 363
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    485 AFIPSELFGSEFFMGQLMKRLPESRICFLEGIWSNLYAANLQDSLYWASEPSQFWDRWVR 544

Qy    364 NQANLDKEQVPLLKIEBPPSTAGRIAEFFTDLLTWRPLAQATHNFLRGLHFHKDYFQHPH 423
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    545 NQANLDKEQVPLLKIEBPPSTAGRIAEFFTDLLTWRPLAQATHNFLRGLHFHKDYFQHPH 604

Qy    424 FSTWKATTLDGLPNQLTPSEPHLCLLDVGYLINTSCLPLLQPTRDVDLILSLDYNLHGAF 483
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    605 FSTWKATTLDGLPNQLTPSEPHLCLLDVGYLINTSCLPLLQPTRDVDLILSLDYNLHGAF 664

Qy    484 QQLQLLGRFCQEQGIPFPPISPSPEEQLQPRECHTFSDPTCPGAPAVLHF--------- 533
          |||||||||||||||||||||||||||||||||||||||||||||||||
Db    665 QQLQLLGRFCQEQGIPFPPISPSPEEQLQPRECHTFSDPTCPGAPAVLHFPLVSDSFREY 724

Qy    534 -SSGVRRTPEERAAGEVNLSSSDSPYHYTKVTYSQEDVDKLIHLTHYVCNNQEQLLEAL 592
           : ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    725 SAPGVRRTPEERAAGEVNLSSSDSPYHYTKVTYSQEDVDKLLHLTHYVCNNQEQLLEAL 784

Qy    593 RQAVQRRRQRRPH 605
          |||||||||||||
Db    785 RQAVQRRRQRRPH 797
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```
RESULT 5
ABG76483
ID   ABG76483 standard; protein; 797 AA.
XX
AC   ABG76483;
XX
DT   10-MAY-2003  (first entry)
XX
DE   Human cytosolic phospholipase A2-beta, cPLA2-beta.
XX
KW   Human; calcium independent cytosolic phospholipase A2-beta; cPLA2-beta;
KW   antiinflammatory; arachidonic acid cascade; enzyme;
KW   inflammatory condition.
XX
OS   Homo sapiens.
XX
PN   US6482625-B1.
XX
PD   19-NOV-2002.
XX
PF   29-JUN-2001;  2001US-00895547.
XX
PR   24-JAN-1997;    97US-00788975.
PR   13-DEC-1999;    99US-00460145.
XX
PA   (GEMY ) GENETICS INST LLC.
XX
PI   Kriz R,  Song C;
XX
DR   WPI; 2003-287361/28.
DR   N-PSDB; ABX11884.
XX
PT   Novel purified calcium-independent cytosolic phospholipase A2-beta
PT   enzyme, useful for screening compounds having antiinflammatory activity
PT   mediated by the arachidonic acid cascade.
XX
PS   Disclosure; Col 21-26; 19pp; English.
XX
CC   The invention relates to a purified phospholipase enzyme (calcium-
CC   independent cytosolic phospholipase A 2-beta enzyme) peptide appearing as
CC   ABG76482 encoded by a polynucleotide appearing as ABX118883. The protein
CC   has an enzymatic activity in a mixed micelle assay (MMA) with 1-palmitoyl
CC   -2- (1^4C)-arachidonyl- phosphatidylcholine. cPLA2-beta is useful for
CC   assaying chemical agents for antiinflammatory activity mediated by the
CC   various components of the arachidonic acid cascade. cPLA2-beta is also
CC   useful in the development of polyclonal and monoclonal antibodies which
```

CC are useful as research or diagnostic tools, and to study phospholipase
CC A 2 activity and inflammatory conditions. The present sequence represents
CC the cPLA2-beta protein
XX
SQ Sequence 797 AA;

Query Match   85.5%; Score 2767.5; DB 6; Length 797;
Best Local Similarity 87.6%; Pred. No. 2.6e-248;
Matches 537; Conservative 5; Mismatches 22; Indels 49; Gaps 6;

```
Qy   24 TGLLVLFCPAPCPFFFFEMESLSVAQAGVQWRDLGSLQPPPLGFKRFSCLSLPSSWDYR  83
Db  203 TGTFRFHCPA-C-----WEQE-LSI----------RLQDAPEEQLKAPLSALPSGGQVVR 244

Qy   84 ------------LRELAVRLGFGPCAEEQAFLSRRKQVVAAALRQALQLDGD 123
Db  245 LVFPTSQEPLMRVELKKEAGLRELAVRLGFGPCAEEQAFLSRRKQVVAAALRQALQLDGD 304

Qy  124 LQEDEIPVVAIMATGGIRAMTSLYGQLAGLKELGLLDCVSYITGASGSTWALANLYEDP 183
Db  305 LQEDEIPVVAIMATGGIRAMTSLYGQLAGLKELGLLDCVSYITGASGSTWALANLYEDP 364

Qy  184 EWSQKDLAGPTELLKTQVTKNKLGVLAPSQLQRYRQELAERARLGYPSCFTNLWALINEA 243
Db  365 EWSQKDLAGPTELLKTQVTKNKLGVLAPSQLQRYRQELAERARLGYPSCFTNLWALINEA 424

Qy  244 LLHDEPHDHKLSDQREALSHGQNPLPIYCALNTKGQSLTTFEFGEWCEFSPYEVGFPKYG 303
Db  425 LLHDEPHDHKLSDQREALSHGQNPLPIYCALNTKGQSLTTFEFGEWCEFSPYEVGFPKYG 484

Qy  304 AFIPSELFGSEFFMGQLMKRLPESRICFLEGIWSNLYAANLQDSLYWASEPSQFWDRWVR 363
Db  485 AFIPSELFGSEFFMGQLMKRLPESRICFLEGIWSNLYAANLQDSLYWASEPSQFWDRWVR 544

Qy  364 NQANLDKEQVPLLKIEEPPSTAGRIAEFFTDLLTWRPLAQATHNFLRGLHFHKDYFQHPH 423
Db  545 NQANLDKEQVPLLKIEEPPSTAGRIAEFFTDLLTWRPLAQATHNFLRGLHFHKDYFQHPH 604

Qy  424 FSTWKATTLDGLPNQLTPSEPHLCLLDVGYLINTSCLPLLQPTRDVDLILSLDYNLHGAF 483
Db  605 FSTWKATTLDGLPNQLTPSEPHLCLLDVGYLINTSCLPLLQPTRDVDLILSLDYNLHGAF 664

Qy  484 QQLQLLGRFCQEQGIPFPPISPSPEEQLQPRECHTFSDPTCPGAPAVLHF---------- 533
Db  665 QQLQLLGRFCQEQGIPFPPISPSPEEQLQPRECHTFSDPTCPGAPAVLHFPLVSDSFREY 724

Qy  534 -SSGVRRTPEEAAAGEVNLSSSDSPYHYTKVTYSQEDVDKLLHLTHYNVCNNQEQLLEAL 592
Db  725 SAPGVRRTPEEAAAGEVNLSSSDSPYHYTKVTYSQEDVDKLLHLTHYNVCNNQEQLLEAL 784

Qy  593 RQAVQRRRQRRPH 605
Db  785 RQAVQRRRQRRPH 797
```

RESULT 6
AAY51557
ID AAY51557 standard; protein; 797 AA.
XX
AC AAY51557;
XX
DT 18-MAY-2000 (first entry)
XX
DE Human PLA2 protein.
XX
KW PLA2; phospholipase A2; phosphatide 2-acyl hydrolase; human; therapy;
KW arachidonic acid; lysophospholipid; Alzheimer's disease.
XX
OS Homo sapiens.
XX
PN US6025178-A.
XX
PD 15-FEB-2000;

XX
CC This invention describes a novel human phospholipase A2 (PLA2) protein
CC (I) and its encoding nucleic acid. The amino acid (I) releases
CC arachidonic acid in specific tissues characterized by unique membrane
CC phospholipids, by generating lysophospholipid species which are
CC deleterious to membrane integrity or by remodeling of unsaturated species
CC of membrane phospholipids through deacylation/reacylation mechanisms. The
CC amino acid is useful in assays to identify inhibitors having a
CC therapeutic benefit, such as inhibiting the central role of PLA2 in the
CC inflammatory component of Alzheimer's disease. The amino acid (I) allows
CC sensitive and rapid screening and identification of inhibitors of
CC phospholipase A2. This sequence represents the human PLA2 protein (also
CC known as phosphatide 2-acyl hydrolase)
XX
SQ Sequence 913 AA;

Query Match   85.5%; Score 2767.5; DB 3; Length 913;
Best Local Similarity 87.6%; Pred. No. 3.2e-248;
Matches 537; Conservative 5; Mismatches 22; Indels 49; Gaps 6;

```
Qy   24 TGLLVLFCPAPCPFFFFEMESLSVAQAGVQWRDLGSLQPPPLGFKRFSCLSLPSSWDYR  83
Db  319 TGTFRFHCPA-C-----WEQE-LSI----------RLQDAPEEQLKAPLSALPSGGQVVR 360

Qy   84 ------------LRELAVRLGFGPCAEEQAFLSRRKQVVAAALRQALQLDGD 123
Db  361 LVFPTSQEPLMRVELKKEAGLRELAVRLGFGPCAEEQAFLSRRKQVVAAALRQALQLDGD 420

Qy  124 LQEDEIPVVAIMATGGIRAMTSLYGQLAGLKELGLLDCVSYITGASGSTWALANLYEDP 183
Db  421 LQEDEIPVVAIMATGGIRAMTSLYGQLAGLKELGLLDCVSYITGASGSTWALANLYEDP 480

Qy  184 EWSQKDLAGPTELLKTQVTKNKLGVLAPSQLQRYRQELAERARLGYPSCFTNLWALINEA 243
Db  481 EWSQKDLAGPTELLKTQVTKNKLGVLAPSQLQRYRQELAERARLGYPSCFTNLWALINEA 540

Qy  244 LLHDEPHDHKLSDQREALSHGQNPLPIYCALNTKGQSLTTFEFGEWCEFSPYEVGFPKYG 303
Db  541 LLHDEPHDHKLSDQREALSHGQNPLPIYCALNTKGQSLTTFEFGEWCEFSPYEVGFPKYG 600

Qy  304 AFIPSELFGSEFFMGQLMKRLPESRICFLEGIWSNLYAANLQDSLYWASEPSQFWDRWVR 363
Db  601 AFIPSELFGSEFFMGQLMKRLPESRICFLEGIWSNLYAANLQDSLYWASEPSQFWDRWVR 660

Qy  364 NQANLDKEQVPLLKIEEPPSTAGRIAEFFTDLLTWRPLAQATHNFLRGLHFHKDYFQHPH 423
Db  661 NQANLDKEQVPLLKIEEPPSTAGRIAEFFTDLLTWRPLAQATHNFLRGLHFHKDYFQHPH 720

Qy  424 FSTWKATTLDGLPNQLTPSEPHLCLLDVGYLINTSCLPLLQPTRDVDLILSLDYNLHGAF 483
Db  721 FSTWKATTLDGLPNQLTPSEPHLCLLDVGYLINTSCLPLLQPTRDVDLILSLDYNLHGAF 780

Qy  484 QQLQLLGRFCQEQGIPFPPISPSPEEQLQPRECHTFSDPTCPGAPAVLHF---------- 533
Db  781 QQLQLLGRFCQEQGIPFPPISPSPEEQLQPRECHTFSDPTCPGAPAVLHFPLVSDSFREY 840
```

Qy   534 -SSGVRRTPEEAAAGEVNLSSSDSPYHYTKVTYSQEDVDKLLHLTHYNVCNNQEQLLEAL 592
           : ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   841 SAPGVRRTPEEAAAGEVNLSSSDSPYHYTKVTYSQEDVDKLLHLTHYNVCNNQEQLLEAL 900

Qy   593 RQAVQRRQRRPH 605
          ||||||||||||
Db   901 RQAVQRRQRRPH 913

RESULT 7
AAB74635
ID   AAB74635 standard; protein; 913 AA.
XX
AC   AAB74635;
XX
DT   23-MAY-2001 (first entry)
XX
DE   Phospholipase A2 (PLA2) protein sequence SEQ ID NO:3.
XX
KW   Phospholipase A2; PLA2; antiinflammatory; inflammatory condition;
KW   rheumatoid arthritis; psoriasis; asthma; cytosolic PLA2; cPLA2.
XX
OS   Homo sapiens.
XX
PN   US6197569-B1.
XX
PD   06-MAR-2001.
XX
PF   07-FEB-2000; 2000US-00500358.
XX
PR   29-MAR-1996;   96US-0014608P.
PR   19-MAR-1997;   97US-0041264P.
PR   28-MAR-1997;   97US-00827208.
XX
PA   (ELIL) LILLY & CO ELI.
XX
PI   Choiu XC, Kramer RM, Pickard RT, Sharp JD, Strifler BA;
XX
DR   WPI; 2001-256372/26.
DR   N-PSDB; AAF74998, AAF74999.
XX
PT   Novel nucleic acid molecules encoding phospholipase A2 enzyme, useful in
PT   screening assays for identifying compounds that inhibit or block
PT   phospholipase A2 enzyme activity.
XX
PS   Claim 1; Col 53-58; 32pp; English.
XX
CC   The present invention describes an isolated polynucleotide (I),
CC   comprising a 3085 base pair phospholipase A2 (PLA2) sequence (given in
CC   AAF74999), encoding a 913 residue phospholipase A2 protein sequence
CC   (given in AAB74635), or a nucleotide sequence which hybridises under
CC   stringent conditions to the above mentioned nucleotide sequence. Also
CC   described are: (1) an isolated polynucleotide (II) comprising an 8517
CC   base pair sequence, given in AAF74998; (2) an expression vector (III)
CC   comprising (I) and an expression control sequence; (3) a host cell
CC   transformed with (III); (4) an expression vector (IV) comprising (II);
CC   operably linked to an expression control sequence; and (5) a host cell
CC   transformed with (IV). (I) is useful for screening compounds which
CC   inhibit or block cytosolic PLA2 (cPLA2) enzyme activity. The host cells
CC   transformed or transfected or transfected with cPLA2 enzymes in large
CC   quantities which are useful in screening assays for discovering agents
CC   that inhibit PLA2. The inhibitors identified are useful for treating
CC   inflammatory conditions such as rheumatoid arthritis, psoriasis, or
CC   asthma. (I) is also useful in the detection of mutant genomic DNA which
CC   has been digested with restriction enzymes and run on an electrophoretic
CC   gel by hybridising to the genomic DNA
XX
SQ   Sequence 913 AA;

Query Match   85.5%; Score 2767.5; DB 4; Length 913;
Best Local Similarity   87.6%; Pred. No. 3.2e-248;
Matches 537; Conservative 5; Mismatches 22; Indels 49; Gaps 6;

Qy   24 TGLLVLFCPAPCPFFFEMESLSVAQAGVQWRDLGSLQPPLGPKRFSCLSLPSSWDYR   83
          : | :   : : : :   : | |||
Db   319 TGTFRFHCPA-C----WEQE-LSI--------RLQDAPEEQLKAPLSALPSGQVVR   360

Qy   84 --------------------LRELAVRLGFGPCAEEQAFLSRRKQVVAAALRQALQLDGD 123
                              ||||||||||||||||||||||||||||||||||||||||
Db   361 LVFPTSQEPLMRVELKKEAGLRELAVRLGFGPCAEEQAFLSRRKQVVAAALRQALQLDGD 420

Qy   124 LQEDEIPVVAIMATGGIRAMTSLYGQLAGLKELGLLDCVSYITGASGSTWALANLYEDP   183
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   421 LQEDEIPVVAIMATGGIRAMTSLYGQLAGLKELGLLDCVSYITGASGSTWALANLYEDP   480

Qy   184 EWSQKDLAGPTELLKTQVTKNLGVLAPSQLQRYRQELAERARLGYPSCFTNLWALINEA   243
          |||:||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   481 EWSPQKDLAGPTELLKTQVTKNLGVLAPSQLQRYRQELAERARLGYPSCFTNLWALINEA 540

Qy   244 LLHDEPHDHKLSDQREALSHGQNPLPIYCALNTKGQSLTTFBFGEWCEFSPYEVGFPKYG 303
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   541 LLHDEPHDHKLSDQREALSHGQNPLPIYCALNTKGQSLTTFBFGEWCEFSPYEVGFPKYG 600

Qy   304 AFIPSELFGSEFFMGQLMKRLPESRICFLEGIWSNLYAANLQDSLYWASEPSQFWDRWVR 363
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   601 AFIPSELFGSEFFMGQLMKRLPESRICFLEGIWSNLYAANLQDSLYWASEPSQFWDRWVR 660

Qy   364 NQANLDKEQVPLLKIEBPPSTAGRIAEFFTDLLTWRPLAQATHNFLRGLHFHKDYFQHPH 423
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   661 NQANLDKEQVPLLKIEBPPSTAGRIAEFFTDLLTWRPLAQATHNFLRGLHFHKDYFQHPH 720

Qy   424 FSTWKATTLDGLPNQLTPSEPHLCLLDVGYLINTSCLPLLQPTRDVDLILSLDYNLHGAF 483
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   721 FSTWKATTLDGLPNQLTPSEPHLCLLDVGYLINTSCLPLLQPTRDVDLILSLDYNLHGAF 780

Qy   484 QQLQLLGRFCQEQGIPFPPISPSPEEQLQPRECHTFSDPTCPGAPAVLHF---------- 533
          |||||||||||||||||||||||||||||||||||||||||||||||||
Db   781 QQLQLLGRFCQEQGIPFPPISPSPEEQLQPRECHTFSDPTCPGAPAVLHFPLVSDSFREY 840

Qy   534 -SSGVRRTPEEAAAGEVNLSSSDSPYHYTKVTYSQEDVDKLLHLTHYNVCNNQEQLLEAL 592
           : ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   841 SAPGVRRTPEEAAAGEVNLSSSDSPYHYTKVTYSQEDVDKLLHLTHYNVCNNQEQLLEAL 900

Qy   593 RQAVQRRQRRPH 605
          ||||||||||||
Db   901 RQAVQRRQRRPH 913

RESULT 8
AAB82415
ID   AAB82415 standard; protein; 913 AA.
XX
AC   AAB82415;
XX
DT   06-AUG-2001 (first entry)
XX
DE   Human phospholipase A2.
XX
KW   Phospholipase A2; PLA2; bPLA2; PLA2-beta; inhibitor; screening;
KW   antiinflammatory; human; Alzheimer's disease; therapy.
XX
OS   Homo sapiens.
XX
PN   US6242206-B1.
XX
PD   05-JUN-2001.
XX
PF   07-FEB-2000; 2000US-00498809.
XX
PR   29-MAR-1996;   96US-0014608P.
PR   19-MAR-1997;   97US-0041264P.
PR   28-MAR-1997;   97US-00827208.
XX
PA   (ELIL) LILLY & CO ELI.
XX

PI   Choiu XC, Kramer RM, Pickard RT, Sharp JD, Strifler BA;
XX
DR   WPI; 2001-366537/38.
DR   N-PSDB; AAF90487, AAF90488.
XX
PT   Assays to evaluate the effectiveness of inhibitors of phospholipase A2,
PT   used to screen candidate compounds, comprise recombinant expression of a
PT   novel phospholipase A2.
XX
PS   Claim 1(a); Col 53-58; 32pp; English.
XX
CC   The present sequence is that of a novel human phospholipase A2 (PLA2,
CC   also referred to bPLA2 or PLA2-beta). PLA2 liberates arachidonic acid
CC   from phospholipids, leading to the production of eicosanoids involved in
CC   inflammatory reaction. A claimed assay for evaluating the effectiveness
CC   of a compound as an inhibitor of PLA2 involves culturing a cell
CC   transformed with an expression vector comprising PLA2 genomic DNA or cDNA
CC   (see AAF90487-88), isolating the PLA2, contacting it with a candidate
CC   compound, and determining whether the PLA2 activity has been inhibited.
CC   The assay provides rapid and efficient screening for new antiinflammatory
CC   drugs that inhibit the arachidonic acid cascade. These may be especially
CC   useful in the treatment of the inflammatory component of Alzheimer's
CC   disease
XX
SQ   Sequence 913 AA;

Query Match   85.5%;   Score 2767.5; DB 4; Length 913;
Best Local Similarity   87.6%;   Pred. No. 3.2e-248;
Matches 537;   Conservative   5; Mismatches   22; Indels 49; Gaps   6;

Qy   24 TGLLVLFCPAPCPFFFFEMESLSVAQGVQWRDLGSLQPPPLGFKRFSCLLSLPSSWDYR 83
          |||| :| || :   :||:   :|||
Db   319 TGTFRFHCPA-C-----WEQE-LSI----------------------RLQDAPEEQLKAPLSALPSGQVVR 360

Qy   84 ------------LRELAVRLGFGFGFCAEEQAFLSRRKQVVAAALRQALQLDGD 123
                      ||||||||||||||||||||||||||||||||||||||||
Db   361 LVFPTSQEPLMRVELKKEAGLRELAVRLGFGFCAEEQAFLSRRKQVVAAALRQALQLDGD 420

Qy   124 LQEDEIPVVAIMATGGGIRAMTSLYGQLAGLKELGLLDCVSYITGASGSTWALANLYEDP 183
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   421 LQEDEIPVVAIMATGGGIRAMTSLYGQLAGLKELGLLDCVSYITGASGSTWALANLYEDP 480

Qy   184 EWSQKDLAGPTELLKTQVTKNKLGVLAPSQLQRYRQELAERARLGYPSCFTNLWALINEA 243
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   481 EWSQKDLAGPTELLKTQVTKNKLGVLAPSQLQRYRQELAERARLGYPSCFTNLWALINEA 540

Qy   244 LLHDEPHDHKLSDQREALSHGQNPLPIYCALNTKGQSLTTFEFGEWCEFSPYEVGFPKYG 303
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   541 LLHDEPHDHKLSDQREALSHGQNPLPIYCALNTKGQSLTTFEFGEWCEFSPYEVGFPKYG 600

Qy   304 AFIPSELFGSEFFMGQLMKRLPESRICFLEGIWSNLYAANLQDSLYWASEPSQFWDRWVR 363
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   601 AFIPSELFGSEFFMGQLMKRLPESRICFLEGIWSNLYAANLQDSLYWASEPSQFWDRWVR 660

Qy   364 NQANLDKEQVPLLKIEEPPSTAGRIAEFFTDLLTWRPLAQATHNFLRGLHFHKDYFQHPH 423
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   661 NQANLDKEQVPLLKIEEPPSTAGRIAEFFTDLLTWRPLAQATHNFLRGLHFHKDYFQHPH 720

Qy   424 FSTWKATTLDGLPNQLTPSEPHLCLLDVGYLINTSCLPLLQPTRDVDLILSLDYNLHGAF 483
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   721 FSTWKATTLDGLPNQLTPSEPHLCLLDVGYLINTSCLPLLQPTRDVDLILSLDYNLHGAF 780

Qy   484 QQLQLLGRFCQEOGIPFPPISPSPEEQLQPRECHTFSDPTCPGAPAVLHF---------- 533
          ||||||||||||||||||||||||||||||||||||||||||||||||||
Db   781 QQLQLLGRFCQEOGIPFPPISPSPEEQLQPRECHTFSDPTCPGAPAVLHFPLVSDSFREY 840

Qy   534 -SSGVRRTPEEAAAGEVNLSSSDSPYHYTKVTYSQEDVDKLLHLTHYNVCNNQEQLLEAL 592
           : ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   841 SAPGVRRTPEEAAAGEVNLSSSDSPYHYTKVTYSQEDVDKLLHLTHYNVCNNQEQLLEAL 900

Qy   593 RQAVQRRRQRRPH 605
          |||||||||||||
Db   901 RQAVQRRRQRRPH 913

RESULT 9
AAB21140
ID   AAB21140 standard; protein; 533 AA.
XX
AC   AAB21140;
XX
DT   19-JAN-2001 (first entry)
XX
DE   Human cytosolic phospholipase A2 cPLA2 beta.
XX
KW   Human; cytosolic phospholipase A2 beta; cPLA2 beta; asthma; arthritis;
KW   inflammatory disease; crystal structure.
XX
OS   Homo sapiens.
XX
PN   WO200047763-A1.
XX
PD   17-AUG-2000.
XX
PF   14-FEB-2000; 2000WO-US003745.
XX
PR   15-FEB-1999; 99US-00250083.
XX
PA   (GEMY) GENETICS INST INC.
XX
PI   Dessen A, Somers WS, Stahl ML, Seehra JS;
XX
DR   WPI; 2000-558219/51.
XX
PT   New crystalline cytosolic phospholipase A2 (cPLA2) for identifying a
PT   species which is an agonist or antagonist of cPLA2 activity or binding
PT   that can be used to prevent or treat inflammation or inflammatory-related
PT   conditions.
XX
PS   Disclosure; Fig 4; 7ipp; English.
XX
CC   The present sequence is the human cytosolic phospholipase A2 (cPLA2) beta
CC   protein. The invention concerns the elucidation of the crystal structure
CC   of the protein and its use in drug design. The protein can be used to
CC   identify treatments for inflammation-related conditions such as
CC   rheumatoid arthritis, psoriasis, asthma, inflammatory bowel disease, and
CC   diseases such as osteoporosis, colitis, myelogenous leukaemia, diabetes,
CC   wasting and atherosclerosis
XX
SQ   Sequence 533 AA;

Query Match   85.5%;   Score 2765.5; DB 3; Length 533;
Best Local Similarity   97.6%;   Pred. No. 2.1e-248;
Matches 520;   Conservative   1; Mismatches   1; Indels   1; Gaps   1;

Qy   84 LRELAVRLGFGFGFCAEEQAFLSRRKQVVAAALRQALQLDGDLQEDEIPVVAIMATGGGIRA 143
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 LRELAVRLGFGFGFCAEEQAFLSRRKQVVAAALRQALQLDGDLQEDEIPVVAIMATGGGIRA 60

Qy   144 MTSLYGQLAGLKELGLLDCVSYITGASGSTWALANLYEDPEWSQKDLAGPTELLKTQVTK 203
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 MTSLYGQLAGLKELGLLDCVSYITGASGSTWALANLYEDPEWSQKDLAGPTELLKTQVTK 120

Qy   204 NKLGVLAPSQLQRYRQELAERARLGYPSCFTNLWALINEALLHDEPHDHKLSDQREALSH 263
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121 NKLGVLAPSQLQRYRQELAERARLGYPSCFTNLWALINEALLHDEPHDHKLSDQREALSH 180

Qy   264 GQNPLPIYCALNTKGQSLTTFEFGEWCEFSPYEVGFPKYGAFIPSELFGSEFFMGQLMKR 323
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181 GQNPLPIYCALNTKGQSLTTFEFGEWCEFSPYEVGFPKYGAFIPSELFGSEFFMGQLMKR 240

Qy   324 LPESRICFLEGIWSNLYAANLQDSLYWASEPSQFWDRWVRNQANLDKEQVPLLKIEEPPS 383
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241 LPESRICFLEGIWSNLYAANLQDSLYWASEPSQFWDRWVRNQANLDKEQVPLLKIEEPPS 300

Qy   384 TAGRIAEFFTDLLTWRPLAQATHNFLRGLHFHKDYFQHPHFSTWKATTLDGLPNQLTPSE 443

```
Db           ||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    301  TAGRIAEFFTDLLTWRPLAQATHNFLRGLHFHKDYFQHPHFSTWKATTLDGLPNQLTPSE  360

Db    444  PHLCLLDVGYLINTSCLPLLQPTRDVDLILSLDYNLHGAFQQLQLLGRFCQEQGIPFPPI  503
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361  PHLCLLDVGYLINTSCLPLLQPTRDVDLILSLDYNLHGAFQQLQLLGRFCQEQGIPFPPI  420

Qy    504  SPSPEEQLQPRECHTFSDPTCPGAPAVLHF-------SSGVRRTPEEAAAGEVNLS  552
           |||||||||||||||||||||||||||||        ||||||||||||||||||
Db    421  SPSPEEQLQPRECHTFSDPTCPGAPAVLHPLVSDSFREYSAPGVRRTPEEAAAGEVNLS  480

Qy    553  SSDSPYHYTKVTYSQEDVDKLLHLTHYNVCNNQEQLLEALRQAVQRRRQRRPH  605
           ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    481  SSDSPYHYTKVTYSQEDVDKLLHLTHYNVCNNQEQLLEALRQAVQRRRQRRPH  533
```

RESULT 10
ABG05871
ID   ABG05871 standard; protein; 1020 AA.
XX
AC   ABG05871;
XX
DT   13-FEB-2002 (first entry)
XX
DE   Novel human diagnostic protein #5862.
XX
KW   Human; chromosome mapping; gene mapping; gene therapy; forensic;
KW   food supplement; medical imaging; diagnostic; genetic disorder.
XX
OS   Homo sapiens.
XX
PN   WO200175067-A2.
XX
PD   11-OCT-2001.
XX
PF   30-MAR-2001; 2001WO-US008631.
XX
PR   31-MAR-2000; 2000US-00540217.
PR   23-AUG-2000; 2000US-00649167.
XX
PA   (HYSE-) HYSEQ INC.
XX
PI   Drmanac RT, Liu C, Tang YT;
XX
DR   WPI; 2001-639362/73.
DR   N-PSDB; AAS70058.
XX
PT   New isolated polynucleotide and encoded polypeptides, useful in
PT   diagnostics, forensics, gene mapping, identification of mutations
PT   responsible for genetic disorders or other traits and to assess
PT   biodiversity.
XX
PS   Claim 20; SEQ ID NO 36230; 103pp; English.
XX
CC   The invention relates to isolated polynucleotide (I) and polypeptide (II)
CC   sequences. (I) is useful as hybridisation probes, polymerase chain
CC   reaction (PCR) primers, oligomers, and for chromosome and gene mapping,
CC   and in recombinant production of (II). The polynucleotides are also used
CC   in diagnostics as expressed sequence tags for identifying normal
CC   genes. (I) is useful in gene therapy techniques to restore normal
CC   activity of (II) or to treat disease states involving (II). (II) is
CC   useful for generating antibodies against it, detecting or quantitating a
CC   polypeptide in tissue, as molecular weight markers and as a food
CC   supplement. (II) and its binding partners are useful in medical imaging
CC   of sites expressing (II). (I) and (II) are useful for treating disorders
CC   involving aberrant protein expression or biological activity. The
CC   polypeptide and polynucleotide sequences have applications in
CC   diagnostics, forensics, gene mapping, identification of mutations
CC   responsible for genetic disorders or other traits to assess biodiversity
CC   and to produce other types of data and products dependent on DNA and
CC   amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic
CC   amino acid sequences of the invention. Note: The sequence data for this
CC   patent did not appear in the printed specification, but was obtained in

CC   electronic format directly from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 1020 AA;

  Query Match   83.5%; Score 2700; DB 4; Length 1020;
  Best Local Similarity   86.4%; Pred. No. 7.5e-242;
  Matches 532; Conservative   5; Mismatches   27; Indels 52; Gaps   9;

```
Qy     24  TGLLVLFCPAPCPFFFEMESLSVAQAGVQWRDLGSLQPPPLGFKRFSCLLSLPSSWDYR   83
           |||  |  ||| |                        :|| || :   : |||   |:|
Db    423  TGTFRFHCPA-C-----WEQE-LSI---------RLQDAPEEQLKAPLSALPSGQVVR  464

Qy     84  ------------------LRELAVRLGFGPCAEEQAFLSRRKQVVAAALRQALQLDGD  123
                             ||||||||||||||||||||||||||||||||||||||||
Db    465  LVFPTSQEPLMRVELKKEAGLRELAVRLGFGPCAEEQAFLSRRKQVVAAALRQALQLDGD  524

Qy    124  LQEDEIPVAIMATGGGIRAMTSLYGOLAGLKELGLLDCVSYITGASGSTWALANLYEDP  183
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    525  LQEDEIPVAIMATGGGIRAMTSLYGOLAGLKELGLLDCVSYITGASGSTWALANLYEDP  584

Qy    184  EWSQKDLAGPTELLKTQVTKNKLGVLAPSQLQRYRQELAERARLGYPSCFTNLWALINEA  243
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    585  EWSQKDLAGPTELLKTQVTKNKLGVLAPSQLQRYRQELAERARLGYPSCFTNLWALINEA  644

Qy    244  LLHDEPHDHKLSDQREALSHGQNPLPIYCALNTKGQSLTTFEFGEWCEFSPYEVGFPKYG  303
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    645  LLHDEPHDHKLSDQREALSHGQNPLPIYCALNTKGQSLTTFEFGEWCEFSPYEVGFPKYG  704

Qy    304  AFIPSELFGSEFFMGQLMKRLPESRICFLEGIWSNLYAANLQDSLYWASEPSQFWDRWV-  362
           |||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||
Db    705  AFIPSELFGSEFFMGQLKKRLPESRICFLEGIWSNLYAANLQDSLYWASEPSQFWDRWVS  764

Qy    363  RNQANLDKEQVPLLKIEEPPSTAGRIAEFFTDLLTWRPLAQATHNFLRGLH-FHKDYFQH  421
           |||||||||||||||||||||||||||||||||||||||||||| |||||: |||||||
Db    765  RNQANLDKEQVPLLKIEEPPSTAGRIAEFFTDLLTWRPLAQATQNFLRGRSIFHKDYFQH  824

Qy    422  PHFSTWKATTLDGLPNQLTPSEPHLCLLDVGY-LINTSCLPLLQPTRDVDLILSLDYNLH  480
           |||||||||||||||||||||||||||||| | |||||||||||||||||||||||||||
Db    825  PHFSTWKATTLDGLPNQLTPSEPHLCLLDGGYTLINTSCLPLLQPTRDVDLILSLDYNLH  884

Qy    481  GAFQQLQLLGRFCQEQGIPFPPISPSPEEQLQPRECHTFSDPTCPGAPAVLHF------  533
           |||||||||||||||||||||||||||||||||||||||||||||||||||
Db    885  GAFQQLQLLGRFCQEQGIPFPPISPSPEEQLQPRRCHTFSDPTCPGAPAVLHFPLVSDSF  944

Qy    534  ----SSGVRRTPEEAAAGEVNLSSSDSPYHYTKVTYSQEDVDKLLHLTHYNVCNNQEQLL  589
               |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    945  REYSAPGVRRTPEEAAAGEVNLSSSDSPYHYTKVTYSQEDVDKLLHLTHYNVCNNQEQLL  1004

Qy    590  EALRQAVQRRRQRRPH  605
           ||||||||||||||||
Db   1005  EALRQAVQRRRQRRPH  1020
```

RESULT 11
ABG20154
ID   ABG20154 standard; protein; 1040 AA.
XX
AC   ABG20154;
XX
DT   18-FEB-2002 (first entry)
XX
DE   Novel human diagnostic protein #20145.
XX
KW   Human; chromosome mapping; gene mapping; gene therapy; forensic;
KW   food supplement; medical imaging; diagnostic; genetic disorder.
XX
OS   Homo sapiens.
XX
PN   WO200175067-A2.
XX
PD   11-OCT-2001.
XX

```
PF   30-MAR-2001; 2001WO-US008631.
XX
PR   31-MAR-2000; 2000US-00540217.
PR   23-AUG-2000; 2000US-00649167.
XX
PA   (HYSE-) HYSEQ INC.
XX
PI   Drmanac RT, Liu C, Tang YT;
XX
DR   WPI; 2001-639362/73.
DR   N-PSDB; AAS84341.
XX
PT   New isolated polynucleotide and encoded polypeptides, useful in
PT   diagnostics, forensics, gene mapping, identification of mutations
PT   responsible for genetic disorders or other traits and to assess
PT   biodiversity.
XX
PS   Claim 20; SEQ ID NO 50513; 103pp; English.
XX
CC   The invention relates to isolated polynucleotide (I) and polypeptide (II)
CC   sequences. (I) is useful as hybridisation probes, polymerase chain
CC   reaction (PCR) primers, oligomers, and for chromosome and gene mapping,
CC   and in recombinant production of (II). The polynucleotides are also used
CC   in diagnostics as expressed sequence tags for identifying expressed
CC   genes. (I) is useful in gene therapy techniques to restore normal
CC   activity of (II) or to treat disease states involving (II). (II) is
CC   useful for generating antibodies against it, detecting or quantitating a
CC   polypeptide in tissue, as molecular weight markers and as a food
CC   supplement. (II) and its binding partners are useful in medical imaging
CC   of sites expressing (II). (I) and (II) are useful for treating disorders
CC   involving aberrant protein expression or biological activity. The
CC   polypeptide and polynucleotide sequences have application in
CC   diagnostics, forensics, gene mapping, identification of mutations
CC   responsible for genetic disorders or other traits to assess biodiversity
CC   and to produce other types of data and products dependent on DNA and
CC   amino acid sequences. ABG0010-ABG30377 represent novel human diagnostic
CC   amino acid sequences of the invention. Note: The sequence data for this
CC   patent did not appear in the printed specification, but was obtained in
CC   electronic format directly from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 1040 AA;

Query Match             80.7%;  Score 2610.5;  DB 4;  Length 1040;
Best Local Similarity   84.3%;  Pred. No. 1.7e-233;
Matches 520; Conservative   7; Mismatches 35;  Indels   55;  Gaps   11;

Qy       24 TGLLVLFCPAPCPFFFFEMESLSVAQGVQWRDLGSLQPPLGFKRFSCLSLPSSWDYR 83
            ||||| ||| |   || |  :| || |:  : |||:: |  : |||| ||| ||
Db      430 TGTFRFHCPA-C-----WEQE-LSI-------RLQDAPEEQLKAPLSALPSGQVVR 471

Qy       84 -------------LRELAVRLGFGPCAEEQAFLSRRKQVVAAALRQALQLDGD 123
                         ||||||||||||||||||||||||||||||||||||||||
Db      472 LVFPTSQEPLMRVELKKEAGLRELAVRLGFGPCAEEQAFLSRRKQVVAAALRQALQLDGD 531

Qy      124 LQEDEIPVVAIMATGGGIRAMTSLYGQLAGLKEIGLLDCVSYITGASGSTWALANLYEDP 183
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      532 LQEDEIPVVAIMATGGGIRAMTSLYGQLAGLKEIGLLDCVSYITGASGSTWALANLYEDP 591

Qy      184 EWSQKDLAGPTELLKTQVTKNKLGVLAPSQLQRYRQELAERARLGYPSCFTNLWALINEA 243
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      592 EWSQKDLAGPTELLKTQVTKNKLGVLAPSQLQRYRQELAERARLGYPSCFTNLWALINEA 651

Qy      244 LLHDEPHDHKLSDQREALSHGQNPLPIYCALNTKGQSLTTFEFGEWCEFSPYEVGFPKYG 303
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      652 LLHDEPHDHKLSDQREALSHGQNPLPIYCALNTKGQSLTTFEFGEWCEFSPYEVGFPKYG 711

Qy      304 AFIPSELFGSEFFMGQLMKRLPESRICFLEGIWSNLYAANLQDSLYWASEPSQFWDRWV- 362
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      712 AFIPSELFGSEFFMGQLKKRLPESRICFLEGIWSNLYAANLQDSLYWASEPSQFWDRWVS 771

Qy      363 RNQANLDKEQVPLLKIEEPPSTAGRIAEFFTDLLTWRPLAQATHNFLRGLH-FHKDYFQH 421
            |||||||||||||||||||||||||||||| |||  |||| |||| |||| ||||||||
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Db      772 RNQANLDKEQVPLLKIEEPPSTAGRIAEFFTDLLTWRPLAQATQNFLRGRSIFHKDYFQH 831
            |||||||||||||||||||||||||||||| |||  |||| :||| |||| ||||||||
Qy      422 PHFSTWKATTLDGLPNQLTPSEPHLCLLDVGY-LINTSCLPLLQPTRDVDLILSLDYNLH 480
            |||||||||||||||||||||||||||||||| |||||||||||||||||||||||||||
Db      832 PHFSTWKATTLDGLPNQLTPSEPHLCLLDGGYTLINTSCLPLLQPTRDVDLILSLDYNLH 891
            ||||||||||||||||||||||||||||| || |||||||||||||||||||||||||||
Qy      481 GAFQQLQLLGRFCQEGIPFPPISPSPEEQLQP-RECHTFSDPTCPGAPAVLHF------ 533
            |||||||||||||||||||||||||||||||| :|||||||||||||||||||
Db      892 GAFQQLQLLGRFCQEGIPFPPISPSPEEQLQPWRSCHTFSDPTCPGAPAVLHFPLVSDS 951
            |||||||||||||||||||||||||||||||| :|||||||||||||||||||
Qy      534 ------SSGVRRTPEAAAGEVNLSSSDSPYHYTKVTYSQEDVDKLLHLTHYNVCNNQEQL 588
                  :||:|||||||||||||||||||||||||||||||||||||||||||||||||
Db      952 FREYSAPGVRRTPEAAAGEVNLSSSDSPYHYTKVTYSQEDVDKLLHLTHYNVCNNQEQL 1011
                  :: |||||||||||||||||||||||||||||||||||||||||||||||||
Qy      589 LEAL--RQAVQRRRQRR 603
                   :|| |||| ||
Db     1012 LGRLCAPGSANGRRQRK 1028
```

```
RESULT 12
AAW75132
ID   AAW75132 standard; protein; 483 AA.
XX
AC   AAW75132;
XX
DT   25-MAR-2003 (revised)
DT   28-JAN-1999 (first entry)
XX
DE   Human secreted protein encoded by gene 11 clone HCENJ40.
XX
KW   Human; secreted protein; fusion protein; gene therapy; protein therapy;
KW   diagnosis; tissue; cancer; tumour; neurodegenerative disorder; leukaemia;
KW   developmental abnormality; foetal deficiency; blood; allergy; renal;
KW   immune system; asthma; lymphocytic disease; brain; hepatic; lymphoma;
KW   inflammation; ischaemic shock; Alzheimer's disease; restenosis; AIDS;
KW   cognitive disorder; schizophrenia; prostate; obesity; osteoclast; thymus;
KW   osteoporosis; arthritis; testis; lung; thyroiditis; thyroid; digestion;
KW   endocrine; metabolism; regulation; malabsorption; gastritis; neoplasm.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Misc-difference 29
FT                   /label= unknown
FT   Misc-difference 483
FT                   /label= unknown
XX
PN   WO9839446-A2.
XX
PD   11-SEP-1998.
XX
PF   06-MAR-1998;  98WO-US004482.
XX
PR   07-MAR-1997;  97US-0038621P.
PR   07-MAR-1997;  97US-0040161P.
PR   07-MAR-1997;  97US-0040162P.
PR   07-MAR-1997;  97US-0040163P.
PR   07-MAR-1997;  97US-0040333P.
PR   07-MAR-1997;  97US-0040334P.
PR   07-MAR-1997;  97US-0040336P.
PR   07-MAR-1997;  97US-0040626P.
PR   11-APR-1997;  97US-0043311P.
PR   11-APR-1997;  97US-0043312P.
PR   11-APR-1997;  97US-0043313P.
PR   11-APR-1997;  97US-0043314P.
PR   11-APR-1997;  97US-0043315P.
PR   11-APR-1997;  97US-0043568P.
PR   11-APR-1997;  97US-0043569P.
PR   11-APR-1997;  97US-0043576P.
PR   11-APR-1997;  97US-0043578P.
PR   11-APR-1997;  97US-0043580P.
PR   11-APR-1997;  97US-0043670P.
```

us-09-830-321a-2.rag

```
XX
PA   (HUMA-) HUMAN GENOME SCI INC.
XX
PI   Ruben SM, Rosen CA, Fischer CL, Soppet DR, Carter KC;
PI   Bednarik DP, Endress GA, Yu G, Ni J, Feng P, Young PE, Greene JM;
PI   Ferrie AM, Duan R, Hu J, Florence KA, Olsen HS, Ebner R, Brewer LA;
PI   Moore PA, Shi Y, Lafleur DW, Li Y, Zeng Z, Kyaw H;
XX
DR   WPI; 1998-609887/51.
DR   N-PSDB; AAV34229.
XX
PT   New isolated human genes and the secreted polypeptides they encode -
PT   useful for diagnosis and treatment of e.g. cancers, neurological
PT   disorders, immune diseases, inflammation or blood disorders.
XX
PS   Claim 1; Page 326-327; 447pp; English.
XX
CC   This sequence represents a secreted human protein encoded by the gene
CC   clone detailed in the descriptor line. The gene can be used to generate
CC   fusion proteins by linking to the gene to a human immunoglobulin Fc
CC   portion (e.g. AAV34145) for increasing the stability of the fused protein
CC   as compared to the human protein only. The invention relates to 70 novel
CC   genes and their fragments (nucleic acid sequences: AAV34154-V34276; amino
CC   acid sequences AAW75057-W75179) which are useful for preventing, treating
CC   or ameliorating medical conditions e.g. by protein or gene therapy. Also,
CC   pathological conditions can be diagnosed by determining the amount of the
CC   new polypeptides in a sample or by determining the presence of mutations
CC   in the new polynucleotides. Specific uses are described for each of the
CC   70 polynucleotides, based on which tissues they are most highly expressed
CC   in (see AAV34154 for described uses). (Updated on 25-MAR-2003 to correct
CC   PF field.) (Updated on 25-MAR-2003 to correct PI field.)
XX
SQ   Sequence 483 AA;

Query Match             77.6%;  Score 2509.5;  DB 2;  Length 483;
Best Local Similarity   96.9%;  Pred No. 1.3e-224;
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Qy        255 SDQREALSHGQNPLPIYCALNTKGQSLTTFEFGEWCEFSPYEVGPFKYGAFIPSELFGSE 314
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Db        121 SDQREALSHGQNPLPIYCALNTKGQSLTTFEFGEWCEFSPYEVGPFKYGAFIPSELFGSE 180

Qy        315 FFMGQLMKRLPESRICFLEGIWSNLYAANLQDSLYWASEPSQFWDRWVRNQANLDKEQVP 374
                  |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 FFMGQLMKRLPESRICFLEGIWSNLYAANLQDSLYWASEPSQFWDRWVRNQANLDKEQVP 240

Qy        375 LLKIEEPPSTAGRIAEFFTDLLTWRPLAQATHNFLRGLHFHKDYFQHPHFSTWKATTLDG 434
                  |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 LLKIEEPPSTAGRIAEFFTDLLTWRPLAQATHNFLRGLHFHKDYFQHPHFSTWKATTLDG 300

Qy        435 LPNQLTPSEPHLCLLDVGYLINTSCLPLLQPTRDVDLILSLLDYNLHGAFQQLLGRFCQ 494
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Qy        495 EQGIPFPPISPSPEEQLQPRECHTFSDPTCPGAPAVLHF----------SSGVRRTPEE 543
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Qy        544 AAAGEVNLSSSDSPYHYTKVTYSQEDVDKLLHLTHYNVCNNQEQLLEALRQAVQRRRQRR 603
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Qy        604 PH 605
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PR 23-MAY-1997; 97US-0047502P.
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PR 05-SEP-1997; 97US-0057650P.
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DT   25-MAR-2003   (revised)
DT   28-JAN-1999   (first entry)
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KW   Human; secreted protein; fusion protein; gene therapy; protein therapy;
KW   diagnosis; tissue; cancer; tumour; neurodegenerative disorder; leukaemia;
KW   developmental abnormality; foetal deficiency; blood; allergy; renal;
KW   immune system; asthma; lymphocytic disease; brain; hepatic; lymphoma;
KW   inflammation; ischaemic shock; Alzheimer's disease; restenosis; AIDS;
KW   cognitive disorder; schizophrenia; prostate; obesity; osteoclast; thymus;
KW   osteoporosis; arthritis; testis; lung; thyroiditis; thyroid; digestion;
KW   endocrine; metabolism; regulation; malabsorption; gastritis; neoplasm.
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OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Misc-difference 29
FT                   /label= unknown
FT   Misc-difference 483
FT                   /label= unknown
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PN   WO9839446-A2.
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PD   11-SEP-1998.
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PF   06-MAR-1998;   98WO-US004482.
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                                            XX
                                            PA   (HUMA-) HUMAN GENOME SCI INC.
                                            XX
                                            PI   Ruben SM, Rosen CA, Fischer CL, Soppet DR, Carter KC;
                                            PI   Bednarik DP, Endress GA, Yu G, Ni J, Feng P, Young PE, Greene JM;
                                            PI   Ferrie AM, Duan R, Hu J, Florence KA, Olsen HS, Ebner R, Brewer LA;
                                            PI   Moore PA, Shi Y, Lafleur DW, Li Y, Zeng Z, Kyaw H;
                                            XX
                                            DR   WPI; 1998-609887/51.
                                            DR   N-PSDB; AAV34164.
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                                            PT   New isolated human genes and the secreted polypeptides they encode -
                                            PT   useful for diagnosis and treatment of e.g. cancers, neurological
                                            PT   disorders, immune diseases, inflammation or blood disorders.
                                            XX
                                            PS   Claim 1; Page 285-287; 447pp; English.
                                            XX
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CC      This sequence represents a secreted human protein encoded by the gene
CC      clone detailed in the descriptor line. The gene can be used to generate
CC      fusion proteins by linking to the gene to a human immunoglobulin Fc
CC      portion (e.g. AAV34145) for increasing the stability of the fused protein
CC      as compared to the human protein only. The invention relates to 70 novel
CC      genes and their fragments (nucleic acid sequences: AAV34154-V34276; amino
CC      acid sequences AAW75057-W75179) which are useful for preventing, treating
CC      or ameliorating medical conditions e.g. by protein or gene therapy. Also,
CC      pathological conditions can be diagnosed by determining the amount of the
CC      new polypeptides in a sample or by determining the presence of mutations
CC      in the new polynucleotides. Specific uses are described for each of the
CC      70 polynucleotides, based on which tissues they are most highly expressed
CC      in (see AAV34154 for described uses). (Updated on 25-MAR-2003 to correct
CC      PF field.) (Updated on 25-MAR-2003 to correct PI field.)
XX
SQ      Sequence 483 AA;
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Query Match         77.6%;     Score 2509.1;  DB 2;   Length 483;
Best Local Similarity  96.9%;  Pred. No. 1.3e-224;
Matches  467;   Conservative     2;  Mismatches      2;  Indels    11;  Gaps     1;
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Qy     255 SDQREALSHGQNPLPIYCALNTKGQSLTTFEFGEWCEFSPYEVGFPKYGAFIPSELFGSE 314
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               |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy     604 PH 605
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Db     481 PH 482
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ID   AB001943 standard;  protein; 483 AA.
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AC   AB001943;
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DT   12-AUG-2003  (first entry)
XX
DE   Novel human secreted protein #11.
XX
KW   Human; immunoglobulin G; IgG; fragment of crystallisation; FC;
KW   immune system disorder; haematopoietic cell disorder;
KW   immunologic deficiency disorder; ataxia telangiectasia; HIV infection;
KW   Wiskott-Aldrich disorder; thrombocytopenia; haemoglobinuria;
KW   blood coagulation disorder; blood platelet disorder; autoimmune disorder;
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KW   Addison's disease; haemolytic anaemia; rheumatoid arthritis; dermatitis;
KW   glomerulonephritis; Grave's disease; allergic reaction;
KW   graft-versus-host disease; hyperproliferative disorder; neoplasm;
KW   infectious disease; nervous system disease; spinal cord disorder;
KW   head trauma; stroke; tissue regeneration; congenital defect; trauma;
KW   wound; burn; incision; ulcer; age disease; osteoporosis;
KW   periodontal disease; liver failure; catabolism; anabolism; metabolism;
KW   food additive; preservative; secreted protein.
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OS   Homo sapiens.
XX
PN   US2003027132-A1.
XX
PD   06-FEB-2003.
XX
PF   04-SEP-1998;                98US-0148545.
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PR	22-AUG-1997;	97US-0056893P.
PR	22-AUG-1997;	97US-0056894P.
PR	22-AUG-1997;	97US-0056903P.
PR	22-AUG-1997;	97US-0056908P.
PR	22-AUG-1997;	97US-0056909P.
PR	22-AUG-1997;	97US-0056910P.
PR	22-AUG-1997;	97US-0056911P.
PR	05-SEP-1997;	97US-0057650P.
PR	05-SEP-1997;	97US-0057761P.
PR	06-MAR-1998;	98WO-US004482.
XX		
PA	(RUBE/)	RUBEN S M.
PA	(ROSE/)	ROSEN C A.
PA	(FISC/)	FISCHER C L.
PA	(SOPP/)	SOPPET D R.
PA	(CART/)	CARTER K C.
PA	(BEDN/)	BEDNARIK D R.
PA	(ENDR/)	ENDRESS G A.
PA	(YUGG/)	YU G.
PA	(NIJJ/)	NI J.
PA	(FENG/)	FENG P.
PA	(YOUN/)	YOUNG P E.
PA	(GREE/)	GREENE J M.
PA	(FERR/)	FERRIE A M.
PA	(DUAN/)	DUAN R.
PA	(HUJJ/)	HU J.
PA	(FLOR/)	FLORENCE K A.
PA	(OLSE/)	OLSEN H S.
PA	(EBNE/)	EBNER R.
PA	(BREW/)	BREWER L A.
XX	(SHIY/)	SHI Y.

PI Ruben SM, Rosen CA, Fischer CL, Soppet DR, Carter KC;
PI Bednarik DR, Endress GA, Yu G, Ni J, Feng P, Young PE, Greene JM;
PI Ferrie AM, Duan R, Hu J, Florence KA, Olsen HS, Ebner R, Brewer LA;
PI Shi Y;
XX
DR WPI; 2003-466138/44.
DR N-PSDB; ACD08035.
XX
PT Novel isolated human secreted HODAZ50 polypeptide useful for diagnosing
PT or treating deficiencies or disorders of the immune system, autoimmune
PT disorders, hyperproliferative disorders, and infectious diseases.
XX
PS Claim 11; Page 177-178; 243pp; English.

XX
CC   The invention describes an isolated human secreted HODAZ50 polypeptide
CC   (I) comprising a sequence at least 95% identical to a sequence selected
CC   from polypeptide fragment of any one of the 123 polypeptide sequences
CC   (PS) fully defined in the specification and having biological activity,
CC   polypeptide domain or epitope of PS, secreted form of PS, full-length
CC   protein of PS, or variant, allelic variant or species homologue of PS.
CC   (I) or a polynucleotide (II) encoding (I) is useful for preventing,
CC   treating, or ameliorating a medical condition in a mammalian subject. (I)
CC   or (II) is also useful for diagnosing a pathological condition or a
CC   susceptibility to a pathological condition in a subject. (I) is useful
CC   for identifying a binding partner which involves contacting the
CC   polypeptide with the binding partner and determining whether the binding
CC   partner affects the activity of the polypeptide. (I) or (II) is useful
CC   for diagnosing or treating deficiencies or disorders of the immune
CC   system, deficiencies or disorders of haematopoietic cells, to treat
CC   immunologic deficiency disorders, ataxia telangiectasia, HIV infection,
CC   Wiskott-Aldrich disorders, thrombocytopenia or haemoglobinuria, blood
CC   coagulation disorders, blood platelet disorders, autoimmune disorders
CC   (e.g. Addison's disease, haemolytic anaemia, rheumatoid arthritis,
CC   dermatitis, glomerulonephritis, Grave's disease), allergic reactions,
CC   graft-versus-host disease, hyperproliferative disorders (e.g., neoplasms
CC   located in the abdomen, bone, breast, digestive system, liver, pancreas,
CC   peritoneum, endocrine glands), infection diseases (e.g. viral,
CC   bacterial, fungal or parasitic infection), central and peripheral nervous
CC   system diseases (e.g. spinal cord disorders, head trauma or stroke), to
CC   differentiate, proliferate and attract cells leading to the regeneration
CC   of tissues to repair, replace or protect tissue damaged by congenital
CC   defects, trauma (wounds, burns, incisions, or ulcers) age disease (e.g.,
CC   osteoporosis, periodontal disease, liver failure) or surgery. (I) or (IV)
CC   is useful to modulate mammalian characteristics, to modulate mammalian
CC   metabolism affecting catabolism, anabolism, processing, utilisation, and
CC   storage of energy, to change a mammal's mental state or physical state,
CC   or as a food additive or preservative, such as to increase or decrease
CC   storage capabilities, fat content, lipid, protein, carbohydrate,
CC   vitamins, minerals, cofactors or other nutritional components. This is
CC   the amino acid sequence of a novel human secreted protein
XX
SQ   Sequence 483 AA;

Query Match   77.6%;   Score 2509.5; DB 6; Length 483;
Best Local Similarity   96.9%;   Pred. No. 1.3e-224;
Matches 467;   Conservative   2;   Mismatches 2;   Indels 11;   Gaps   1;

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Qy   195 ELLKTQVTKNKLGVLAPSQLQRYRQELAERARLGYPSCFTNLWALINEALLHDEPHDHKL 254
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 ELLKTQVTKNKLGVLAPSQLQRYRQELAERARLGYPSCFTNLWALINEALLHDEPHDHKL 120

Qy   255 SDQREALSHGQNPLPIYCALNTKGQSLTTFEFGEWCEFSPYEVGFPPKYGAFIPSELFGSE 314
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121 SDQREALSHGQNPLPIYCALNTKGQSLTTFEFGEWCEFSPYEVGFPPKYGAFIPSELFGSE 180

Qy   315 FFMGQLMKRLPESRICFLEGIWSNLYAANLQDSLYWASEPSQFWDRWVRNQANLDKEQVP 374
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181 FFMGQLMKRLPESRICFLEGIWSNLYAANLQDSLYWASEPSQFWDRWVRNQANLDKEQVP 240

Qy   375 LLKIEEPPSTAGRIAEFFTDLLTWRPLAQATHNFLRGLHFHKDYFQHPHFSTWKATTLDG 434
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241 LLKIEEPPSTAGRIAEFFTDLLTWRPLAQATHNFLRGLHFHKDYFQHPHFSTWKATTLDG 300

Qy   435 LPNQLTPSEPHLCLLDVGYLINTSCLPLLQPTRDVDLLILSLDYNLHGAFQQLQLGRFCQ 494
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Db   301 LPNQLTPSEPHLCLLDVGYLINTSCLPLLQPTRDVDLLILSLDYNLHGAFQQLQLGRFCQ 360

Qy   495 EQGIPFPPISPSPPEQLQPRECHTFSDPTCPGAPAVLHF------------SSGVRRTPEE 543
           |||||||||||||||||||||||||||||||||||||||| :|||||||||
Db   361 EQGIPFPPISPSPPEQLQPRECHTFSDPTCPGAPAVLHPLVSDSFREYSAPGVRRTPEE 420

Qy   544 AAGEVNLSSSDSPYHYTKVTYSQEDVDKLLHLTHYNVCNNQEQLLEALRQAVQRRRQRR 603

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Qy        604 PH 605
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Db        481 PH 482


RESULT 15
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ID   AB002008 standard; protein; 483 AA.
XX
AC   AB002008;
XX
DT   12-AUG-2003  (first entry)
XX
DE   Novel human secreted protein #76.
XX
KW   Human; immunoglobulin G; IgG; fragment of crystallisation; Fc;
KW   immune system disorder; haematopoietic cell disorder;
KW   immunologic deficiency disorder; ataxia telangiectasia; HIV infection;
KW   Wiskott-Aldrich disorder; thrombocytopenia; haemoglobinuria;
KW   blood coagulation disorder; blood platelet disorder; autoimmune disorder;
KW   Addison's disease; haemolytic anaemia; rheumatoid arthritis; dermatitis;
KW   glomerulonephritis; Grave's disease; allergic reaction;
KW   graft-versus-host disease; hyperproliferative disorder; neoplasm;
KW   infectious disease; nervous system disease; spinal cord disorder;
KW   head trauma; stroke; tissue regeneration; congenital defect; trauma;
KW   wound; burn; incision; ulcer; age disease; osteoporosis;
KW   periodontal disease; liver failure; catabolism; anabolism; metabolism;
KW   food additive; preservative; secreted protein.
XX
OS   Homo sapiens.
XX
PN   US2003027132-A1.
XX
PD   06-FEB-2003.
XX
PF   04-SEP-1998;   98US-00148545.
XX
PR   07-MAR-1997;   97US-0038621P.
PR   07-MAR-1997;   97US-0040161P.
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PR   07-MAR-1997;   97US-0040163P.
PR   07-MAR-1997;   97US-0040333P.
PR   07-MAR-1997;   97US-0040334P.
PR   07-MAR-1997;   97US-0040336P.
PR   07-APR-1997;   97US-0040626P.
PR   11-APR-1997;   97US-0043311P.
PR   11-APR-1997;   97US-0043312P.
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PR   23-MAY-1997;   97US-0047633P.
PR   06-JUN-1997;   97US-0048964P.
PR   06-JUN-1997;   97US-0048974P.
PR   22-AUG-1997;   97US-0056630P.
PR   22-AUG-1997;   97US-0056631P.
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PR   22-AUG-1997;   97US-0056911P.
PR   05-SEP-1997;   97US-0057650P.
PR   05-SEP-1997;   97US-0057761P.
PR   06-MAR-1998;   98WO-US004482.
XX
PA   (RUBE/)  RUBEN S M.
PA   (ROSE/)  ROSEN C A.
PA   (FISC/)  FISCHER C L.
PA   (SOPP/)  SOPPET D R.
PA   (CART/)  CARTER K C.
PA   (BEDN/)  BEDNARIK D R.
PA   (ENDR/)  ENDRESS G A.
PA   (YUGG/)  YU G.
PA   (NIJJ/)  NI J.
PA   (FENG/)  FENG P.
PA   (YOUN/)  YOUNG P E.
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PA   (HUJJ/)   HU J.
PA   (FLOR/)   FLORENCE K A.
PA   (OLSE/)   OLSEN H S.
PA   (EBNE/)   EBNER R.
PA   (BREW/)   BREWER L A.
XX   (SHIY/)   SHI Y.
PI   Ruben SM, Rosen CA, Fischer CL, Soppet DR, Carter KC;
PI   Bednarik DR, Endress GA, Yu G, Ni J, Feng P, Young PE, Greene JM;
PI   Ferrie AM, Duan R, Hu J, Florence KA, Olsen HS, Ebner R, Brewer LA;
PI   Shi Y;
XX
DR   WPI; 2003-466138/44.
DR   N-PSDB; ACD08100.
XX
PT   Novel isolated human secreted HODAZ50 polypeptide useful for diagnosing
PT   or treating deficiencies or disorders of the immune system, autoimmune
PT   disorders, hyperproliferative disorders, and infectious diseases.
XX
PS   Claim 11; Page 210; 243pp; English.
XX
CC   The invention describes an isolated human secreted HODAZ50 polypeptide   (I)
CC   (I) comprising a sequence at least 95% identical to a sequence selected
CC   from polypeptide fragment of any one of the 123 polypeptide sequences
CC   (PS) fully defined in the specification and having biological activity,
CC   polypeptide domain or epitope of PS, secreted form of PS, full-length
CC   protein of PS, or variant, allelic variant or species homologue of PS.
CC   (I) or a polynucleotide (II) encoding (I) is useful for preventing,
CC   treating, or ameliorating a medical condition in a mammalian subject.   (I)
CC   or (II) is also useful for diagnosing a pathological condition or a
CC   susceptibility to a pathological condition in a subject. (I) is useful
CC   for identifying a binding partner which involves contacting the
CC   polypeptide with the binding partner and determining whether the binding
CC   partner affects the activity of the polypeptide. (I) or (II) is useful
CC   for diagnosing or treating deficiencies or disorders of the immune
CC   system, deficiencies or disorders of haematopoietic cells, to treat
CC   immunologic deficiency disorders, ataxia telangiectasia, HIV infection,
CC   Wiskott-Aldrich disorders, thrombocytopenia or haemoglobinuria, blood
CC   coagulation disorders, blood platelet disorders, autoimmune disorders
CC   (e.g., Addison's disease, haemolytic anaemia, rheumatoid arthritis,
CC   dermatitis, glomerulonephritis, Grave's disease), allergic reactions,
CC   graft-versus-host disease, hyperproliferative disorders (e.g., neoplasms
CC   located in the abdomen, bone, breast, digestive system, liver, pancreas,
CC   peritoneum, endocrine glands), infectious diseases (e.g., viral,
CC   bacterial, fungal or parasitic infection), central and peripheral nervous
CC   system diseases (e.g., spinal cord disorders, head trauma or stroke), to
CC   differentiate, proliferate and attract cells leading to the regeneration
CC   of tissues to repair, replace or protect tissue damaged by congenital
CC   defects, trauma (wounds, burns, incisions, or ulcers) age disease (e.g.,
CC   osteoporosis, periodontal disease, liver failure) or surgery. (I) or (IV)
CC   is useful to modulate mammalian characteristics, to modulate mammalian
CC   metabolism affecting catabolism, anabolism, processing, utilisation, and
CC   storage of energy, to change a mammal's mental state or physical state,
CC   or as a food additive or preservative, such as to increase or decrease
CC   storage capabilities, fat content, lipid, protein, carbohydrate,
CC   vitamins, minerals, cofactors or other nutritional components. This is
CC   the amino acid sequence of a novel human secreted protein
XX
SQ   Sequence 483 AA;

Query Match             77.6%;  Score 2509.5;  DB 6;  Length 483;
Best Local Similarity   96.9%;  Pred. No. 1.3e-224;
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Qy     315 FFMGQLMKRLPESRICFLEGIWSNLYAANLQDSLYWASEPSQFWDRWVRNQANLDKEQVP 374
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Qy     375 LLKIEPPSTAGRIAEFFTDLLTWRPLAQATHNFLRGLHFHKDYFQHPHFSTWKATTLDG 434
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Qy     435 LPNQLTPSEPHLCLLDVGYLINTSCLPLLQPTRDVDLILSLDYNLHGAFQQLQLLGRFCQ 494
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OM protein - protein search, using sw model

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              GenCore version 5.1.6
       Copyright (c) 1993 - 2004 Compugen Ltd.
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Title: US-09-830-321A-2
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Scoring table: BLOSUM62
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Total number of hits satisfying chosen parameters: 389414

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
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                 Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Match	Length	DB	ID	Description
1	2767.5	85.5	778	778	3	US-09-460-145-2	Sequence 2, Appli
2	2767.5	85.5	778	778	4	US-09-895-547-2	Sequence 2, Appli
3	2767.5	85.5	797	797	3	US-09-460-145-4	Sequence 4, Appli
4	2767.5	85.5	797	797	4	US-09-895-547-4	Sequence 4, Appli
5	2767.5	85.5	913	913	3	US-09-827-208-3	Sequence 3, Appli
6	2767.5	85.5	913	913	3	US-09-500-358-3	Sequence 3, Appli
7	2767.5	85.5	913	913	4	US-09-498-809-3	Sequence 3, Appli
8	2509.5	77.6	483	483	4	US-09-148-545-144	Sequence 144, App
9	2509.5	77.6	483	483	4	US-09-148-545-209	Sequence 209, App
10	619	19.1	749	749	1	US-08-046-508-2	Sequence 2, Appli
11	498.5	15.4	541	541	3	US-09-045-185-2	Sequence 2, Appli
12	490.5	15.2	541	541	3	US-08-890-615-2	Sequence 2, Appli
13	490.5	15.2	541	541	4	US-09-246-290A-2	Sequence 2, Appli
14	208	6.4	638	638	4	US-09-687-538B-4	Sequence 4, Appli
15	208	6.4	654	654	4	US-09-437-687A-2	Sequence 2, Appli
16	208	6.4	654	654	4	US-10-263-250-2	Sequence 2, Appli
17	203.5	6.3	90	90	4	US-09-621-976-4397	Sequence 4397, Ap
18	200.5	6.2	640	640	4	US-09-687-538B-2	Sequence 2, Appli
19	200	6.2	87	87	4	US-09-205-258-342	Sequence 342, App
20	198.5	6.1	66	66	4	US-09-621-976-5606	Sequence 5606, Ap
21	195.5	6.0	552	552	3	US-09-295-186-10	Sequence 10, Appl
22	195.5	6.0	573	573	3	US-09-295-186-11	Sequence 11, Appl
23	193	6.0	397	397	5	PCT-US95-17111A-121	Sequence 121, App
24	189	5.8	117	117	4	US-09-621-976-4623	Sequence 4623, Ap
25	188	5.8	627	627	4	US-09-687-538B-6	Sequence 6, Appli
26	186.5	5.8	648	648	4	US-09-437-687A-16	Sequence 16, Appl
27	186.5	5.8	648	648	4	US-10-263-250-16	Sequence 16, Appl
28	185	5.7	375	375	2	US-08-454-557C-121	Sequence 121, App
29	185	5.7	375	375	2	US-08-340-426D-121	Sequence 121, App
30	185	5.7	375	375	4	US-08-450-673C-121	Sequence 121, App
31	182.5	5.6	87	87	4	US-09-621-976-4482	Sequence 4482, Ap
32	177.5	5.5	649	649	3	US-09-295-186-18	Sequence 18, Appl
33	177	5.5	612	612	3	US-09-295-186-16	Sequence 16, Appl
34	176	5.4	776	776	4	US-10-020-079-24	Sequence 24, Appl
35	176	5.4	789	789	4	US-10-020-079-22	Sequence 22, Appl
36	176	5.4	863	863	4	US-10-020-079-32	Sequence 32, Appl
37	176	5.4	876	876	4	US-10-020-079-30	Sequence 30, Appl
38	176	5.4	889	889	4	US-10-020-079-20	Sequence 20, Appl
39	176	5.4	895	895	4	US-10-020-079-18	Sequence 18, Appl
40	176	5.4	976	976	4	US-10-020-079-28	Sequence 28, Appl
41	176	5.4	982	982	4	US-10-020-079-26	Sequence 26, Appl
42	171	5.3	120	120	4	US-09-621-976-5592	Sequence 5592, Ap
43	171	5.3	132	132	4	US-09-636-215-573	Sequence 573, App
44	171	5.3	132	132	4	US-09-685-166A-573	Sequence 573, App
45	171	5.3	135	135	4	US-09-685-166A-884	Sequence 884, App

ALIGNMENTS

RESULT 1
US-09-460-145-2

; Sequence 2, Application US/09460145
; Patent No. 6287838
; GENERAL INFORMATION:
;   APPLICANT: Kriz, Ron
;   APPLICANT: Song, Chuanzheng
;   TITLE OF INVENTION: CYTOSOLIC PHOSPHOLIPASE A2-BETA ENZYMES
;   NUMBER OF SEQUENCES: 9
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE: Genetics Institute, Inc.
;   STREET: 87 CambridgePark Drive
;   CITY: Cambridge
;   STATE: MA
;   COUNTRY: USA
;   ZIP: 02140
;   COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: PatentIn Release #1.0, Version #1.30
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/09/460,145
;   FILING DATE:
;   CLASSIFICATION:
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: 08/788,975
;   FILING DATE:
;   ATTORNEY/AGENT INFORMATION:
;   NAME: Brown, Scott A.
;   REGISTRATION NUMBER: 32,724
;   REFERENCE/DOCKET NUMBER: GI5289
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE: (617) 498-8224
;   TELEFAX: (617) 876-5851
; INFORMATION FOR SEQ ID NO: 2:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH: 778 amino acids
;   TYPE: amino acid
;   STRANDEDNESS:
;   TOPOLOGY: linear
;   MOLECULE TYPE: protein
US-09-460-145-2

Query Match   85.5%;   Score 2767.5; DB 3;   Length 778;
Best Local Similarity 87.6%;   Pred. No. 2.1e-268;
Matches 537; Conservative 5; Mismatches 22; Indels 49; Gaps 6;

Qy 24 TGLLVLFCPAPCPFFFFEMESLSVAQAGVQWRDLGSLQPPPLGFKRFSCLSLPSSWDYR 83
          ||||| ||||| |||| | : ::|| | ||| ||| ||| : |||

```
          REGISTRATION NUMBER: 32,724
          REFERENCE/DOCKET NUMBER: GI5289
     TELECOMMUNICATION INFORMATION:
          TELEPHONE: (617) 498-8224
          TELEFAX: (617) 876-5851
INFORMATION FOR SEQ ID NO: 2:
     SEQUENCE CHARACTERISTICS:
          LENGTH: 778 amino acids
          TYPE: amino acid
          STRANDEDNESS: <Unknown>
          TOPOLOGY: linear
     MOLECULE TYPE: protein
     SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-895-547-2

Query Match           85.5%;  Score 2767.5;  DB 4;  Length 778;
Best Local Similarity 87.6%;  Pred. No. 2.1e-268;
Matches 537;  Conservative 5;  Mismatches 22;  Indels 49;  Gaps 6;

Qy   24 TGLLVLFCPAPCPFFFPEMESLSVAQAGVQWRDLGSLQPPLGFKRFSCLSLPSSWDYR  83
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Db  184 TGTFRFHCPA-C-----WEQE-LSI----------RLQDAPEEQLKAPLSALPSGQVVR 225

Qy   84 ------------LRELAVRLGFGPCAEEQAFLSRRKQVVAAALRQALQLDGD 123
                     |||||||||||||||||||||||||||||||||||
Db  226 LVFPTSQEPLMRVELKKEAGLRELAVRLGFGPCAEEQAFLSRRKQVVAAALRQALQLDGD 285

Qy  124 LQEDEIPVVAIMATGGGIRAMTSLYGQLAGLKELGLLDCVSYITGASGSTWALANLYEDP 183
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  286 LQEDEIPVVAIMATGGGIRAMTSLYGQLAGLKELGLLDCVSYITGASGSTWALANLYEDP 345

Qy  184 EWSQKDLAGPTELLKTQVTKNKLGVLAPSQLQRYRQELAERARLGYPSCFTNLWALINEA 243
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  346 EWSQKDLAGPTELLKTQVTKNKLGVLAPSQLQRYRQELAERARLGYPSCFTNLWALINEA 405

Qy  244 LLHDEPHDHKLSDQREALSHGQNPLPIYCALNTKGQSLTTFEFGEWCEFSPYEVGFPKYG 303
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  406 LLHDEPHDHKLSDQREALSHGQNPLPIYCALNTKGQSLTTFEFGEWCEFSPYEVGFPKYG 465

Qy  304 AFIPSELFGSEFFMGQLMKRLPESRICFLEGIWSNLYAANLQDSLYWASEPSQFWDRWVR 363
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  466 AFIPSELFGSEFFMGQLMKRLPESRICFLEGIWSNLYAANLQDSLYWASEPSQFWDRWVR 525

Qy  364 NQANLDKEQVPLLKIEEPPSTAGRIAEFFTDLLTWRPLAQATHNFLRGLHFHKDYFQHPH 423
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Db  526 NQANLDKEQVPLLKIEEPPSTAGRIAEFFTDLLTWRPLAQATHNFLRGLHFHKDYFQHPH 585

Qy  424 FSTWKATTLDGLPNQLTPSEPHLCLLDVGYLINTSCLPLLQPTRDVDLILSLDYNLHGAF 483
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  586 FSTWKATTLDGLPNQLTPSEPHLCLLDVGYLINTSCLPLLQPTRDVDLILSLDYNLHGAF 645

Qy  484 QQLQLLGRFCQEQGIPFPPISPSPEEQLQPRECHTFSDPTCPGAPAVLHF---------- 533
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Db  646 QQLQLLGRFCQEQGIPFPPISPSPEEQLQPRECHTFSDPTCPGAPAVLHFPLVSDSFREY 705

Qy  534 -SSGVRRTPEEAAAGEVNLSSSDSPYHYTKVTYSQEDVDKLLHLTHYNVCNNQEQLLEAL 592
         : |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  706 SAPGVRRTPEEAAAGEVNLSSSDSPYHYTKVTYSQEDVDKLLHLTHYNVCNNQEQLLEAL 765

Qy  593 RQAVQRRRQRRPH 605
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Db  766 RQAVQRRRQRRPH 778

RESULT 3
US-09-460-145-4
; Sequence 4, Application US/09460145
; Patent No. 6287838
; GENERAL INFORMATION:
;   APPLICANT: Kriz, Ron
;   APPLICANT: Song, Chuanzheng
;   TITLE OF INVENTION: CYTOSOLIC PHOSPHOLIPASE A2-BETA ENZYMES
;   NUMBER OF SEQUENCES: 9
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Db  184 TGTFRFHCPA-C-----WEQE-LSI----------RLQDAPEEQLKAPLSALPSGQVVR 225
Qy   84 ------------LRELAVRLGFGPCAEEQAFLSRRKQVVAAALRQALQLDGD 123
Db  226 LVFPTSQEPLMRVELKKEAGLRELAVRLGFGPCAEEQAFLSRRKQVVAAALRQALQLDGD 285
Qy  124 LQEDEIPVVAIMATGGGIRAMTSLYGQLAGLKELGLLDCVSYITGASGSTWALANLYEDP 183
Db  286 LQEDEIPVVAIMATGGGIRAMTSLYGQLAGLKELGLLDCVSYITGASGSTWALANLYEDP 345
Qy  184 EWSQKDLAGPTELLKTQVTKNKLGVLAPSQLQRYRQELAERARLGYPSCFTNLWALINEA 243
Db  346 EWSQKDLAGPTELLKTQVTKNKLGVLAPSQLQRYRQELAERARLGYPSCFTNLWALINEA 405
Qy  244 LLHDEPHDHKLSDQREALSHGQNPLPIYCALNTKGQSLTTFEFGEWCEFSPYEVGFPKYG 303
Db  406 LLHDEPHDHKLSDQREALSHGQNPLPIYCALNTKGQSLTTFEFGEWCEFSPYEVGFPKYG 465
Qy  304 AFIPSELFGSEFFMGQLMKRLPESRICFLEGIWSNLYAANLQDSLYWASEPSQFWDRWVR 363
Db  466 AFIPSELFGSEFFMGQLMKRLPESRICFLEGIWSNLYAANLQDSLYWASEPSQFWDRWVR 525
Qy  364 NQANLDKEQVPLLKIEEPPSTAGRIAEFFTDLLTWRPLAQATHNFLRGLHFHKDYFQHPH 423
Db  526 NQANLDKEQVPLLKIEEPPSTAGRIAEFFTDLLTWRPLAQATHNFLRGLHFHKDYFQHPH 585
Qy  424 FSTWKATTLDGLPNQLTPSEPHLCLLDVGYLINTSCLPLLQPTRDVDLILSLDYNLHGAF 483
Db  586 FSTWKATTLDGLPNQLTPSEPHLCLLDVGYLINTSCLPLLQPTRDVDLILSLDYNLHGAF 645
Qy  484 QQLQLLGRFCQEQGIPFPPISPSPEEQLQPRECHTFSDPTCPGAPAVLHF---------- 533
Db  646 QQLQLLGRFCQEQGIPFPPISPSPEEQLQPRECHTFSDPTCPGAPAVLHFPLVSDSFREY 705
Qy  534 -SSGVRRTPEEAAAGEVNLSSSDSPYHYTKVTYSQEDVDKLLHLTHYNVCNNQEQLLEAL 592
Db  706 SAPGVRRTPEEAAAGEVNLSSSDSPYHYTKVTYSQEDVDKLLHLTHYNVCNNQEQLLEAL 765
Qy  593 RQAVQRRRQRRPH 605
Db  766 RQAVQRRRQRRPH 778

RESULT 2
US-09-895-547-2
; Sequence 2, Application US/09895547
; Patent No. 6482625
; GENERAL INFORMATION:
;   APPLICANT: Kriz, Ron
;             Song, Chuanzheng
;   TITLE OF INVENTION: CYTOSOLIC PHOSPHOLIPASE A2-BETA ENZYMES
;   NUMBER OF SEQUENCES: 9
;   CORRESPONDENCE ADDRESS:
;      ADDRESSEE: Genetics Institute, Inc.
;      STREET: 87 CambridgePark Drive
;      CITY: Cambridge
;      STATE: MA
;      COUNTRY: USA
;      ZIP: 02140
;   COMPUTER READABLE FORM:
;      MEDIUM TYPE: Floppy disk
;      COMPUTER: IBM PC compatible
;      OPERATING SYSTEM: PC-DOS/MS-DOS
;      SOFTWARE: PatentIn Release #1.0, Version #1.30
;   CURRENT APPLICATION DATA:
;      APPLICATION NUMBER: US/09/895,547
;      FILING DATE: 29-Jun-2001
;      CLASSIFICATION: <Unknown>
;   PRIOR APPLICATION DATA:
;      APPLICATION NUMBER: 09/460,145
;      FILING DATE: <Unknown>
;   ATTORNEY/AGENT INFORMATION:
;      NAME: Brown, Scott A.
```

```
; CORRESPONDENCE ADDRESS:
;    ADDRESSEE: Genetics Institute, Inc.
;    STREET: 87 CambridgePark Drive
;    CITY: Cambridge
;    STATE: MA
;    COUNTRY: USA
;    ZIP: 02140
; COMPUTER READABLE FORM:
;    MEDIUM TYPE: Floppy disk
;    COMPUTER: IBM PC compatible
;    OPERATING SYSTEM: PC-DOS/MS-DOS
;    SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
;    APPLICATION NUMBER: US/09/460,145
;    FILING DATE:
;    CLASSIFICATION:
; PRIOR APPLICATION DATA:
;    APPLICATION NUMBER: 08/788,975
;    FILING DATE:
; ATTORNEY/AGENT INFORMATION:
;    NAME: Brown, Scott A.
;    REGISTRATION NUMBER: 32,724
;    REFERENCE/DOCKET NUMBER: GI5289
; TELECOMMUNICATION INFORMATION:
;    TELEPHONE: (617) 498-8224
;    TELEFAX: (617) 876-5851
; INFORMATION FOR SEQ ID NO: 4:
;    SEQUENCE CHARACTERISTICS:
;    LENGTH: 797 amino acids
;    TYPE: amino acid
;    STRANDEDNESS:
;    TOPOLOGY: linear
;    MOLECULE TYPE: protein

US-09-460-145-4

Query Match             85.5%;  Score 2767.5;  DB 3;  Length 797;
Best Local Similarity   87.6%;  Pred. No. 2.2e-268;
Matches  537;  Conservative    5;  Mismatches  22;  Indels  49;  Gaps   6;

Qy    24 TGLLVLFCPAPCPFFFFEMESLSVAQGVQWRDLGSLQPPPLGFKRFSCLSLPSSWDYR 83
Db   203 TGTFRFHCPA-C-----WEQE-LSI-------RLQDAPEEQLKAPLSALPSGQVVR 244

Qy    84 ------------LRELAVRLGFGPCAEEQAFLSRRKQVVAAALRQALQLDGD 123
Db   245 LVFPTSQEPLMRVELKKEAGLRELAVRLGFGPCAEEQAFLSRRKQVVAAALRQALQLDGD 304

Qy   124 LQEDEIPVVAIMATGGGIRAMTSLYGQLAGLKELGLLDCVSYITGASGSTWALANLYEDP 183
Db   305 LQEDEIPVVAIMATGGGIRAMTSLYGQLAGLKELGLLDCVSYITGASGSTWALANLYEDP 364

Qy   184 EWSQKDLAGPTELLKTQVTKNKLGVLAPSLQRYRQELAERARLGYPSCFTNLWALINEA 243
Db   365 EWSQKDLAGPTELLKTQVTKNKLGVLAPSLQRYRQELAERARLGYPSCFTNLWALINEA 424

Qy   244 LLHDEPHDHKLSDQRRALSHGQNPLPIYCALNTKGQSLTTFEFGEWCEFSPYEVGFPKYG 303
Db   425 LLHDEPHDHKLSDQRRALSHGQNPLPIYCALNTKGQSLTTFEFGEWCEFSPYEVGFPKYG 484

Qy   304 AFIPSELFGSEFFMGQLMKRLPESRICFLEGIWSNLYAANLQDSLYWASEPSQFWDRWVR 363
Db   485 AFIPSELFGSEFFMGQLMKRLPESRICFLEGIWSNLYAANLQDSLYWASEPSQFWDRWVR 544

Qy   364 NQANLDKEQVPLLKIEEPPSTAGRIAEFFTDLLTWRPLAQATHNFLRGLHFHKDYFQHPH 423
Db   545 NQANLDKEQVPLLKIEEPPSTAGRIAEFFTDLLTWRPLAQATHNFLRGLHFHKDYFQHPH 604

Qy   424 FSTWKATTLDGLPNQLTPSEPHLCLLDVGYLINTSCLPLLQPTRDVDLIILSLDYNLHGAF 483
Db   605 FSTWKATTLDGLPNQLTPSEPHLCLLDVGYLINTSCLPLLQPTRDVDLIILSLDYNLHGAF 664

Qy   484 QQLQLLGRFCQEQGIPFPPISPSPEEQLQPRECHTFSDPTCPGAPAVLHF-------- 533
Db   665 QQLQLLGRFCQEQGIPFPPISPSPEEQLQPRECHTFSDPTCPGAPAVLHFPLVSDSFREY 724

Qy   534 -SSGVRRTPEEAAAGEVNLSSSDSPYHYTKVTYSQEDVDKLLHLTHYNVCNNQQLLEAL 592
Db   725 SAPGVRRTPEEAAAGEVNLSSSDSPYHYTKVTYSQEDVDKLLHLTHYNVCNNQQLLEAL 784

Qy   593 RQAVQRRRQRRPH 605
Db   785 RQAVQRRRQRRPH 797


RESULT 4
US-09-895-547-4
; Sequence 4, Application US/0989547
; Patent No. 6482625
; GENERAL INFORMATION:
;    APPLICANT: Kriz, Ron
;               Song, Chuanzheng
;    TITLE OF INVENTION: CYTOSOLIC PHOSPHOLIPASE A2-BETA ENZYMES
;    NUMBER OF SEQUENCES: 9
;    CORRESPONDENCE ADDRESS:
;       ADDRESSEE: Genetics Institute, Inc.
;       STREET: 87 CambridgePark Drive
;       CITY: Cambridge
;       STATE: MA
;       COUNTRY: USA
;       ZIP: 02140
;    COMPUTER READABLE FORM:
;       MEDIUM TYPE: Floppy disk
;       COMPUTER: IBM PC compatible
;       OPERATING SYSTEM: PC-DOS/MS-DOS
;       SOFTWARE: Patentin Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;       APPLICATION NUMBER: US/09/895,547
;       FILING DATE: 29-Jun-2001
;       CLASSIFICATION: <Unknown>
;    PRIOR APPLICATION DATA:
;       APPLICATION NUMBER: 09/460,145
;       FILING DATE: <Unknown>
;    ATTORNEY/AGENT INFORMATION:
;       NAME: Brown, Scott A.
;       REGISTRATION NUMBER: 32,724
;       REFERENCE/DOCKET NUMBER: GI5289
;    TELECOMMUNICATION INFORMATION:
;       TELEPHONE: (617) 498-8224
;       TELEFAX: (617) 876-5851
; INFORMATION FOR SEQ ID NO: 4:
;    SEQUENCE CHARACTERISTICS:
;       LENGTH: 797 amino acids
;       TYPE: amino acid
;       STRANDEDNESS: <Unknown>
;       TOPOLOGY: linear
;    MOLECULE TYPE: protein
;    SEQUENCE DESCRIPTION: SEQ ID NO: 4:

US-09-895-547-4

Query Match             85.5%;  Score 2767.5;  DB 4;  Length 797;
Best Local Similarity   87.6%;  Pred. No. 2.2e-268;
Matches  537;  Conservative    5;  Mismatches  22;  Indels  49;  Gaps   6;

Qy    24 TGLLVLFCPAPCPFFFFEMESLSVAQGVQWRDLGSLQPPPLGFKRFSCLSLPSSWDYR 83
Db   203 TGTFRFHCPA-C-----WEQE-LSI-------RLQDAPEEQLKAPLSALPSGQVVR 244

Qy    84 ------------LRELAVRLGFGPCAEEQAFLSRRKQVVAAALRQALQLDGD 123
Db   245 LVFPTSQEPLMRVELKKEAGLRELAVRLGFGPCAEEQAFLSRRKQVVAAALRQALQLDGD 304

Qy   124 LQEDEIPVVAIMATGGGIRAMTSLYGQLAGLKELGLLDCVSYITGASGSTWALANLYEDP 183
Db   305 LQEDEIPVVAIMATGGGIRAMTSLYGQLAGLKELGLLDCVSYITGASGSTWALANLYEDP 364

Qy   184 EWSQKDLAGPTELLKTQVTKNKLGVLAPSLQRYRQELAERARLGYPSCFTNLWALINEA 243
Db   365 EWSQKDLAGPTELLKTQVTKNKLGVLAPSLQRYRQELAERARLGYPSCFTNLWALINEA 424

Qy   244 LLHDEPHDHKLSDQRRALSHGQNPLPIYCALNTKGQSLTTFEFGEWCEFSPYEVGFPKYG 303
Db   425 LLHDEPHDHKLSDQRRALSHGQNPLPIYCALNTKGQSLTTFEFGEWCEFSPYEVGFPKYG 484

Qy   304 AFIPSELFGSEFFMGQLMKRLPESRICFLEGIWSNLYAANLQDSLYWASEPSQFWDRWVR 363
Db   485 AFIPSELFGSEFFMGQLMKRLPESRICFLEGIWSNLYAANLQDSLYWASEPSQFWDRWVR 544

Qy   364 NQANLDKEQVPLLKIEEPPSTAGRIAEFFTDLLTWRPLAQATHNFLRGLHFHKDYFQHPH 423
Db   545 NQANLDKEQVPLLKIEEPPSTAGRIAEFFTDLLTWRPLAQATHNFLRGLHFHKDYFQHPH 604

Qy   424 FSTWKATTLDGLPNQLTPSEPHLCLLDVGYLINTSCLPLLQPTRDVDLIILSLDYNLHGAF 483
Db   605 FSTWKATTLDGLPNQLTPSEPHLCLLDVGYLINTSCLPLLQPTRDVDLIILSLDYNLHGAF 664

Qy   484 QQLQLLGRFCQEQGIPFPPISPSPEEQLQPRECHTFSDPTCPGAPAVLHF-------- 533
Db   665 QQLQLLGRFCQEQGIPFPPISPSPEEQLQPRECHTFSDPTCPGAPAVLHFPLVSDSFREY 724

Qy   534 -SSGVRRTPEEAAAGEVNLSSSDSPYHYTKVTYSQEDVDKLLHLTHYNVCNNQQLLEAL 592
Db   725 SAPGVRRTPEEAAAGEVNLSSSDSPYHYTKVTYSQEDVDKLLHLTHYNVCNNQQLLEAL 784

Qy   593 RQAVQRRRQRRPH 605
Db   785 RQAVQRRRQRRPH 797
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Db   365 EWSQKDLAGPTELLKTQVTKNKLGVLAPSQLQRYRQELAERARLGYPSCFTNLWALINEA 424
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   244 LLHDEPHDHKLSDQREALSHGQNPLPIYCALNTKGQSLTTFEFGEWCEFSPYEVGFPKYG 303
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   425 LLHDEPHDHKLSDQREALSHGQNPLPIYCALNTKGQSLTTFEFGEWCEFSPYEVGFPKYG 484

Qy   304 AFIPSELFGSEFFMGQLMKRLPESRICFLEGIWSNLYAANLQDSLYWASEPSQFWDRWVR 363
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   485 AFIPSELFGSEFFMGQLMKRLPESRICFLEGIWSNLYAANLQDSLYWASEPSQFWDRWVR 544

Qy   364 NQANLDKEQVPLLKIEEPPSTAGRIAEFFTDLLTWRPLAQATHNFLRGLHFHKDYFQHPH 423
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   545 NQANLDKEQVPLLKIEEPPSTAGRIAEFFTDLLTWRPLAQATHNFLRGLHFHKDYFQHPH 604

Qy   424 FSTWKATTLDGLPNQLTPSEPHLCLLDVGYLINTSCLPLLQPTRDVDLILSLDYNLHGAF 483
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   605 FSTWKATTLDGLPNQLTPSEPHLCLLDVGYLINTSCLPLLQPTRDVDLILSLDYNLHGAF 664

Qy   484 QQLQLLGRFCQEQGIPFPPISPSPEEQLQPRECHTFSDPTCPGAPAVLHF---------- 533
          |||||||||||||||||||||||||||||||||||||||||||||||||||
Db   665 QQLQLLGRFCQEQGIPFPPISPSPEEQLQPRECHTFSDPTCPGAPAVLHFPLVSDSFREY 724

Qy   534 -SSGVRRTPEEAAAGEVNLSSSDSPYHYTKVTYSQEDVDKLLHLTHYNVCNNQEQLLEAL 592
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   725 SAPGVRRTPEEAAAGEVNLSSSDSPYHYTKVTYSQEDVDKLLHLTHYNVCNNQEQLLEAL 784

Qy   593 RQAVQRRRQRRPH 605
          |||||||||||||
Db   785 RQAVQRRRQRRPH 797
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RESULT 5
US-08-827-208-3
; Sequence 3, Application US/08827208
; Patent No. 6025178
; GENERAL INFORMATION:
; APPLICANT: Chiou, Xue-Chiou C.
; APPLICANT: Kramer, Ruth M.
; APPLICANT: Pickard, Richard T.
; APPLICANT: Sharp, John D.
; APPLICANT: Strifler, Beth A.
; TITLE OF INVENTION: HUMAN PHOSPHOLIPASE A2 AND RELATED
; TITLE OF INVENTION: NUCLEIC ACID COMPOUNDS
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Eli Lilly and Company
; STREET: Lilly Corporate Center
; CITY: Indianapolis
; STATE: Indiana
; COUNTRY: United States of America
; ZIP: 46285
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/827,208
; FILING DATE: 28-MAR-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/014,608
; FILING DATE: 29-MAR-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/041,264
; FILING DATE: 19-MAR-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Gaylo, Paul J.
; REGISTRATION NUMBER: 36,808
; REFERENCE/DOCKET NUMBER: X-10610
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (317) 276-0756

; TELEFAX: (317) 276-3861
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 913 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-827-208-3

Query Match   85.5%;   Score 2767.5;   DB 3;   Length 913;
Best Local Similarity 87.6%;   Pred. No. 2.7e-268;
Matches 537; Conservative 5; Mismatches 22; Indels 49; Gaps 6;

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Qy    24 TGLLVLFCPAPCPFFFEMESLSVAQAGVQWRDLGSLQPPLGFKRFSCLSLPSSWDYR    83
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Db   319 TGTFRFHCPA-C-----WEQE-LSI------------RLQDAPEEQLKAPLSALPSGQVVR 360

Qy    84 --------------LRELAVRLGFGPCAEEQAFLSRRKQVVAALRQALQLDGD        123
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Db   361 --------------LRELAVRLGFGPCAEEQAFLSRRKQVVAALRQALQLDGD        420

Qy   124 LQEDEIPVVAIMATGGGIRAMTSLYGQLAGLKELGLLDCVSYITGASGSTWALANLYEDP 183
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Db   421 LQEDEIPVVAIMATGGGIRAMTSLYGQLAGLKELGLLDCVSYITGASGSTWALANLYEDP 480

Qy   184 EWSQKDLAGPTELLKTQVTKNKLGVLAPSQLQRYRQELAERARLGYPSCFTNLWALINEA 243
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Db   481 EWSQKDLAGPTELLKTQVTKNKLGVLAPSQLQRYRQELAERARLGYPSCFTNLWALINEA 540

Qy   244 LLHDEPHDHKLSDQREALSHGQNPLPIYCALNTKGQSLTTFEFGEWCEFSPYEVGFPKYG 303
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   541 LLHDEPHDHKLSDQREALSHGQNPLPIYCALNTKGQSLTTFEFGEWCEFSPYEVGFPKYG 600

Qy   304 AFIPSELFGSEFFMGQLMKRLPESRICFLEGIWSNLYAANLQDSLYWASEPSQFWDRWVR 363
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Db   601 AFIPSELFGSEFFMGQLMKRLPESRICFLEGIWSNLYAANLQDSLYWASEPSQFWDRWVR 660

Qy   364 NQANLDKEQVPLLKIEEPPSTAGRIAEFFTDLLTWRPLAQATHNFLRGLHFHKDYFQHPH 423
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Db   661 NQANLDKEQVPLLKIEEPPSTAGRIAEFFTDLLTWRPLAQATHNFLRGLHFHKDYFQHPH 720

Qy   424 FSTWKATTLDGLPNQLTPSEPHLCLLDVGYLINTSCLPLLQPTRDVDLILSLDYNLHGAF 483
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Db   721 FSTWKATTLDGLPNQLTPSEPHLCLLDVGYLINTSCLPLLQPTRDVDLILSLDYNLHGAF 780

Qy   484 QQLQLLGRFCQEQGIPFPPISPSPEEQLQPRECHTFSDPTCPGAPAVLHF---------- 533
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Db   781 QQLQLLGRFCQEQGIPFPPISPSPEEQLQPRECHTFSDPTCPGAPAVLHFPLVSDSFREY 840

Qy   534 -SSGVRRTPEEAAAGEVNLSSSDSPYHYTKVTYSQEDVDKLLHLTHYNVCNNQEQLLEAL 592
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Db   841 SAPGVRRTPEEAAAGEVNLSSSDSPYHYTKVTYSQEDVDKLLHLTHYNVCNNQEQLLEAL 900

Qy   593 RQAVQRRRQRRPH 605
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Db   901 RQAVQRRRQRRPH 913
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RESULT 6
US-09-500-358-3
; Sequence 3, Application US/09500358
; Patent No. 6197569
; GENERAL INFORMATION:
; APPLICANT: Chiou, Xue-Chiou C.
; APPLICANT: Kramer, Ruth M.
; APPLICANT: Pickard, Richard T.
; APPLICANT: Sharp, John D.
; APPLICANT: Strifler, Beth A.
; TITLE OF INVENTION: HUMAN PHOSPHOLIPASE A2 AND RELATED
; TITLE OF INVENTION: NUCLEIC ACID COMPOUNDS
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Eli Lilly and Company

;   STREET: Lilly Corporate Center
;   CITY: Indianapolis
;   STATE: Indiana
;   COUNTRY: United States of America
;   ZIP: 46285
; COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/09/500,358
;   FILING DATE:
;   CLASSIFICATION:
; PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: US/08/827,208
;   FILING DATE: 28-MAR-1997
;   APPLICATION NUMBER: US 60/014,608
;   FILING DATE: 29-MAR-1996
; PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: US 60/041,264
;   FILING DATE: 19-MAR-1997
; ATTORNEY/AGENT INFORMATION:
;   NAME: Gaylo, Paul J.
;   REGISTRATION NUMBER: 36,808
;   REFERENCE/DOCKET NUMBER: X-10610
; TELECOMMUNICATION INFORMATION:
;   TELEPHONE: (317) 276-0756
;   TELEFAX: (317) 276-3861
; INFORMATION FOR SEQ ID NO: 3:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH: 913 amino acids
;   TYPE: amino acid
;   TOPOLOGY: linear
;   MOLECULE TYPE: protein
US-09-500-358-3

Query Match   85.5%; Score 2767.5; DB 3; Length 913;
Best Local Similarity   87.6%; Pred. No. 2.7e-268;
Matches 537; Conservative   5; Mismatches 22; Indels 49; Gaps   6;

Qy   24 TGLLVLFCPAPCPFFFFEMESLSVAQAGVQWRDLGSLQPPLGFKRFSCLSLPSSWDYR 83
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Db 319 TGTFRFHCPA-C------WEQE-LSI--------RLQDAPEEQLKAPLSALPSGQVVR 360

Qy   84 --------------LRELAVRLGFGPCAEEQAFLSRRKQVVAAALRQALQLDGD 123
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Db 361 LVFPTSQEPLMRVELKKEAGLRELAVRLGFGPCAEEQAFLSRRKQVVAAALRQALQLDGD 420

Qy 124 LQEDEIPVVAIMATGGGIRAMTSLYGQLAGLKELGLLDCVSYITGASGSTWALANLYEDP 183
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Db 421 LQEDEIPVVAIMATGGGIRAMTSLYGQLAGLKELGLLDCVSYITGASGSTWALANLYEDP 480

Qy 184 EWSQKDLAGPTELLKTQVTKNKLGVLAPSQLQRYRQELAERRARLGYPSCFTNLWALINEA 243
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Db 481 EWSQKDLAGPTELLKTQVTKNKLGVLAPSQLQRYRQELAERRARLGYPSCFTNLWALINEA 540

Qy 244 LLHDEPHDHKLSDQREALSHGQNPLPIYCALNTKGQSLTTFEFGEWCEFSPYEVGFPKYG 303
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Db 541 LLHDEPHDHKLSDQREALSHGQNPLPIYCALNTKGQSLTTFEFGEWCEFSPYEVGFPKYG 600

Qy 304 AFIPSELFGSEFFMGQLMKRLPESRICFLEGIWSNLYAANLQDSLYWASEPSQFWDRWVR 363
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Db 601 AFIPSELFGSEFFMGQLMKRLPESRICFLEGIWSNLYAANLQDSLYWASEPSQFWDRWVR 660

Qy 364 NQANLDKEQVPLLKIEPPSTAGRIAEFFDLLTWRPLAQATHNFLRGLHFHKDYFQHPH 423
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Db 661 NQANLDKEQVPLLKIEPPSTAGRIAEFFDLLTWRPLAQATHNFLRGLHFHKDYFQHPH 720

Qy 424 FSTWKATTLDGLPNQLTPSEPHLCLLDVGYLINTSCLPLLQPTRDVDLILSLDYNLHGAF 483
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Db 721 FSTWKATTLDGLPNQLTPSEPHLCLLDVGYLINTSCLPLLQPTRDVDLILSLDYNLHGAF 780

Qy 484 QQLQLLGRFCQEQGIPPPISPSPEEQLQPRRCHTFSDPTCPGAPAVLHF-------- 533
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Db 781 QQLQLLGRFCQEQGIPPPISPSPEEQLQPRRCHTFSDPTCPGAPAVLHFPLVSDSFREY 840

Qy 534 -SSGVRRTPEEAAAGEVNLSSSDSPYHYTKVTYSQEDVDKLLHLTHYNVCNNQEQLLEAL 592
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Db 841 SAPGVRRTPEEAAAGEVNLSSSDSPYHYTKVTYSQEDVDKLLHLTHYNVCNNQEQLLEAL 900

Qy 593 RQAVQRRRQRRPH 605
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Db 901 RQAVQRRRQRRPH 913

RESULT 7
US-09-498-809-3
; Sequence 3, Application US/09498809
; Patent No. 6242206
; GENERAL INFORMATION:
; APPLICANT: Chiou, Xue-Chiou C.
; APPLICANT: Kramer, Ruth M.
; APPLICANT: Pickard, Richard T.
; APPLICANT: Sharp, John D.
; APPLICANT: Stifler, Beth A.
; TITLE OF INVENTION: HUMAN PHOSPHOLIPASE A2 AND RELATED
; TITLE OF INVENTION: NUCLEIC ACID COMPOUNDS
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
;   ADDRESSEE: Eli Lilly and Company
;   STREET: Lilly Corporate Center
;   CITY: Indianapolis
;   STATE: Indiana
;   COUNTRY: United States of America
;   ZIP: 46285
; COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/09/498,809
;   FILING DATE:
;   CLASSIFICATION:
; PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: 08/827,208
;   FILING DATE:
; PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: US 60/041,264
;   FILING DATE: 19-MAR-1997
; ATTORNEY/AGENT INFORMATION:
;   NAME: Gaylo, Paul J.
;   REGISTRATION NUMBER: 36,808
;   REFERENCE/DOCKET NUMBER: X-10610
; TELECOMMUNICATION INFORMATION:
;   TELEPHONE: (317) 276-0756
;   TELEFAX: (317) 276-3861
; INFORMATION FOR SEQ ID NO: 3:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH: 913 amino acids
;   TYPE: amino acid
;   TOPOLOGY: linear
;   MOLECULE TYPE: protein
US-09-498-809-3

Query Match   85.5%; Score 2767.5; DB 3; Length 913;
Best Local Similarity   87.6%; Pred. No. 2.7e-268;
Matches 537; Conservative   5; Mismatches 22; Indels 49; Gaps   6;

Qy   24 TGLLVLFCPAPCPFFFFEMESLSVAQAGVQWRDLGSLQPPLGFKRFSCLSLPSSWDYR 83
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Db 319 TGTFRFHCPA-C------WEQE-LSI--------RLQDAPEEQLKAPLSALPSGQVVR 360

Qy   84 --------------LRELAVRLGFGPCAEEQAFLSRRKQVVAAALRQALQLDGD 123
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Db   361 LVFPTSQEPLMRVELKKEAGLRELAVRLGFGPCAEEQAFLSRRKQVVAAALRQALQLDGD 420

Qy   124 LQEDEIPVVAIMATGGGIRAMTSLYGQLAGLKELGLLDCVSYITGASGSTWALANLYEDP 183
         |||||||||||||||||||||||||||||||||||||||||||||||||
Db   421 LQEDEIPVVAIMATGGGIRAMTSLYGQLAGLKELGLLDCVSYITGASGSTWALANLYEDP 480

Qy   184 EWSQKDLAGPTELLKTQVTKNKLGVLAPSQLQRYRQELAERRARLGYPSCFTNLWALINEA 243
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Db   481 EWSQKDLAGPTELLKTQVTKNKLGVLAPSQLQRYRQELAERRARLGYPSCFTNLWALINEA 540

Qy   244 LLHDEPHDHKLSDQREALSHGQNPLPIYCALNTKGQSLTTFEFGEWCEFSPYEVGFPKYG 303
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Db   541 LLHDEPHDHKLSDQREALSHGQNPLPIYCALNTKGQSLTTFEFGEWCEFSPYEVGFPKYG 600

Qy   304 AFIPSELFGSEFFMGQLMKRLPESRICFLEGIWSNLYAANLQDSLYWASEPSQFWDRWVR 363
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Db   601 AFIPSELFGSEFFMGQLMKRLPESRICFLEGIWSNLYAANLQDSLYWASEPSQFWDRWVR 660

Qy   364 NQANLDKEQVPLLKIEEPPSTAGRIAEFFTDLLTWRPLAQATHNFLRGLHFHKDYFQHPH 423
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Db   661 NQANLDKEQVPLLKIEEPPSTAGRIAEFFTDLLTWRPLAQATHNFLRGLHFHKDYFQHPH 720

Qy   424 FSTWKATTLDGLPNQLTPSEPHLCLLDVGYLINTSCLPLLQPTRDVDLILSLDYNLHGAF 483
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Db   721 FSTWKATTLDGLPNQLTPSEPHLCLLDVGYLINTSCLPLLQPTRDVDLILSLDYNLHGAF 780

Qy   484 QQLQLLGRFCQEQGIPFPPISPSPEEQLQPRECHTFSDPTCPGAPAVLHF---------- 533
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Db   781 QQLQLLGRFCQEQGIPFPPISPSPEEQLQPRECHTFSDPTCPGAPAVLHFPLVSDSFREY 840

Qy   534 -SSGVRRTPEEAAAGEVNLSSSDSPYHYTKVTYSQEDVDKLLHLTHYNVCNNQEQLLEAL 592
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Db   841 SAPGVRRTPEEAAAGEVNLSSSDSPYHYTKVTYSQEDVDKLLHLTHYNVCNNQEQLLEAL 900

Qy   593 RQAVQRRRQRRPH 605
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Db   901 RQAVQRRRQRRPH 913
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RESULT 8
US-09-148-545-144
; Sequence 144, Application US/09148545
; Patent No. 6590075
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 70 Human Secreted Proteins
; FILE REFERENCE: PZ001P1
; CURRENT APPLICATION NUMBER: US/09/148,545
; CURRENT FILING DATE: 1998-09-04
; EARLIER APPLICATION NUMBER: PCT/US98/04482
; EARLIER FILING DATE: 1998-03-06
; EARLIER APPLICATION NUMBER: 60/040,162
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/040,333
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/038,621
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; EARLIER APPLICATION NUMBER: 60/040,161
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; EARLIER FILING DATE: 1997-05-23
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; EARLIER APPLICATION NUMBER: 60/047,597
; EARLIER FILING DATE: 1997-05-23

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; EARLIER FILING DATE: 1997-05-23
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; EARLIER FILING DATE: 1997-05-23
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; EARLIER FILING DATE: 1997-05-23
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; EARLIER APPLICATION NUMBER: 60/047,492
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,598
; EARLIER FILING DATE: 1997-05-23
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; EARLIER FILING DATE: 1997-05-23
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; EARLIER APPLICATION NUMBER: 60/047,612
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; EARLIER APPLICATION NUMBER: 60/047,601
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; EARLIER FILING DATE: 1997-04-11
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; EARLIER APPLICATION NUMBER: 60/043,671
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; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,315
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/048,974
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/056,886
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,877
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,889
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,893
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,630
; EARLIER FILING DATE: 1997-05-23

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;; EARLIER FILING DATE: 1997-08-22
;; EARLIER APPLICATION NUMBER: 60/056,878
;; EARLIER APPLICATION NUMBER: 60/056,662
;; EARLIER FILING DATE: 1997-08-22
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;; EARLIER APPLICATION NUMBER: 60/056,882
;; EARLIER FILING DATE: 1997-08-22
;; EARLIER APPLICATION NUMBER: 60/056,637
;; EARLIER FILING DATE: 1997-08-22
;; EARLIER APPLICATION NUMBER: 60/056,903
;; EARLIER FILING DATE: 1997-08-22
;; EARLIER APPLICATION NUMBER: 60/056,888
;; EARLIER FILING DATE: 1997-08-22
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;; EARLIER APPLICATION NUMBER: 60/056,880
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;; EARLIER APPLICATION NUMBER: 60/056,894
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;; EARLIER APPLICATION NUMBER: 60/056,911
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;; EARLIER APPLICATION NUMBER: 60/056,636
;; EARLIER FILING DATE: 1997-08-22
;; EARLIER APPLICATION NUMBER: 60/056,874
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;; EARLIER FILING DATE: 1997-08-22
;; EARLIER APPLICATION NUMBER: 60/056,864
;; EARLIER FILING DATE: 1997-08-22
;; EARLIER APPLICATION NUMBER: 60/056,631
;; EARLIER FILING DATE: 1997-08-22
;; EARLIER APPLICATION NUMBER: 60/056,845
;; EARLIER FILING DATE: 1997-08-22
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;; EARLIER FILING DATE: 1997-08-22
;; EARLIER APPLICATION NUMBER: 60/047,595
;; EARLIER FILING DATE: 1997-05-23
;; EARLIER APPLICATION NUMBER: 60/057,761
;; EARLIER FILING DATE: 05-Sep-1997
;; EARLIER APPLICATION NUMBER: 60/047,599
;; EARLIER FILING DATE: 1997-05-23
;; EARLIER APPLICATION NUMBER: 60/047,588
;; EARLIER FILING DATE: 1997-05-23
;; EARLIER APPLICATION NUMBER: 60/047,585
;; EARLIER FILING DATE: 1997-05-23
;; EARLIER APPLICATION NUMBER: 60/047,586
;; EARLIER FILING DATE: 1997-05-23
;; EARLIER APPLICATION NUMBER: 60/047,590
;; EARLIER FILING DATE: 1997-05-23
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;; EARLIER FILING DATE: 1997-05-23
;; EARLIER APPLICATION NUMBER: 60/047,589
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;; EARLIER APPLICATION NUMBER: 60/047,593
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;; EARLIER APPLICATION NUMBER: 60/047,614
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;; EARLIER FILING DATE: 1997-04-11
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;; EARLIER APPLICATION NUMBER: 60/047,501
;; EARLIER FILING DATE: 1997-05-23
;; EARLIER APPLICATION NUMBER: 60/043,670
;; EARLIER FILING DATE: 1997-04-11
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;; EARLIER FILING DATE: 1997-08-22
;; EARLIER APPLICATION NUMBER: 60/056,664
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;; EARLIER APPLICATION NUMBER: 60/056,876
;; EARLIER FILING DATE: 1997-08-22
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;; EARLIER APPLICATION NUMBER: 60/056,881
;; EARLIER FILING DATE: 1997-08-22
;; EARLIER APPLICATION NUMBER: 60/056,909
;; EARLIER FILING DATE: 1997-08-22
;; EARLIER APPLICATION NUMBER: 60/056,875
;; EARLIER FILING DATE: 1997-08-22
;; EARLIER APPLICATION NUMBER: 60/056,862
;; EARLIER FILING DATE: 1997-08-22
;; EARLIER APPLICATION NUMBER: 60/056,887
;; EARLIER FILING DATE: 1997-08-22
;; EARLIER APPLICATION NUMBER: 60/056,908
;; EARLIER FILING DATE: 1997-08-22
;; EARLIER APPLICATION NUMBER: 60/048,964
;; EARLIER FILING DATE: 1997-06-06
;; EARLIER APPLICATION NUMBER: 60/057,650
;; EARLIER FILING DATE: 1997-09-05
;; EARLIER APPLICATION NUMBER: 60/056,884
;; EARLIER FILING DATE: 1997-08-22
;; NUMBER OF SEQ ID NOS: 280
;; SOFTWARE: PatentIn Ver. 2.0
;;
;; SEQ ID NO 144
;; LENGTH: 483

Query Match             77.6%;  Score 2509.5;  DB 4;  Length 483;
Best Local Similarity   96.9%;  Pred. No. 7.3e-243;
Matches  467;  Conservative   2;  Mismatches   2;  Indels   2;  Gaps  11;

Qy  135 MATGGGIRAMTSLYGQLAGLKELGLLDCVSYITGASGSTWALANLYEDPEWSQKDLAGPT 194
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Db    1 MATGGGIRAMTSLYGQLAGLKELGLLDCXSYITGASGSTWALANLYKDPEWSQKDLAGPT  60

Qy  195 ELLKTQVTKNKLGVLAPSQLQRYRQELAERARLGYPSCFTNLWALINEALLHDEPHDHKL 254
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Db   61 ELLKTQVTKNKLGVLAPSQLQRYRQELAERARLGYPSCFTNLWALINEALLHDEPHDHKL 120

Qy  255 SDQREALSHGQNPLPIYCALNTKGQSLTTFEFGEWCEFSPYEVGPPKYGAFIPSELFGSE 314
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Qy  315 FFMGQLMKRLPESRICFLEGIWSNLYAANLQDSLYWASEPSQFWDRWVRNQANLDKEQVP 374
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Qy  375 LLKIEEPPSTAGRIAEFFTDLLTWRPLAQATHNFLRGLHFHKDYFQHPHFSTWKATTLDG 434
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Qy  435 LPNQLTPSEPHLCLLDVGYLINTSCLPLLQPTRDVDLILSLDYNLHGAFQQLLGRFCQ 494
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Db  421 AAAGEVNLSSSDSPYHYTKVTYSQEDVDKLLHLTHYNVCNNQEQLLEALRQAVQRRRQRR 480

Qy  604 PH 605
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Db  481 PH 482

RESULT 9
US-09-148-545-209
; Sequence 209, Application US/09148545
; Patent No. 6590075
; GENERAL INFORMATION:
;   APPLICANT: Rosen et al.
;   TITLE OF INVENTION: 70 Human Secreted Proteins
;   FILE REFERENCE: PZ001P1
;   CURRENT APPLICATION NUMBER: US/09/148,545
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EARLIER APPLICATION NUMBER: PCT/US98/04482
EARLIER FILING DATE: 1998-03-06
EARLIER APPLICATION NUMBER: 60/040,162
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EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/056,886
EARLIER FILING DATE: 1997-08-22
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EARLIER APPLICATION NUMBER: 60/057,761
EARLIER FILING DATE: 05-Sep-1997
EARLIER APPLICATION NUMBER: 60/047,599
EARLIER FILING DATE: 1997-05-23
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EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,586
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;  EARLIER FILING DATE: 1997-05-23
;  EARLIER APPLICATION NUMBER: 60/047,590
;  EARLIER FILING DATE: 1997-05-23
;  EARLIER APPLICATION NUMBER: 60/047,594
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;  EARLIER APPLICATION NUMBER: 60/047,589
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;  EARLIER APPLICATION NUMBER: 60/047,593
;  EARLIER FILING DATE: 1997-05-23
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;  EARLIER FILING DATE: 1997-05-23
;  EARLIER APPLICATION NUMBER: 60/043,578
;  EARLIER FILING DATE: 1997-04-11
;  EARLIER APPLICATION NUMBER: 60/043,576
;  EARLIER FILING DATE: 1997-04-11
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;  EARLIER FILING DATE: 1997-05-23
;  EARLIER APPLICATION NUMBER: 60/043,670
;  EARLIER FILING DATE: 1997-04-11
;  EARLIER APPLICATION NUMBER: 60/056,632
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;  EARLIER APPLICATION NUMBER: 60/056,664
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;  EARLIER APPLICATION NUMBER: 60/056,876
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;  EARLIER APPLICATION NUMBER: 60/056,909
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;  EARLIER FILING DATE: 1997-08-22
;  EARLIER APPLICATION NUMBER: 60/048,964
;  EARLIER FILING DATE: 1997-06-06
;  EARLIER APPLICATION NUMBER: 60/057,650
;  EARLIER FILING DATE: 1997-09-05
;  EARLIER APPLICATION NUMBER: 60/056,884
;  EARLIER FILING DATE: 1997-08-22
;  NUMBER OF SEQ ID NOS: 280
;  SOFTWARE: PatentIn Ver. 2.0
;  SEQ ID NO 209
;  LENGTH: 483

Query Match             77.6%;  Score 2509.5;  DB 4;  Length 483;
Best Local Similarity   96.9%;  Pred. No. 7.3e-243;
Matches   467;  Conservative   2;  Mismatches   2;  Indels  11;  Gaps    1;

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Db       1 MATGGGIRAMTSLYGQLAGLKELGLLDCVSYITGASGSTWALANLYKDPEWSQKDLAGPT 60

Qy     195 ELLKTQVTKNKLGVLAPSQLQRYRQELAERARLGYPSCFTNLWALINEALLHDEPHDHKL 254
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Db      61 ELLKTQVTKNKLGVLAPSQLQRYRQELAERARLGYPSCFTNLWALINEALLHDEPHDHKL 120

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Qy     495 EQGIPFPPISPSPEEQLQPRECHTFSDPTCPGAPAVLHF---------SSGVVRTPEE 543
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Qy     604 PH 605
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RESULT 10
US-08-046-508-2
;  Sequence 2, Application US/08046508
;  Patent No. 5328842
;  GENERAL INFORMATION:
;     APPLICANT: Chiou et al.
;     TITLE OF INVENTION: COMPOUNDS, VECTORS AND METHODS FOR
;     TITLE OF INVENTION: EXPRESSING HUMAN CYTOSOLIC PHOSPHOLIPASE A2
;     NUMBER OF SEQUENCES: 2
;     CORRESPONDENCE ADDRESS:
;        ADDRESSEE: Patent Division/RSM
;        STREET: Lilly Corporate Center
;        CITY: Indianapolis
;        STATE: Indiana
;        COUNTRY: USA
;        ZIP: 46285
;     COMPUTER READABLE FORM:
;        MEDIUM TYPE: Floppy disk
;        COMPUTER: Macintosh
;        OPERATING SYSTEM: Macintosh
;        SOFTWARE: Microsoft Word
;     CURRENT APPLICATION DATA:
;        APPLICATION NUMBER: US/08/046,508
;        FILING DATE:
;        CLASSIFICATION: 435
;     ATTORNEY/AGENT INFORMATION:
;        NAME: Joseph A. Jones
;        REGISTRATION NUMBER: 26,472
;        REFERENCE/DOCKET NUMBER: X-8477
;     TELECOMMUNICATION INFORMATION:
;        TELEPHONE: 317-276-5183
;        TELEFAX: 317-276-1294
;  INFORMATION FOR SEQ ID NO: 2:
;     SEQUENCE CHARACTERISTICS:
;        LENGTH: 749 amino acids
;        TYPE: amino acid
;        TOPOLOGY: linear
;        MOLECULE TYPE: protein
US-08-046-508-2

Query Match             19.1%;  Score 619;  DB 1;  Length 749;
Best Local Similarity   27.1%;  Pred. No. 6.9e-53;
Matches   174;  Conservative   125;  Mismatches   238;  Indels  106;  Gaps    22;

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Qy     100 QAFLSRRKQVVAAALRQAL--QLDGDLQBDEIPVVAIMATGGGIRAMTSLYGQLAGLKE 156
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US-09-045-185-2

Query Match      15.4%;   Score 498.5;  DB 3;  Length 541;
Best Local Similarity   27.8%;  Pred. No. 4.9e-41;
Matches 158;  Conservative 86;  Mismatches 190;  Indels 135;  Gaps 23;

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Qy 512 Q----PRECHTFSDPTCPGAPAVLHFSSGVRRTP--EEAAAGEVNLSSSDSPYHYTKV 563
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Qy 333 EGIWSNLYA-----------ANLQDSLYWASEPSQFWDRWVRNQANLDKEQVPLL 376
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Qy 377 KIEEPPSTAGRIA--EFFTD-----------LLTWRPLAQATHNFLRGLHFH 415
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Qy 416 KDYFQHP--HFSTWKATTLDGL------PNQ-----LTPSEPHLCLLDVGYLINTSCL 460
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Qy 461 PLIQPTRDVDLILSLDYNLHGA-----FQQLQLLGRFCQEQGIPFPPISPSPEEQLQPRE 515
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Qy 559 HYTKVTYSQEDVDKLLHLTHYNVCNNQEQLLEALRQAVQRRRQ 601
Db 679 STNFQYPNQAFKRLHDLMHFNTLNNIDVIKEAMVESIEYRRQ 721
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RESULT 11
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; Sequence 2, Application US/09045185
; Patent No. 6103510
; GENERAL INFORMATION:
; APPLICANT: Kramer, Ruth M.
; APPLICANT: Pickard, Richard T.
; APPLICANT: Sharp, John D.
; APPLICANT: Strifler, Beth A.
; TITLE OF INVENTION: HUMAN PHOSPHOLIPASE A2 AND RELATED
; TITLE OF INVENTION: NUCLEIC ACID COMPOUNDS
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Eli Lilly and Company
; STREET: Lilly Corporate Center
; CITY: Indianapolis
; STATE: Indiana
; COUNTRY: United States of America
; ZIP: 46285
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/045,185
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Gaylo, Paul J.
; REGISTRATION NUMBER: 36,808
; REFERENCE/DOCKET NUMBER: P-11369
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (317) 276-0756
; TELEFAX: (317) 276-3861
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 541 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein

RESULT 12
US-08-890-615-2
; Sequence 2, Application US/08890615
; Patent No. 6121031
; GENERAL INFORMATION:
; APPLICANT: Song, Chuanzheng
; APPLICANT: Kriz, Ron
; APPLICANT: Knopf, John
; TITLE OF INVENTION: CYTOSOLIC PHOSPHOLIPASE A2-GAMMA ENZYMES
; TITLE OF INVENTION: AND POLYNUCLEOTIDES ENCODING SAME
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genetics Institute, Inc.
; STREET: 87 CambridgePark Drive
; CITY: Cambridge
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02140
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
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; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/890,615
; FILING DATE:

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;       CLASSIFICATION: 435
;       ATTORNEY/AGENT INFORMATION:
;       NAME: Brown, Scott A.
;       REGISTRATION NUMBER: 32,724
;       REFERENCE/DOCKET NUMBER: GI5300
;       TELECOMMUNICATION INFORMATION:
;       TELEPHONE: 617-498-8224
;       TELEFAX: 617-876-5851
; INFORMATION FOR SEQ ID NO: 2::
;       SEQUENCE CHARACTERISTICS:
;       LENGTH: 541 amino acids
;       TYPE: amino acid
;       STRANDEDNESS:
;       TOPOLOGY: linear
;       MOLECULE TYPE: protein
;       FEATURE:
;       NAME/KEY: Active-site
;       LOCATION: 6..242
;       FEATURE:
;       NAME/KEY: Active-site
;       LOCATION: 366..535
US-08-890-615-2
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Query Match           15.2%;   Score 490.5;   DB 3;   Length 541;
Best Local Similarity 27.6%;   Pred. No. 3.1e-40;
Matches 157;  Conservative 86;  Mismatches 191;  Indels 135;  Gaps 23;

Qy   98 EEQAFLSRRKQVVAAALRQALQLDGDLQEDEIPVVAIMATGGGIRAMTSLYGQLAGLKEL 157
           ||:|:||:|:|||:    :: ||:|||::|:|||| :||:|| |:::|
Db   15 EEKAAVERRRLHVLKALKKL----RIEADEAPVVAVLGSGGGLRAHIACLGVLSEMKEQ   69

Qy  158 GLLDCVSYITGASGSTWALANLYE--DPEWSQKDLAGPTELLKTQVTKNKLGVLAPSQL 214
           ||||||:|||||||||||||:  :||||:|: ||  |||||::|
Db   70 GLLDAVTYLAGVSGSTWAISSLYTNDGDMEALEAD------LKHRFTRQEW-----DL 116

Qy  215 QRYRQELAERARLGYPSCFTNLWA-LINEALLHDEPHDHKLSDQREALSHGQNPLPIYCA 273
           |:|: |:    :||    |:|:  ||| ||:|:
Db  117 AKSLQKTIQAARSENYS-LTDFWAYMVISKQTRELPESH-LSNMKKPVEEGTLPYPIFAA 174

Qy  274 ---LNTKGQSLTTFEFGEWCEFSPYEVGFPKYGAFIPSELFGSEFFMGQLMKRLPESRI 329
             ||| || ||:||| ::: |:::|| || :||::
Db  175 IDNDLQPSWQEARAPE--TWFEFTPHHAGFSALGAFVSITHFGSKFKKGRLVRTHPERDL 232

Qy  330 CFLEGIWSN----------------------------------LYA--ANLQDSLY 349
           || |:||                                    :|:  |:|
Db  233 TFLRGLWGSALGNTEVIREYIFDQLRNLTLKGLWRRAVANAKSIGHLIFARLLRLQESSQ 292

Qy  350 W--------ASEPSQFW----DRWVRNQANLDKEQVPLLKIEEPPSTAGRIAEFF----- 392
           |        |:||||||        :::||
Db  293 GEHPPPEDEGGEPEHTWLTEMLENWTR--TSLEKQEQP---HEDPERKGSLSNLMDFVK 346

Qy  393 -TDLLTWRPLAQATHNFLRGLHFHKDYFQHPHFSTWKATTLDGLPNQLTPSEPHLCLLDV 451
            |||:  :||||        :|||
Db  347 KTGICASKWEWGTTHNFL--------YKH----------GGIRDKIMSSRKHLHLVDA 386

Qy  452 GYLINTSCLPLLQPTRDVDLIILSLDYNLHGAFQQLQLLGRFCQEQGIPFPPISPSPEEQL 511
           :|||                :::|:: ||||: |::|
Db  387 GLAINTPFPLVLPPTREVHLILSFDFSAGDPFETIRATTDYCRRHKIPFPQVE---EAEL 443

Qy  512 Q-----PRECHTFSDPTCPGAPAVLHFSSGVRRTP--EEAAAGEVNLSSSDSPYHYTKV 563
           :       :|  :|||:|       ||:|
Db  444 DLWSKAPASCYILKGET---GPVVIHF-------PLFNIDACGGDIEAWSDTYDTFKLAD 493

Qy  564 TYSQEDVDKLLHLTHYNVCNNQEQLLEAL 592
           ||::|| ||: |:|:::|
Db  494 TYTLDVVVLLLALAKKNVRENKKILREL 522
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RESULT 13
US-09-246-290A-2
; Sequence 2, Application US/09246290A
; Patent No. 6440683
; GENERAL INFORMATION:
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;       APPLICANT: Song, Chuanzheng
;       APPLICANT: Kriz, Ronald
;       APPLICANT: Knopf, John
;       TITLE OF INVENTION: CYTOSOLIC PHOSPHOLIPASE A2-GAMMA ENZYMES
;       TITLE OF INVENTION: AND POLYNUCLEOTIDES ENCODING SAME
;       FILE REFERENCE: GFN-5300DV
;       CURRENT APPLICATION NUMBER: US/09/246,290A
;       CURRENT FILING DATE: 1999-02-08
;       PRIOR APPLICATION NUMBER: US 08/890,615
;       PRIOR FILING DATE: 1997-07-09
;       NUMBER OF SEQ ID NOS: 9
;       SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2
;       LENGTH: 541
;       TYPE: PRT
;       ORGANISM: Homo sapiens
;       FEATURE:
;       NAME/KEY: ACT_SITE
;       LOCATION: (6)...(242)
;       NAME/KEY: ACT_SITE
;       LOCATION: (366)...(535)
US-09-246-290A-2
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Query Match           15.2%;   Score 490.5;   DB 4;   Length 541;
Best Local Similarity 27.6%;   Pred. No. 3.1e-40;
Matches 157;  Conservative 86;  Mismatches 191;  Indels 135;  Gaps 23;

Qy   98 EEQAFLSRRKQVVAAALRQALQLDGDLQEDEIPVVAIMATGGGIRAMTSLYGQLAGLKEL 157
           ||:|:||:|:|||:    :: ||:|||::|:|||| :||:|| |:::|
Db   15 EEKAAVERRRLHVLKALKKL----RIEADEAPVVAVLGSGGGLRAHIACLGVLSEMKEQ   69

Qy  158 GLLDCVSYITGASGSTWALANLYE--DPEWSQKDLAGPTELLKTQVTKNKLGVLAPSQL 214
           ||||||:|||||||||||||:  :||||:|: ||  |||||::|
Db   70 GLLDAVTYLAGVSGSTWAISSLYTNDGDMEALEAD------LKHRFTRQEW-----DL 116

Qy  215 QRYRQELAERARLGYPSCFTNLWA-LINEALLHDEPHDHKLSDQREALSHGQNPLPIYCA 273
           |:|: |:    :||    |:|:  ||| ||:|:
Db  117 AKSLQKTIQAARSENYS-LTDFWAYMVISKQTRELPESH-LSNMKKPVEEGTLPYPIFAA 174

Qy  274 ---LNTKGQSLTTFEFGEWCEFSPYEVGFPKYGAFIPSELFGSEFFMGQLMKRLPESRI 329
             ||| || ||:||| ::: |:::|| || :||::
Db  175 IDNDLQPSWQEARAPE--TWFEFTPHHAGFSALGAFVSITHFGSKFKKGRLVRTHPERDL 232

Qy  330 CFLEGIWSN----------------------------------LYA--ANLQDSLY 349
           || |:||                                    :|:  |:|
Db  233 TFLRGLWGSALGNTEVIREYIFDQLRNLTLKGLWRRAVANAKSIGHLIFARLLRLQESSQ 292

Qy  350 W--------ASEPSQFW----DRWVRNQANLDKEQVPLLKIEEPPSTAGRIAEFF----- 392
           |        |:||||||        :::||
Db  293 GEHPPPEDEGGEPEHTWLTEMLENWTR--TSLEKQEQP---HEDPERKGSLSNLMDFVK 346

Qy  393 -TDLLTWRPLAQATHNFLRGLHFHKDYFQHPHFSTWKATTLDGLPNQLTPSEPHLCLLDV 451
            |||:  :||||        :|||
Db  347 KTGICASKWEWGTTHNFL--------YKH----------GGIRDKIMSSRKHLHLVDA 386

Qy  452 GYLINTSCLPLLQPTRDVDLIILSLDYNLHGAFQQLQLLGRFCQEQGIPFPPISPSPEEQL 511
           :|||                :::|:: ||||: |::|
Db  387 GLAINTPFPLVLPPTREVHLILSFDFSAGDPFETIRATTDYCRRHKIPFPQVE---EAEL 443

Qy  512 Q-----PRECHTFSDPTCPGAPAVLHFSSGVRRTP--EEAAAGEVNLSSSDSPYHYTKV 563
           :       :|  :|||:|       ||:|
Db  444 DLWSKAPASCYILKGET---GPVVIHF-------PLFNIDACGGDIEAWSDTYDTFKLAD 493

Qy  564 TYSQEDVDKLLHLTHYNVCNNQEQLLEAL 592
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Db  494 TYTLDVVVLLLALAKKNVRENKKILREL 522
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RESULT 14
US-09-687-538B-4
; Sequence 4, Application US/09687538B
; Patent No. 6514739
; GENERAL INFORMATION:
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; APPLICANT: Udagawa, Hiroaki
; APPLICANT: Frandsen, Torben
; APPLICANT: Nielsen, Tom
; APPLICANT: Kauppinen, Markus
; APPLICANT: Christensen, Soeren
; TITLE OF INVENTION: Lysophospholipase
; FILE REFERENCE: 5958.210-US
; CURRENT APPLICATION NUMBER: US/09/687,538B
; CURRENT FILING DATE: 1999-10-20
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 638
; TYPE: PRT
; ORGANISM: Aspergillus niger
US-09-687-538B-4

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Query Match            6.4%;    Score 208;  DB 4;  Length 638;
Best Local Similarity  20.1%;   Pred. No: 9e-12;
Matches 108;  Conservative 74;  Mismatches 156;  Indels 200;  Gaps 26;

Qy  129  IPVVAIMATGGIRAMTSLYGQLAGLKEL----------GLLDCVSYITGASGSTWALA  177
Db  114  IPNIAIAASGGGYRALTNGAGALKAFDSRSDNATNSGQLGGLLQAATVVSGLSGGSWLVG  173
Qy  178  NLY----------EDPEWSQKDLAGPTELLKTQVTKNKLGVLAPSQ  213
Db  174  SMFVNFSSIGELQASEKVWRFDKSLLEGPNFDHIQIVSTVEYWK-DIT  221
Qy  214  LQRYRQELAERARLGYPSCFTNLWA----------LINE  253
Db  222  ----------EEVDGKANAGFNTSFTDYWGRALSYQLVNASDDKGGPDYTWSSIALMDD----------ALLHDEPHDHK  270
Qy  254  LSDQREALSHGQNLPIYCA-LNTKGQ----------SLTTFPFGEWCEFSPYEVGFPKYGAFIP  307
Db  271  ----------FKNGQYMPIVVADGRNPGEIIVETNATVYEVNPW-EFGSFD----------PSVYAFAP  319
Qy  308  SELFGSEFFMGQLMKRLPESRIC----------FLEGIWSNLYAANLQDSLYWASEPSQFWD  359
Db  320  LQYIGSRFENGS----------IPDNGTCVSGFDNAGFIMGSSSTLF----------NQF--  359
Qy  360  RWVRNQANLDKEQVPLLKIEEPPSTAGRIAEFFTDLLTWRPLAQATHNFLRGLHFHKDYF  419
Db  360  ----------LLQINSTSIPTI----------LKDAFTDIL--EDLGBRNDDI----------AVVS  394
Qy  420  QHPHFSTWKATTLDGLPNQLTPSEPHLCLLDVGYL----------INTSCLPLLQPTRDVDLIL  473
Db  395  PNP-FSGYRDS----------SEDYATAKDLDVVDGGEDGENIPLHPLIQPERAVDVIF  442
Qy  474  SLDYNLHGAF--QQLQLLGRFCQEQGIPPPISPSPEEQLQPRBCHTFSDPTCPGAPAV  530
Db  443  AIDSSADTDYWPNGTSLVATY----------ERSLEPSIANGTAFPAVPDDQNTF  487
Qy  531  LHFSSGVRRTPEEAAAGEVNLSSS----------DSPYHYT-----KVTYSQEDVDKLL  574
Db  488  VNL--GLNSRPTFPGCDPKNISGTAPLVIYLPNSPYTYDSNFSTFKLITYSDEERDSVI  543
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RESULT 15
US-09-437-687A-2
; Sequence 2, Application US/09437687A
; Patent No. 6489154
; GENERAL INFORMATION:
; APPLICANT: Randy M. Berka
; APPLICANT: Michael W. Rey
; APPLICANT: Tony Byun
; APPLICANT: Ryoko Itami
; APPLICANT: No. 6489154iko Tsutsumi
; APPLICANT: Alan Klotz
; TITLE OF INVENTION: Polypeptides Having Lysophospholipase
; TITLE OF INVENTION: Activity And Nucleic Acids Encoding Same
; FILE REFERENCE: 5713.200-US
; CURRENT APPLICATION NUMBER: US/09/437,687A

; CURRENT FILING DATE: 1998-11-10
; PRIOR APPLICATION NUMBER: 09/189,486
; PRIOR FILING DATE: 1998-11-10
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 654
; TYPE: PRT
; ORGANISM: Fusarium venenatum
US-09-437-687A-2

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Query Match            6.4%;    Score 208;  DB 4;  Length 654;
Best Local Similarity  21.7%;   Pred. No. 9.4e-12;
Matches 146;  Conservative 82;  Mismatches 216;  Indels 230;  Gaps 35;

Qy   36  PFFFFFEMESLSVAQGVQWRDLGSLQPPLGFKRFSCLSLPSS----------WDYRLRE  86
Db    4  PLVFTLWLTSSAIAAPD---DAGLVAAPAIG-KSLSIRALPDSPSGGYAPKVVDCPSTR  58
Qy   87  LAVRLGFGPCAEEQAFLSRRKQVVAAALRQALQ------LDGD-LQEDE---IPVVA  133
Db   59  PKIRLADGLLSDQEEAWVRRRRNNTIDPMKDLLSRVNISGPDAEKWIEKNKNNATALPNIA  118
Qy  134  IMATGGIRAMTSLYGQLAGLKE----------LGLLDCVSYITGASGSTWALANLYED---  182
Db  119  IAASGGGYRALMNGAGFISAADSRNNESGPISGLLQSSTYLAGLSGGGWLVGSIFANNFT  178
Qy  183  --PEWSQKD----------LAGPTELLKTQVTKNKLGVLAPSQLQRYRQELAERARLG  228
Db  179  TIPDLQKGKGSDIWAFDRSIFKGP----------EKSGLNVLNTAKYWDDIKDTVDEKADG  230
Qy  229  YPSCFTNLWALINEALLHDEPHDHKLSDQREA----------LSHGQNLPLIYCA-  273
Db  231  WNTTLTDWW------GRAL----------SYQLIDASEGGPAYTFSSIADTSNFKDADTPFFPILVAD  281
Qy  274  ----------LNTKGQSLTTFPFGEWCEFSPYEVGFPKYGAFIPSELFGSEFFMGQLMKR  323
Db  282  GRAPQQRIVSLNATVYEFNPEFEFGTWDPTS----------YG-FAPVEYIGSNFTNGTIEK-  331
Qy  324  LPESRIC----------FLEGIWSNLYAANLQDSLYWASEPSQFWDRWVRNQANLDKEQVPL  375
Db  332  ---GGBCVRGFDQFGFVMGTSSSLFNQFLNNITKIGE----------ENDIPS  372
Qy  376  LKIEEPPSTAGRIAEFFTDLLTWRPLAQATHNFLRGLHFH----------KDYFQHPHFSTWKAT-  430
Db  373  L----------VVKAIQGFLVALDTNDEDIADYSPNP-FYQWNVTG  407
Qy  431  -TLDGLPNQLTPSEPHLCLLDVGY-LINTSCLPLLQPTRDVDLILSLDYN----------  478
Db  408  KSYNAKDHQLT----------LVDGGEDLQNIPLHPLIQPVRGVDIIFAIDSSADTDNNWPNG  460
Qy  479  --LHGAFQQL-QLLGRFCQEQGIPPPPISPSPE----------EQLQPR----------ECHTFSDPT  523
Db  461  TALRATYDRVDSSLG----NGTQFPSI-PSAETFINEKLNQRPTLFGCDADNFTLSDGK  514
Qy  524  CPGAPAVLHFSSGVRRTPEEAAAGEVNLSSSDSPYHYTKVTYSQEDVDKLLHLTHYNVCN  583
Db  515  AP-PPLVFYI----------PNAPYTFLSNVSTFD----------LSYSIPERDSI----------  549
Qy  584  NQEQLLEALRQAVQ  597
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Search completed: October 5, 2004, 19:24:58
Job time : 41.9133 secs

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              GenCore version 5.1.6
    Copyright (c) 1993 - 2004  Compugen Ltd.

OM protein - protein search, using sw model

Run on:  October 5, 2004, 19:25:05 ; Search time 137.133 Seconds
                                     (without alignments)
                                     1419.702 Million cell updates/sec

Title:          US-09-830-321A-2
Perfect score:  3235
Sequence:       1 MIFVELSPTLALCLERVASH.........EQLLEALRQAVQRRRQRRPH 605

Scoring table:  BLOSUM62
                Gapop 10.0 , Gapext 0.5

Searched:       1351062 seqs, 321799191 residues

Total number of hits satisfying chosen parameters:     1351062

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing:  Minimum Match 0%
                  Maximum Match 100%
                  Listing first 45 summaries

Database :  Published Applications AA:*
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     2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Match Length	DB	ID	Description
1	2767.5	85.5	778	14	US-10-266-388-2	Sequence 2, Appli
2	2767.5	85.5	797	14	US-10-266-388-4	Sequence 4, Appli
3	2767.5	85.5	1012	16	US-10-408-765A-638	Sequence 638, App
4	2509.5	77.6	483	9	US-09-981-876-144	Sequence 144, App
5	2509.5	77.6	483	9	US-09-981-876-209	Sequence 209, App
6	2509.5	77.6	483	10	US-09-148-545-144	Sequence 144, App
7	2509.5	77.6	483	10	US-09-148-545-209	Sequence 209, App
8	1492	46.1	1026	12	US-10-332-426-6	Sequence 6, Appli
9	1243.5	38.4	996	16	US-10-467-248-1	Sequence 1, Appli
10	1139.5	35.2	849	15	US-10-380-873B-1	Sequence 1, Appli
11	1138	35.2	853	15	US-10-380-873B-38	Sequence 38, Appl
12	1127	34.8	854	15	US-10-380-873B-22	Sequence 22, Appl
13	1112	34.4	848	12	US-10-332-426-3	Sequence 3, Appli
14	619	19.1	749	12	US-10-211-462-50	Sequence 50, Appl
15	619	19.1	749	12	US-10-157-898-2	Sequence 2, Appli
16	619	19.1	749	13	US-10-062-730-2	Sequence 2, Appli
17	619	19.1	749	14	US-10-021-660-118	Sequence 118, App
18	599.5	18.5	748	12	US-10-157-898-4	Sequence 4, Appli
19	490.5	15.2	541	14	US-10-211-462-93	Sequence 93, Appl
20	490.5	15.2	541	14	US-10-021-660-127	Sequence 127, App
21	490.5	15.2	541	16	US-10-741-601-296	Sequence 296, App
22	490.5	15.2	541	16	US-10-741-601-297	Sequence 297, App
23	461	14.3	597	14	US-10-181-612-4	Sequence 4, Appli
24	419	13.0	180	12	US-10-296-115-917	Sequence 917, App
25	368.5	11.4	261	15	US-10-380-873B-26	Sequence 26, Appl
26	361	11.2	454	15	US-10-380-873B-3	Sequence 3, Appli
27	358	11.1	442	16	US-10-468-519-1	Sequence 1, Appli
28	347.5	10.7	441	16	US-10-468-519-8	Sequence 8, Appli
29	344	10.6	445	16	US-10-468-519-5	Sequence 5, Appli
30	339	10.5	384	16	US-10-741-601-295	Sequence 295, App
31	232	7.2	151	14	US-10-017-161-1210	Sequence 1210, Ap
32	232	7.2	151	15	US-10-292-798-1020	Sequence 1020, Ap
33	220	6.8	150	15	US-10-094-749-1682	Sequence 1682, Ap
34	217	6.7	135	12	US-10-424-599-242280	Sequence 242280,
35	216	6.7	101	15	US-10-094-749-2181	Sequence 2181, Ap
36	211	6.5	137	15	US-10-276-774-1959	Sequence 1959, Ap
37	211	6.5	157	15	US-10-108-260A-4272	Sequence 4272, Ap
38	210	6.5	157	12	US-10-276-774-1940	Sequence 1940, Ap
39	208.5	6.4	137	12	US-10-276-774-1949	Sequence 1949, Ap
40	208.5	6.4	183	9	US-09-989-920-245	Sequence 245, App
41	208.5	6.4	361	9	US-09-995-494-107	Sequence 107, App
42	208	6.4	97	12	US-10-276-774-2008	Sequence 2008, Ap
43	208	6.4	638	14	US-10-309-437-4	Sequence 4, Appli
44	208	6.4	654	14	US-10-263-250-2	Sequence 2, Appli
45	206	6.4	213	12	US-10-296-115-911	Sequence 911, App

ALIGNMENTS

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RESULT 1
US-10-266-388-2
; Sequence 2, Application US/10266388
; Publication No. US20030124702A1
; GENERAL INFORMATION:
;  APPLICANT: Kriz, Ron
;  APPLICANT: Song, Chuanzheng
;  TITLE OF INVENTION: CYTOSOLIC PHOSPHOLIPASE A2-BETA ENZYMES
;  NUMBER OF SEQUENCES: 9
;  CORRESPONDENCE ADDRESS:
;   ADDRESSEE: Genetics Institute, Inc.
;   STREET: 87 CambridgePark Drive
;   CITY: Cambridge
;   STATE: MA
;   COUNTRY: USA
;   ZIP: 02140
;  COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: PatentIn Release #1.0, Version #1.30
;  CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/10/266,388
;   FILING DATE: 07-Oct-2002
;   CLASSIFICATION: <Unknown>
;  PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: US/09/895,547
;   FILING DATE: 29-Jun-2001
;   APPLICATION NUMBER: 09/460,145
;   FILING DATE: <Unknown>
;  ATTORNEY/AGENT INFORMATION:
;   NAME: Brown, Scott A.
;   REGISTRATION NUMBER: 32,724
;   REFERENCE/DOCKET NUMBER: GI5289
;  TELECOMMUNICATION INFORMATION:
;   TELEPHONE: (617) 498-8224
;   TELEFAX: (617) 876-5851
; INFORMATION FOR SEQ ID NO: 2:
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Left column (SEQ ID NO: 2 / RESULT 2)

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;
;
;
;
        SEQUENCE CHARACTERISTICS:
          LENGTH: 778 amino acids
          TYPE: amino acid
          STRANDEDNESS: <Unknown>
          TOPOLOGY: linear
        MOLECULE TYPE: protein
        SEQUENCE DESCRIPTION: SEQ ID NO: 2:

US-10-266-388-2

Query Match       85.5%;  Score 2767.5;  DB 14;  Length 778;
Best Local Similarity 87.6%;  Pred. No. 1.2e-254;
Matches  537;  Conservative  5;  Mismatches  22;  Indels  49;  Gaps  6;

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Qy   84 ----------------------LRELAVRLGFGPCAEEQAFLSRRKQVVAAALRQALQLDGD  123
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Db  226 LVFPTSQEPLMRVELKKEAGLRELAVRLGFGPCAEEQAFLSRRKQVVAAALRQALQLDGD  285

Qy  124 LQEDEIPVVAIMATGGGIRAMTSLYGQLAGLKELGLLDCVSYITGASGSTWALANLYEDP  183
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Db  286 LQEDEIPVVAIMATGGGIRAMTSLYGQLAGLKELGLLDCVSYITGASGSTWALANLYEDP  345

Qy  184 EWSQKDLAGPTELLKTQVTKNKLGVLAPSQLQRYRQELAERARLGYPSCFTNLWALINEA  243
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  346 EWSQKDLAGPTELLKTQVTKNKLGVLAPSQLQRYRQELAERARLGYPSCFTNLWALINEA  405

Qy  244 LLHDEPHDHKLSDQREALSHGQNPLPIYCALNTKGQSLTTFEFGEWCEFSPYEVGFPKYG  303
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  406 LLHDEPHDHKLSDQREALSHGQNPLPIYCALNTKGQSLTTFEFGEWCEFSPYEVGFPKYG  465

Qy  304 AFIPSELFGSEFFMGQLMKRLPESRICFLEGIWSNLYAANLQDSLYWASEPSQFWDRWVR  363
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  466 AFIPSELFGSEFFMGQLMKRLPESRICFLEGIWSNLYAANLQDSLYWASEPSQFWDRWVR  525

Qy  364 NQANLDKEQVPLLKIEEPPSTAGRIAEFFTDLLTWRPLAQATHNFLRGLHFHKDYFQHPH  423
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  526 NQANLDKEQVPLLKIEEPPSTAGRIAEFFTDLLTWRPLAQATHNFLRGLHFHKDYFQHPH  585

Qy  424 FSTWKATTLDGLPNQLTPSEPHLCLLDVGYLINTSCLPLLQPTRDVDLIISLDYNLHGAF  483
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  586 FSTWKATTLDGLPNQLTPSEPHLCLLDVGYLINTSCLPLLQPTRDVDLIISLDYNLHGAF  645

Qy  484 QQLQLLGRFCQEQGIPFPPISPSPPEEQLQPRECHTFSDPTCPGAPAVLHF----------  533
        ||||||||||||||||||||||||||||||||||||||||||||||||||
Db  646 QQLQLLGRFCQEQGIPFPPISPSPPEEQLQPRECHTFSDPTCPGAPAVLHFPLVSDSFREY  705

Qy  534 -SSGVRRTPEEAAAGEVNLSSSDSPYHYTKVTYSQEDVDKLLHLTHYNVCNNQEQLLEAL  592
         : |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  706 SAPGVRRTPEEAAAGEVNLSSSDSPYHYTKVTYSQEDVDKLLHLTHYNVCNNQEQLLEAL  765

Qy  593 RQAVQRRRQRRPH  605
        |||||||||||||
Db  766 RQAVQRRRQRRPH  778
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RESULT 2

US-10-266-388-4

; Sequence 4, Application US/10266388
; Publication No. US20030124702A1
; GENERAL INFORMATION:
APPLICANT: Kriz, Ron
          Song, Chuanzheng
TITLE OF INVENTION: CYTOSOLIC PHOSPHOLIPASE A2-BETA ENZYMES
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
  ADDRESSEE: Genetics Institute, Inc.
  STREET: 87 CambridgePark Drive
  CITY: Cambridge
  STATE: MA
  COUNTRY: USA

Right column (SEQ ID NO: 4)

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INFORMATION FOR SEQ ID NO: 4:
        SEQUENCE CHARACTERISTICS:
          LENGTH: 797 amino acids
          TYPE: amino acid
          STRANDEDNESS: <Unknown>
          TOPOLOGY: linear
        MOLECULE TYPE: protein
        SEQUENCE DESCRIPTION: SEQ ID NO: 4:

US-10-266-388-4

Query Match       85.5%;  Score 2767.5;  DB 14;  Length 797;
Best Local Similarity 87.6%;  Pred. No. 1.2e-254;
Matches  537;  Conservative  5;  Mismatches  22;  Indels  49;  Gaps  6;

US-10-266-388-4

Qy   24 TGLLVLFCPAPCPFFFFEMESLSVAQAGVQWRDLGSLQPPPLGFKRFSCLSLPSSWDYR   83
           |||| |  | |     :  | :  |||
Db  203 TGTFRFHCPA-C-----WEQE-LSI--------RLQDAPEEQLKAPLSALPSGGQVVR  244

Qy   84 ----------------------LRELAVRLGFGPCAEEQAFLSRRKQVVAAALRQALQLDGD  123
                               ||||||||||||||||||||||||||||||||||||||||
Db  245 LVFPTSQEPLMRVELKKEAGLRELAVRLGFGPCAEEQAFLSRRKQVVAAALRQALQLDGD  304

Qy  124 LQEDEIPVVAIMATGGGIRAMTSLYGQLAGLKELGLLDCVSYITGASGSTWALANLYEDP  183
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  305 LQEDEIPVVAIMATGGGIRAMTSLYGQLAGLKELGLLDCVSYITGASGSTWALANLYEDP  364

Qy  184 EWSQKDLAGPTELLKTQVTKNKLGVLAPSQLQRYRQELAERARLGYPSCFTNLWALINEA  243
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  365 EWSQKDLAGPTELLKTQVTKNKLGVLAPSQLQRYRQELAERARLGYPSCFTNLWALINEA  424

Qy  244 LLHDEPHDHKLSDQREALSHGQNPLPIYCALNTKGQSLTTFEFGEWCEFSPYEVGFPKYG  303
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  425 LLHDEPHDHKLSDQREALSHGQNPLPIYCALNTKGQSLTTFEFGEWCEFSPYEVGFPKYG  484

Qy  304 AFIPSELFGSEFFMGQLMKRLPESRICFLEGIWSNLYAANLQDSLYWASEPSQFWDRWVR  363
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  485 AFIPSELFGSEFFMGQLMKRLPESRICFLEGIWSNLYAANLQDSLYWASEPSQFWDRWVR  544

Qy  364 NQANLDKEQVPLLKIEEPPSTAGRIAEFFTDLLTWRPLAQATHNFLRGLHFHKDYFQHPH  423
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  545 NQANLDKEQVPLLKIEEPPSTAGRIAEFFTDLLTWRPLAQATHNFLRGLHFHKDYFQHPH  604

Qy  424 FSTWKATTLDGLPNQLTPSEPHLCLLDVGYLINTSCLPLLQPTRDVDLIISLDYNLHGAF  483
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  605 FSTWKATTLDGLPNQLTPSEPHLCLLDVGYLINTSCLPLLQPTRDVDLIISLDYNLHGAF  664

Qy  484 QQLQLLGRFCQEQGIPFPPISPSPPEEQLQPRECHTFSDPTCPGAPAVLHF----------  533
        ||||||||||||||||||||||||||||||||||||||||||||||||||
Db  665 QQLQLLGRFCQEQGIPFPPISPSPPEEQLQPRECHTFSDPTCPGAPAVLHFPLVSDSFREY  724

Qy  534 -SSGVRRTPEEAAAGEVNLSSSDSPYHYTKVTYSQEDVDKLLHLTHYNVCNNQEQLLEAL  592
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Db   725 SAPGVRRTPEEAAAGEVNLSSSDSPYHYTKVTYSQEDVDKLLHLTHYNVCNNQEQLLEAL 784
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Qy   593 RQAVQRRRQRRPH 605
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Db   785 RQAVQRRRQRRPH 797
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Db   534 -SSGVRRTPEEAAAGEVNLSSSDSPYHYTKVTYSQEDVDKLLHLTHYNVCNNQEQLLEAL 592
             : |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   940 SAPGVRRTPEEAAAGEVNLSSSDSPYHYTKVTYSQEDVDKLLHLTHYNVCNNQEQLLEAL 999

Qy   593 RQAVQRRRQRRPH 605
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Db  1000 RQAVQRRRQRRPH 1012
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RESULT 3
US-10-408-765A-638
; Sequence 638, Application US/10408765A
; Publication No. US20040101874A1
; GENERAL INFORMATION:
;   APPLICANT: Ghosh, Soumitra S.
;   APPLICANT: Fahy, Eoin D.
;   APPLICANT: Zhang, Bing
;   APPLICANT: Gibson, Bradford W.
;   APPLICANT: Taylor, Steven W.
;   APPLICANT: Glenn, Gary M.
;   APPLICANT: Warnock, Dale E.
;   TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION
;   TITLE OF INVENTION: IDENTIFIED IN THE MITOCHONDRIAL PROTEOME
;   FILE REFERENCE: 660088.465
;   CURRENT APPLICATION NUMBER: US/10/408,765A
;   CURRENT FILING DATE: 2003-04-04
;   NUMBER OF SEQ ID NOS: 3077
;   SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 638
;   LENGTH: 1012
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-408-765A-638

Query Match   85.5%; Score 2767.5; DB 16; Length 1012;
Best Local Similarity   87.6%; Pred. No. 1.7e-254;
Matches   537; Conservative 5; Mismatches 22; Indels 49; Gaps 6;

Qy   24 TGLLVLFCPAPCPFFFFEMESLSVAQGVQWRDLGSLQPPPLGFKRFSCLSLPSSWDYR 83
            |||:|| | : :| :|:| |||| || |::|
Db   418 TGTFRFHCPA-C----WEQE-LSI-------RLQDAPEEQLKAPLSALPSGQVVR 459

Qy   84 ----------------------------LRELAVRLGFGPCAEEQAFLSRRKQVVAAALRQALQLDGD 123
                                        |||||||||||||||||||||||||||||||||||||||
Db   460 LVFPTSQEPLMRVELKKEAGLRELAVRLGFGPCAEEQAFLSRRKQVVAAALRQALQLDGD 519

Qy   124 LQEDEIPVAIMATGGGIRAMTSLYGQLAGLKELGLLDCVSYITGASGSTWALANLYEDP 183
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   520 LQEDEIPVAIMATGGGIRAMTSLYGQLAGLKELGLLDCVSYITGASGSTWALANLYEDP 579

Qy   184 EWSQKDLAGPTELLKTQVTKNKLGVLAPSQLQRYRQELAERARLGYPSCFTNLWALINEA 243
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   580 EWSQKDLAGPTELLKTQVTKNKLGVLAPSQLQRYRQELAERARLGYPSCFTNLWALINEA 639

Qy   244 LLHDEPHDHKLSDQREALSHGQNPLPIYCALNTKGQSLTTFEFGEWCEFSPYEVGFPKYG 303
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   640 LLHDEPHDHKLSDQREALSHGQNPLPIYCALNTKGQSLTTFEFGEWCEFSPYEVGFPKYG 699

Qy   304 AFIPSELFGSEFFMGQLMKRLPESRICFLEGIWSNLYAANLQDSLYWASEPSQFWDRWVR 363
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   700 AFIPSELFGSEFFMGQLMKRLPESRICFLEGIWSNLYAANLQDSLYWASEPSQFWDRWVR 759

Qy   364 NQANLDKEQVPLLKIEEPPSTAGRIAEFFTDLLTWRPLAQATHNFLRGLHFHKDYFQHPH 423
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   760 NQANLDKEQVPLLKIEEPPSTAGRIAEFFTDLLTWRPLAQATHNFLRGLHFHKDYFQHPH 819

Qy   424 FSTWKATTLDGLPNQLTPSEPHLCLLDVGYLINTSCLPLLQPTRDVDLILSLDYNLHGAF 483
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   820 FSTWKATTLDGLPNQLTPSEPHLCLLDVGYLINTSCLPLLQPTRDVDLILSLDYNLHGAF 879

Qy   484 QQLQLLGRFCQEQGIPFPPISPSPEEQLQPRECHTFSDPTCPGAPAVLHF--------- 533
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Db   880 QQLQLLGRFCQEQGIPFPPISPSPEEQLQPRECHTFSDPTCPGAPAVLHFPLVSDSFREY 939
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RESULT 4
US-09-981-876-144
; Sequence 144, Application US/09981876
; Patent No. US2002016466A1
; GENERAL INFORMATION:
;   APPLICANT: Rosen et al.
;   TITLE OF INVENTION: 70 Human Secreted Proteins
;   FILE REFERENCE: PZ001P1
;   CURRENT APPLICATION NUMBER: US/09/981,876
;   CURRENT FILING DATE: 2001-10-19
;   PRIOR APPLICATION NUMBER: 09/148,545
;   PRIOR FILING DATE: 1998-09-04
;   PRIOR APPLICATION NUMBER: 60/040,162
;   PRIOR FILING DATE: 1997-03-07
;   PRIOR APPLICATION NUMBER: 60/040,333
;   PRIOR FILING DATE: 1997-03-07
;   PRIOR APPLICATION NUMBER: 60/038,621
;   PRIOR FILING DATE: 1997-03-07
;   PRIOR APPLICATION NUMBER: 60/040,161
;   PRIOR FILING DATE: 1997-03-07
;   PRIOR APPLICATION NUMBER: 60/040,626
;   PRIOR FILING DATE: 1997-03-07
;   PRIOR APPLICATION NUMBER: 60/040,334
;   PRIOR FILING DATE: 1997-03-07
;   PRIOR APPLICATION NUMBER: 60/040,336
;   PRIOR FILING DATE: 1997-03-07
;   PRIOR APPLICATION NUMBER: 60/047,615
;   PRIOR FILING DATE: 1997-05-23
;   PRIOR APPLICATION NUMBER: 60/047,600
;   PRIOR FILING DATE: 1997-05-23
;   PRIOR APPLICATION NUMBER: 60/047,597
;   PRIOR FILING DATE: 1997-05-23
;   PRIOR APPLICATION NUMBER: 60/047,502
;   PRIOR FILING DATE: 1997-05-23
;   PRIOR APPLICATION NUMBER: 60/047,633
;   PRIOR FILING DATE: 1997-05-23
;   PRIOR APPLICATION NUMBER: 60/047,583
;   PRIOR FILING DATE: 1997-05-23
;   PRIOR APPLICATION NUMBER: 60/047,617
;   PRIOR FILING DATE: 1997-05-23
;   PRIOR APPLICATION NUMBER: 60/047,618
;   PRIOR FILING DATE: 1997-05-23
;   PRIOR APPLICATION NUMBER: 60/047,503
;   PRIOR FILING DATE: 1997-05-23
;   PRIOR APPLICATION NUMBER: 60/047,592
;   PRIOR FILING DATE: 1997-05-23
;   PRIOR APPLICATION NUMBER: 60/047,581
;   PRIOR FILING DATE: 1997-05-23
;   PRIOR APPLICATION NUMBER: 60/047,500
;   PRIOR FILING DATE: 1997-05-23
;   PRIOR APPLICATION NUMBER: 60/047,587
;   PRIOR FILING DATE: 1997-05-23
;   PRIOR APPLICATION NUMBER: 60/047,492
;   PRIOR FILING DATE: 1997-05-23
;   PRIOR APPLICATION NUMBER: 60/047,598
;   PRIOR FILING DATE: 1997-05-23
;   PRIOR APPLICATION NUMBER: 60/047,613
;   PRIOR FILING DATE: 1997-05-23
;   PRIOR APPLICATION NUMBER: 60/047,582
;   PRIOR FILING DATE: 1997-05-23

PRIOR APPLICATION NUMBER: 60/047,596
PRIOR FILING DATE: 1997-05-23
PRIOR APPLICATION NUMBER: 60/047,612
PRIOR FILING DATE: 1997-05-23
PRIOR APPLICATION NUMBER: 60/047,632
PRIOR FILING DATE: 1997-05-23
PRIOR APPLICATION NUMBER: 60/047,601
PRIOR FILING DATE: 1997-05-23
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PRIOR APPLICATION NUMBER: 60/043,313
PRIOR FILING DATE: 1997-04-11
PRIOR APPLICATION NUMBER: 60/043,672
PRIOR FILING DATE: 1997-04-11
PRIOR APPLICATION NUMBER: 60/043,315
PRIOR FILING DATE: 1997-04-11
PRIOR APPLICATION NUMBER: 60/048,974
PRIOR FILING DATE: 1997-06-06
PRIOR APPLICATION NUMBER: 60/056,886
PRIOR FILING DATE: 1997-08-22
PRIOR APPLICATION NUMBER: 60/056,877
PRIOR FILING DATE: 1997-08-22
PRIOR APPLICATION NUMBER: 60/056,889
PRIOR FILING DATE: 1997-08-22
PRIOR APPLICATION NUMBER: 60/056,893
PRIOR FILING DATE: 1997-08-22
PRIOR APPLICATION NUMBER: 60/056,630
PRIOR FILING DATE: 1997-08-22
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PRIOR APPLICATION NUMBER: 60/056,879
PRIOR FILING DATE: 1997-09-05
PRIOR APPLICATION NUMBER: 60/056,880
PRIOR FILING DATE: 1997-08-22
PRIOR APPLICATION NUMBER: 60/056,894
PRIOR FILING DATE: 1997-08-22
PRIOR APPLICATION NUMBER: 60/056,911
PRIOR FILING DATE: 1997-08-22
PRIOR APPLICATION NUMBER: 60/056,636
PRIOR FILING DATE: 1997-08-22
PRIOR APPLICATION NUMBER: 60/056,874
PRIOR FILING DATE: 1997-08-22
PRIOR APPLICATION NUMBER: 60/056,910
PRIOR FILING DATE: 1997-08-22
PRIOR APPLICATION NUMBER: 60/056,864

PRIOR FILING DATE: 1997-08-22
PRIOR APPLICATION NUMBER: 60/056,631
PRIOR FILING DATE: 1997-08-22
PRIOR APPLICATION NUMBER: 60/056,845
PRIOR FILING DATE: 1997-08-22
PRIOR APPLICATION NUMBER: 60/056,892
PRIOR FILING DATE: 1997-08-22
PRIOR APPLICATION NUMBER: 60/047,595
PRIOR FILING DATE: 1997-05-23
PRIOR APPLICATION NUMBER: 60/057,761
PRIOR FILING DATE: 05-Sep-1997
PRIOR APPLICATION NUMBER: 60/047,599
PRIOR FILING DATE: 1997-04-11
PRIOR FILING DATE: 1997-05-23
PRIOR APPLICATION NUMBER: 60/047,588
PRIOR FILING DATE: 1997-05-23
PRIOR APPLICATION NUMBER: 60/047,585
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PRIOR APPLICATION NUMBER: 60/047,594
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PRIOR APPLICATION NUMBER: 60/047,589
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PRIOR APPLICATION NUMBER: 60/047,593
PRIOR FILING DATE: 1997-05-23
PRIOR APPLICATION NUMBER: 60/047,614
PRIOR FILING DATE: 1997-05-23
PRIOR APPLICATION NUMBER: 60/043,578
PRIOR FILING DATE: 1997-04-11
PRIOR APPLICATION NUMBER: 60/043,576
PRIOR FILING DATE: 1997-04-11
PRIOR APPLICATION NUMBER: 60/043,670
PRIOR FILING DATE: 1997-04-11
PRIOR APPLICATION NUMBER: 60/047,501
PRIOR FILING DATE: 1997-05-23
PRIOR APPLICATION NUMBER: 60/056,632
PRIOR FILING DATE: 1997-08-22
PRIOR APPLICATION NUMBER: 60/056,664
PRIOR FILING DATE: 1997-08-22
PRIOR APPLICATION NUMBER: 60/056,876
PRIOR FILING DATE: 1997-08-22
PRIOR APPLICATION NUMBER: 60/056,881
PRIOR FILING DATE: 1997-08-22
PRIOR APPLICATION NUMBER: 60/056,909
PRIOR FILING DATE: 1997-08-22
PRIOR APPLICATION NUMBER: 60/056,875
PRIOR FILING DATE: 1997-08-22
PRIOR APPLICATION NUMBER: 60/056,862
PRIOR FILING DATE: 1997-08-22
PRIOR APPLICATION NUMBER: 60/056,887
PRIOR FILING DATE: 1997-08-22
PRIOR APPLICATION NUMBER: 60/056,908
PRIOR FILING DATE: 1997-08-22
PRIOR APPLICATION NUMBER: 60/048,964
PRIOR FILING DATE: 1997-06-06
PRIOR APPLICATION NUMBER: 60/057,650
PRIOR FILING DATE: 1997-09-05
PRIOR APPLICATION NUMBER: 60/056,884
PRIOR FILING DATE: 1997-08-22

NUMBER OF SEQ ID NOS: 280
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 144
LENGTH: 483

Query Match   77.6%; Score 2509.5; DB 9; Length 483;
Best Local Similarity   96.9%; Pred. No. 2.4e-230;
Matches 467; Conservative   2; Mismatches   2; Indels   11; Gaps 1;

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Qy    135 MATGGGIRAMTSLYGQLAGLKELGLLDCVSYITGASGSTWALANLYEDPEWSQKDLAGPT 194
          ||||||||||||||||||||||||||| ||||||||||||||||:||||||||||||||
Db      1 MATGGGIRAMTSLYGQLAGLKELGLLDCXSYITGASGSTWALANLYKDPEWSQKDLAGPT 60
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Qy   195  ELLKTQVTKNKLGVLAPSQLQRYRQELAERARLGYPSCFTNLWALINEALLHDEPHDHKL  254
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    61  ELLKTQVTKNKLGVLAPSQLQRYRQELAERARLGYPSCFTNLWALINEALLHDEPHDHKL  120

Qy   255  SDQREALSHGQNPLPIYCALNTKGQSLTTFEFGEWCEFSPYEVGFPKYGAFIPSELFGSE  314
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121  SDQREALSHGQNPLPIYCALNTKGQSLTTFEFGEWCEFSPYEVGFPKYGAFIPSELFGSE  180

Qy   315  FFMGQLMKRLPESRICFLEGIWSNLYAANLQDSLYWASEPSQFWDRWVRNQANLDKEQVP  374
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181  FFMGQLMKRLPESRICFLEGIWSNLYAANLQDSLYWASEPSQFWDRWVRNQANLDKEQVP  240

Qy   375  LLKIEEPSTAGRIAEFFTDLLTWRPLAQATHNFLRGLHFHKDYFQHPHFSTWKATTLDG   434
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241  LLKIEEPSTAGRIAEFFTDLLTWRPLAQATHNFLRGLHFHKDYFQHPHFSTWKATTLDG   300

Qy   435  LPNQLTPSEPHLCLLDVGYLINTSCLPLLQPTRDVDLILSLDYNLHGAFQQLQLLGRFCQ  494
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   301  LPNQLTPSEPHLCLLDVGYLINTSCLPLLQPTRDVDLILSLDYNLHGAFQQLQLLGRFCQ  360

Qy   495  EQGIPFPPISPSPEEQLQPRECHTFSDPTCPGAPAVLHF--------SSGVRRTPEE     543
          |||||||||||||||||||||||||||||||||||||||        : |||||||||
Db   361  EQGIPFPPISPSPEEQLQPRECHTFSDPTCPGAPAVLHFPLVSDSFREYSAPGVRRTPEE  420

Qy   544  AAAGEVNLSSSDSPYHYTKVTYSQEDVDKLLHLTHYNVCNNQEQLLEALRQAVQRRRQRR  603
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||| |||
Db   421  AAAGEVNLSSSDSPYHYTKVTYSQEDVDKLLHLTHYNVCNNQEQLLEALRQAVQRRQRR   480

Qy   604  PH  605
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Db   481  PH  482
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RESULT 5
US-09-981-876-209
; Sequence 209, Application US/09981876
; Patent No. US2002016466A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 70 Human Secreted Proteins
; FILE REFERENCE: PZ001P1
; CURRENT APPLICATION NUMBER: US/09/981,876
; CURRENT FILING DATE: 2001-10-19
; PRIOR APPLICATION NUMBER: 09/148,545
; PRIOR FILING DATE: 1998-09-04
; PRIOR APPLICATION NUMBER: 60/040,162
; PRIOR FILING DATE: 1997-03-07
; PRIOR APPLICATION NUMBER: 60/038,621
; PRIOR FILING DATE: 1997-03-07
; PRIOR APPLICATION NUMBER: 60/040,333
; PRIOR FILING DATE: 1997-03-07
; PRIOR APPLICATION NUMBER: 60/040,161
; PRIOR FILING DATE: 1997-03-07
; PRIOR APPLICATION NUMBER: 60/040,626
; PRIOR FILING DATE: 1997-03-07
; PRIOR APPLICATION NUMBER: 60/040,334
; PRIOR FILING DATE: 1997-03-07
; PRIOR APPLICATION NUMBER: 60/040,336
; PRIOR FILING DATE: 1997-03-07
; PRIOR APPLICATION NUMBER: 60/040,163
; PRIOR FILING DATE: 1997-03-07
; PRIOR APPLICATION NUMBER: 60/047,615
; PRIOR FILING DATE: 1997-05-23
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; NUMBER OF SEQ ID NOS: 280
; SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 209
; LENGTH: 483

Query Match   77.6%; Score 2509.5; DB 9; Length 483;
Best Local Similarity 96.9%; Pred. No. 2.4e-230;
Matches 467; Conservative 2; Mismatches 2; Indels 11; Gaps 1;

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; Sequence 144, Application US/09148545
; Publication No. US2003027132A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 70 Human Secreted Proteins
; FILE REFERENCE: PZ001P1
; CURRENT APPLICATION NUMBER: US/09/148,545
; CURRENT FILING DATE: 1998-09-04
; EARLIER APPLICATION NUMBER: PCT/US98/04482
; EARLIER FILING DATE: 1998-03-06
; EARLIER APPLICATION NUMBER: 60/040,162
; EARLIER FILING DATE: 1997-03-07

EARLIER APPLICATION NUMBER: 60/040,333
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; Sequence 209, Application US/09148545
; Publication No. US20030027132A1
; GENERAL INFORMATION:
;   APPLICANT: Rosen et al.
;   TITLE OF INVENTION: 70 Human Secreted Proteins
;   FILE REFERENCE: PZ001P1
;   CURRENT APPLICATION NUMBER: US/09/148,545
;   CURRENT FILING DATE: 1998-09-04
;   EARLIER APPLICATION NUMBER: PCT/US98/04482
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;   SOFTWARE: PatentIn Ver. 2.0
;
; SEQ ID NO 144
;   LENGTH: 483

Query Match   77.6%; Score 2509.5; DB 10; Length 483;
Best Local Similarity 96.9%; Pred. No. 2.4e-230;
Matches 467; Conservative 2; Mismatches 2; Indels 11; Gaps 1;

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Db   1 MATGGGIRAMTSLYGQLAGKELGLLDCKSYITCGASGSTWALANLYKDPEWSQKDLAGPT 60

Qy 195 ELLKTQVTKNKLGVLAPSQLQRYRQELAERARLGYPSCFTNLWALINERALLHDEPHDHKL 254
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 ELLKTQVTKNKLGVLAPSQLQRYRQELAERARLGYPSCFTNLWALINERALLHDEPHDHKL 120

Qy 255 SDQREALSHGQNPLPIYCALNTKGQSLTTFEFGEWCEFSPYEVGFPKYGAFIPSELFGSE 314
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Db 121 SDQREALSHGQNPLPIYCALNTKGQSLTTFEFGEWCEFSPYEVGFPKYGAFIPSELFGSE 180

Qy 315 FFMGQLMKRLPESRICFLEGIWSNLYAANLQDSLYWASEPSQFWDRWVRNQANLDKEQVP 374
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 181 FFMGQLMKRLPESRICFLEGIWSNLYAANLQDSLYWASEPSQFWDRWVRNQANLDKEQVP 240

Qy 375 LLKTEEPPSTAGRIABFFTDLLTWRPLAQATHNFLRGLHFHKDYFQHPHFSTWKATTLDG 434
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 241 LLKTEEPPSTAGRIABFFTDLLTWRPLAQATHNFLRGLHFHKDYFQHPHFSTWKATTLDG 300

Qy 435 LPNQLTPSEPHLCLLDVGYLINTSCLPLLQPTRDVDLILSLDYNLHGAFQQLQLLGRFCQ 494
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 301 LPNQLTPSEPHLCLLDVGYLINTSCLPLLQPTRDVDLILSLDYNLHGAFQQLQLLGRFCQ 360

Qy 495 EQGIPFPPISPSPEEQLQPRECHTFSDPTCPGAPAVLHF--------SSGVRRTPEE 543
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EARLIER APPLICATION NUMBER: 60/047,582
EARLIER FILING DATE: 1997-05-23
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EARLIER APPLICATION NUMBER: 60/047,612
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,632
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,601
EARLIER FILING DATE: 1997-05-23
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EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/056,886
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EARLIER APPLICATION NUMBER: 60/056,889
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EARLIER APPLICATION NUMBER: 60/056,893
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EARLIER APPLICATION NUMBER: 60/056,910

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EARLIER APPLICATION NUMBER: 60/047,595
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/057,761
EARLIER FILING DATE: 05-Sep-1997
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EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,588
EARLIER FILING DATE: 1997-05-23
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EARLIER FILING DATE: 1997-05-23
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EARLIER FILING DATE: 1997-04-11
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EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/043,670
EARLIER FILING DATE: 1997-04-11
EARLIER APPLICATION NUMBER: 60/056,632
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,664
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EARLIER APPLICATION NUMBER: 60/056,876
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EARLIER APPLICATION NUMBER: 60/056,881
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EARLIER APPLICATION NUMBER: 60/056,887
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EARLIER APPLICATION NUMBER: 60/056,908
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/048,964
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/057,650
EARLIER FILING DATE: 1997-09-05
EARLIER APPLICATION NUMBER: 60/056,884
EARLIER FILING DATE: 1997-08-22
NUMBER OF SEQ ID NOS: 280
SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 209
LENGTH: 483

Query Match       77.6%;   Score 2509.5;   DB 10;   Length 483;
Best Local Similarity  96.9%;   Pred. No. 2.4e-230;
Matches  467;  Conservative   2;  Mismatches   2;  Indels  11;  Gaps   1;

Qy    135 MATGGGIRAMTSLYGQLAGLKELGLLDCVSYITGASGSTWALANLYEDPEWSQKDLAGPT 194

;  FEATURE:
;  NAME/KEY: misc_feature
;  OTHER INFORMATION: Incyte ID No. US20040029136A1  7477093CD1
US-10-332-426-6

Query Match        46.1%;   Score 1492;   DB 12;   Length 1026;
Best Local Similarity  51.6%;   Pred. No. 1.3e-132;
Matches 296;  Conservative 92;  Mismatches 152;   Indels 34;   Gaps  8;

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Qy    61 LQPPLGFKRFSCLSLPSSWDYRLR--------BLAVRIGFGPCAEEQAFLSRRKQVVAA  112
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Db   452 LRPLTIGKEVTMDVPAPNAPGVRLQLKAEGCPEELAVHIGFNLCAEEQAFLSRRKQVVAK  511

Qy   113 ALRQALQLDGDLQEDEIPVVAIMATGGIRAMTSLYGQLAGLKEIGLLDCVSYITGASGS   172
          ||:|||||||||||||:||||||||||||||||||||||||||||||||||||:|||||
Db   512 ALKQALQLDRDLQEDEVPVGIMATGGARAMTSLYGHLLALQKLGLGLLDCVTYPSGISGS   571

Qy   173 TWALANLYEDPEWSQKDLAGPTELLKTQVTKNKLGVLAPSQLQRYRQELAERARLGYPSC   232
          ||:|  |||||||:||||||:|||||||||||||||||||||||||||||||||||||
Db   572 TWTMAHLYGDPEWSQRDLEGPIRYAREHLAKSKLEVFSPERLASYRRELRAEQGHPTT    631

Qy   233 FTNLWALINEALLHDEPHDHKLSDQREALSHGQNPLPIYCALNTKGQSLTTFEFGEWCEF   292
          ||:|  ||| |||||||||||:||||||||||||||||||||||||||||||||:||||
Db   632 FVDLWALVLESMLHGQVMDQKLSGQRAALERGQNPLPLYLSLNVKENNLETLDFKEWVEF   691

Qy   293 SPYEVGFPPKYGAFIPSELFGSEFFMGQLMKRLPESRICFLEGIWSNLYAANLQDSLYWAS   352
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   692 SPYEVGFLKYGAFVPPELFGSEFFMGRLMRRIPEPRICFLEAIWSNIFSLNLLDAWYDLT   751

Qy   353 EPSQFWDRWVRNQA-NLDKEQVPLL------KIEE--PPSTAGRIAEFFTDLLTWRPLA   402
          :::||    |||||  :: |  :| ||      :||         |   |||||:|||
Db   752 SSGESWKQHIKDKIRSLEKE--PLTTSGTSSRLEASWLQPGTA--LAQAFKGFLTGRPLH   807

Qy   403 QATHNFLRGLHFHKDYFQHPHFSTWKATTLDGLPNQLTPSEPHLCLLDVGYLINTSCLPL   462
          ||||||||||||||||:|||||||||||||||||:|||||||||:||||||||||||||
Db   808 QRSPNFLQGLQLHQDYCSHKDFSTWADYQLDSMPSQLTPKEPRLCLVDAAYFINTSSPSM   867

Qy   463 LQPTRDVDLILSLDYNLHGAFQQLQLLGRFCQEQGIPFPFPISPSPEEQLQPRECHTFSDP   522
           |    | | |:|  :  |  |        ---------SSGVRRTPEEAAAGEVNLSSSDSPYHYTKVTYSQEDVD  571
Db   868 FRPGRRLDLILSFDYSLSAPFEALQQTELYCRARGLPFFRVEPSPQDHQPRECHLFSDP   927

Qy   523 TCPGAPAVLHP----------------------SSGVRRTPEEAAAGEVNLSSSDSPYHYTKVTYSQEDVD  571
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Db   928 ACPEAPILLHFPLVNASFKDHSAPGVQRSPAELQGGQVDLTGATCPYTLSNMTYKEDFE   987

Qy   572 KLLLHLTHYNVCNNQELLEALRQAVQRRR-QRRP  604
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Db   988 RLLRLSDYNVQTSQGAILQAIRTALKHRTLEARP  1021
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RESULT 8
US-10-332-426-6
; Sequence 6, Application US/10332426
; Publication No. US20040029136A1
; GENERAL INFORMATION:
; APPLICANT: INCYTE GENOMICS, INC.; TANG, Y. Tom;
; APPLICANT: AZIMZAI, Yalda; DAS, Debopriya;
; APPLICANT: THORNTON, Michael; LU, Dyung Aina M.;
; APPLICANT: TRIBOULEY, Catherine M.; YUE, Henry;
; APPLICANT: GANDHI, Ameena R.; CHAWLA, Narinder K.;
; APPLICANT: KHAN, Farrah A.; LU, Yan;
; APPLICANT: YAO, Monique G.; HAFALIA, April J. A.;
; APPLICANT: ELLIOTT, Vicki S.; ARVIZU, Chandra S.;
; APPLICANT: LAL, Preeti; RAMKUMAR, Jayalaxmi;
; APPLICANT: NGUYEN, Danniel B.; BAUGHN, Mariah R.
; TITLE OF INVENTION: LIPID METABOLISM MOLECULES
; FILE REFERENCE: PI-0152 USN
; CURRENT APPLICATION NUMBER: US/10/332,426
; CURRENT FILING DATE: 2003-01-06
; PRIOR APPLICATION NUMBER: US 60/216,803
; PRIOR FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: US 60/216,801
; PRIOR FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: US 60/218,233
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 60/220,046
; PRIOR FILING DATE: 2000-07-21
; PRIOR APPLICATION NUMBER: US 60/220,739
; PRIOR FILING DATE: 2000-07-26
; PRIOR APPLICATION NUMBER: US 60/222,824
; PRIOR FILING DATE: 2000-08-04
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PERL Program
; SEQ ID NO 6
; LENGTH: 1026
; TYPE: PRT
; ORGANISM: Homo sapiens

RESULT 9
US-10-467-248-1
; Sequence 1, Application US/10467248
; Publication No. US20040086905A1
; GENERAL INFORMATION:
; APPLICANT: DAS, Debopriya; YAO, Monique G.;
; APPLICANT: ARVIZU, Chandra S.; BAUGHN, Mariah R.;
; APPLICANT: LU, Yan; HAFALIA, April J.A.;
; APPLICANT: CHAWLA, Narinder K.; GRIFFIN, Jennifer A.;
; APPLICANT: LU, Dyung Aina M.; YUE, Henry;
; APPLICANT: DING, Li; ELLIOTT, Vicki S.;
; APPLICANT: FORSYTHE, Ian J.; RAMKUMAR, Jayalaxmi;
; APPLICANT: GANDHI, Ameena R.; ISON, Craig H.;
; APPLICANT: WARREN, Bridget A.; TANG, Y. Tom;
; APPLICANT: EMERLING, Brooke M.; HONCHELL, Cynthia D.;
; APPLICANT: LYNE, Michael; BARROSO, Ines
; TITLE OF INVENTION: LIPID-ASSOCIATED MOLECULES
; FILE REFERENCE: PI-0358 USN
; CURRENT APPLICATION NUMBER: US/10/467,248
; CURRENT FILING DATE: 2003-08-06
; PRIOR APPLICATION NUMBER: PCT/US02/03813
; PRIOR FILING DATE: 2002-02-06
; PRIOR APPLICATION NUMBER: US 60/266,910

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Db     1 MATGGGIRAMTSLYGQLAGLKELGLLDCXSYITGASGSTWALANLYKDPEWSQKDLAGPT   60
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Qy   195 ELLKTQVTKNKLGVLAPSLYGQLAGLKELGLLDCXSYITGASGSTWALANLYKDPEWSQKDLAGPT  254

Db    61 ELLKTQVTKNKLGVLAPSLYGQLAGLKELGLLDCXSYITGASGSTWALINEALLHDEPHDHKL  120
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Qy   255 SDQREALSHGQNPLPIYCALNTKGQSLTTFEFGEWCEFSPYEVGFPPKYGAFIPSELFGSE  314

Db   121 SDQREALSHGQNPLPIYCALNTKGQSLTTFEFGEWCEFSPYEVGFPPKYGAFIPSELFGSE  180
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   315 FFMGQLMKRLPESRICFLEGIWSNLYAANLQDSLYWASEPSQFWDRWVRNQANLDKEQVP  374

Db   181 FFMGQLMKRLPESRICFLEGIWSNLYAANLQDSLYWASEPSQFWDRWVRNQANLDKEQVP  240
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Qy   375 LLKIEEPPSTAGRIAEFFTDLLTWRPLAQATHNFLRGLHFHKDYFQHPHFSTWKATTLDG  434

Db   241 LLKIEEPPSTAGRIAEFFTDLLTWRPLAQATHNFLRGLHFHKDYFQHPHFSTWKATTLDG  300
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Qy   435 LPNQLTPSEPHLCLLDVGYLINTSCLPLLQPTRDVDLILSLDYNLHGAFQQLQLLGRFCQ  494

Db   301 LPNQLTPSEPHLCLLDVGYLINTSCLPLLQPTRDVDLILSLDYNLHGAFQQLQLLGRFCQ  360
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Qy   495 EQGIPFPFPISPSPEEQLQPRECHTFSDP----SSGVRRTPEE  543

Db   361 EQGIPFPFPISPSPEEQLQPRECHTFSDPTCPGAPAVLHFPLVSDSFREYSAPGVRRTPEE  420
          ||||||||||||||||||||||||||||                     ||||||||||
Qy   544 AAAGEVNLSSSDSPYHYTKVTYSQEDVDKLLLHLTHYNVCNNQELLEALRQAVQRRRQRR  603

Db   421 AAAGEVNLSSSDSPYHYTKVTYSQEDVDKLLLHLTHYNVCNNQELLEALRQAVQRRRQRR  480
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Qy   604 PH  605

Db   481 PH  482
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; PRIOR FILING DATE: 2001-02-06
; PRIOR APPLICATION NUMBER: US 60/276,891
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: US 60/276,855
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: US 60/279,760
; PRIOR FILING DATE: 2001-03-28
; PRIOR APPLICATION NUMBER: US 60/283,818
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: US 60/285,405
; PRIOR FILING DATE: 2001-04-20
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PERL Program
; SEQ ID NO 1
; LENGTH: 996
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No: 7472774CD1
US-10-467-248-1

Query Match   38.4%;   Score 1243.5; DB 16; Length 996;
Best Local Similarity   44.8%;   Pred. No. 6.6e-109;
Matches 261; Conservative 86; Mismatches 187; Indels 49; Gaps 9;

Qy   56 RDLGSLQPPLGFKRFSCLS------LPSSWDYRL-------RELAVRLGFGPCAEEQA 101
Db   419 RKKGPISQP-----LDCLSDGQVMTLPVGESYELHMKSTPCPETLDVRLGFSLCPAELE 472

Qy   102 FLSRRKQVVAALRQALQLDGDLQEDEIPVVAIMATGGGIRAMTSLYGQLAGLKELGLLD 161
Db   473 FLQKRKVVVAKALKQVVLQLEEDLQEDEVPLIAIMATGGGTRSMTSMYGHLLGLQKINLLD 532

Qy   162 CVSYITGASGSTWALANLYEDPEWSQKDLAGPTELLKTQVTKNKLGVLAPSQLQRYRQEL 221
Db   533 CASYITGLSGATWTMATLYRDPDWGSKNLEPAIFEARRHVVKDKLPSLFPDQLRKFQEEL 592

Qy   222 AERARLGYPSCFTNLWALINEALLHDEPHDHKLSDQREALSHGQNPLPIYCALNTKGQSL 281
Db   593 RQRSQEGYRVTFTDFWGLLIETCLGDERNECKLSDQRAALSCGQNPLPIYLTINVKDD-- 650

Qy   282 TTFEFGEWCEFSPYEVGFPKYGAFIPSELFGSEFFMGQLMKRLPESRICFLEGIWSNLYA 341
Db   651 VSNQDVRWFEFSPYEVGLQKYGAFIPSELFGSEFFMGRLVKRIPESRICYMLGLWSSIFS 710

Qy   342 ANLQDSLYWASEPSQFWDRWVRNQANLDKEQVPLLKIEEPPSTAGRIAE---------- 390
Db   711 LNLLDAWNLSHTSEEFFHRWTREKVQ-DIEDEPIL--PEIPKCDANILETTVVIPGSWLS 767

Qy   391 -FFTDLLTWRPLAQATHNFLRGLHFHKDYFQHPHFSTWKATTLDGLPNQLTPSEPHLCLL 449
Db   768 NSFREILTHRSFVSEFHNFLSGLQLHTNYLQNGQFSRWKDTVLDGFPNQLTESANHLCLL 827

Qy   450 DVGYLINTSCLPLLQPTRDVDLILSLDYNLHGAFQOLQLLGRFCQEQGIPFPPISPSPEE 509
Db   828 DTAFFVNSSYPPLLRPERKADLIIHLNYCAGSQTKPIKQTCEYCTVQNIFPKYE-LPDE 886

Qy   510 QLQPRECHTFSDPTCPGAPAVLHF---------SSGVRRTPEAAAGEVNLSSSDSPY 558
Db   887 NENLKBCYLMENPQEPDAPIVTFFPLINDTFRKYKAPGVERSPEELEQGQVDIYGPKTPY 946

Qy   559 HYTKVTYSQEDVDKLLHLTHYNVCNNQEQLLEALRQAVQRRRQ 601
Db   947 ATKELTYTEATFDKLVKLSEYNILNNKDTLLQALRLAVEKKKR 989

RESULT 10
US-10-380-873B-1
; Sequence 1, Application US/10380873B
; Publication No. US20040014089A1
; GENERAL INFORMATION:
; APPLICANT: Hiromasa MIYAJI, et al.

; TITLE OF INVENTION: Polypeptide having phospholipase A2 activity
; FILE REFERENCE: 2139.34
; CURRENT APPLICATION NUMBER: US/10/380,873B
; CURRENT FILING DATE: 2003-07-09
; PRIOR APPLICATION NUMBER: JP 00/144466
; PRIOR FILING DATE: 2000-09-19
; PRIOR APPLICATION NUMBER: JP 01/284044
; PRIOR FILING DATE: 2001-05-16
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 1
; LENGTH: 849
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-380-873B-1

Query Match   35.2%;   Score 1139.5; DB 15; Length 849;
Best Local Similarity   41.8%;   Pred. No. 4.4e-99;
Matches 250; Conservative 94; Mismatches 213; Indels 41; Gaps 9;

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Db   250 MELLAAVQSGPSTELEAQTSKLGEGILLSSLPLQCEEQCSVALGEGQEVALSMKVEMSS 309

Qy   86 -ELAVRLGFGPCAEEQAFLSRRKQVVAAALRQALQLDGDLQEDEIPVVAIMATGGGIRAM 144
Db   310 GDLDLRLGFDLSDGEQEFLDRRKQVVSKALQQVIGLSEALDSGQVPVVAVLGSGGGTRAM 369

Qy   145 TSLYGQLAGLKELGLLDCVSYITGASGSTWALANLYEDPEWSQKDLAGPTELLKTQVTKN 204
Db   370 SSLYGSLAGLQELGLLDTVTYLSGVSGSSTWCISTLYRDPAWSQVALQGPIERAQVHVCSS 429

Qy   205 KLGVLAPSQLQRYRQELAERARLGYPSCFTNLWALINEALLHDEPHDHKLSDQREALSHG 264
Db   430 KMGALSTERLQYYTQELGVRERSGHSVSLIDLWGLLVEYLLYQEENPAKLSDQQEAVRQG 489

Qy   265 QNPLPIYCALNTKGQSLTTFEFGEWCEFSPYEVGFPKYGAFIPSELFGSEFFMGQLMKRL 324
Db   490 QNPYPIYTSVNVR-TNLSGEDFAEWCEFTPYEVGFPKYGAYVPTELFGSELFMGRLLQLQ 548

Qy   325 PESRICFLEGIWSNLYAANLQDSLYWASEPSQFWDRWVRNQANL-DKEQVPLLKIEPP- 382
Db   549 PEPRICYLQGMWGSAFATSLDEIFLKTAGSGLSFLEWYRGSVNITDCQKP--QLHNPSR 606

Qy   383 -----STAGRIAEFFTDLLTWRPLAQATHNFLRGLHFHKDYFQHPHFSTWKATTLDGLP 436
Db   607 LRTRLLTPQGPPSQAVLDIFTSRFTSAQSFNFTRGLCLHKDYVAGREFVAWKDTHPDAFP 666

Qy   437 NQLTPSEPHLCLLDVGYLINTSCLPLLQPTRDVDLILSLDYNLHGAFQOLQLLGRFCQEQ 496
Db   667 NQLTPMRDCLYLVDGGFAINSPFPLALLPQRAVDLILSFDYISLEAPFEVLKMTEKYCLDR 726

Qy   497 GIPFPPISPSPEEQLQPRECHTFSDPTCPGAPAVLHF---------SSGV-RRTPEEA 544
Db   727 GIPFPSIEVGPEDVEEARECYLFAKAEDDPRSPIVLHFPLVNRTPRTHLAPGVERQTAEK 786

Qy   545 AAGEVNLSSSDSPYHYTKVTYSQEDVDKLLHLTHYNVCNNQEQLLEALRQAVQRRRQR 602
Db   787 AFGDFVINRPDTPYGMMNFTYEPQDFYRLVALSRYNVLNNVETLKCALQLALDRHQAR 844

RESULT 11
US-10-380-873B-38
; Sequence 38, Application US/10380873B
; Publication No. US20040014089A1
; GENERAL INFORMATION:
; APPLICANT: Hiromasa MIYAJI, et al.
; TITLE OF INVENTION: Polypeptide having phospholipase A2 activity
; FILE REFERENCE: 2139.34
; CURRENT APPLICATION NUMBER: US/10/380,873B
; CURRENT FILING DATE: 2003-07-09
; PRIOR APPLICATION NUMBER: JP 00/146466
; PRIOR FILING DATE: 2000-09-19

```
;    PRIOR APPLICATION NUMBER: JP 01/284044
;    PRIOR FILING DATE: 2001-05-16
;    NUMBER OF SEQ ID NOS: 47
;    SOFTWARE: PatentIn Ver. 2.0
;    SEQ ID NO 38
;    LENGTH: 853
;    TYPE: PRT
;    ORGANISM: Mus musculus
US-10-380-873B-38

Query Match     35.2%;    Score 1138;    DB 15;    Length 853;
Best Local Similarity   42.4%;    Pred. No. 6.2e-99;
Matches  235;  Conservative 102;  Mismatches 189;  Indels  28;  Gaps    7;

Qy     74 LSLPSWDYRLRELAVRLGFGPCAEEQAFLSRRKQVVAAALRQALQLDGDLQEDEIPVVA 133
          ||||   :: :  ::|||  |||||| ||  |||  ||||||||||| | | |||||
Db    295 VSLRMKADMSSGDLDIRLGFDLCDGEQEFLDKRKQVASKALQRVMGLSEALHCDQVPVVA 354

Qy    134 IMATGGIRAMTSLYGQLAGLKELGLLDCVSYITGASGSTWALANLYEDPEWSQKDLAGP 193
          |||| |||  ||||| : :|||||  ||||||| |:|||||||||||||||||||| ||
Db    355 VLGSGGGTRAMTSLYGSLAGLQELGLLDAVTYLSGVSGSSWCISTLYRDPSWSQKALQGP 414

Qy    194 TELLKTQVTKNKLGVLAPSQLQRYRQELAERARLGYPSCFTNLWALINEALLHDEPHDHK 253
          ||| ||| ||||  |||||| ||||||| :||||||| |||||||||||||||| ||||
Db    415 IKYASERVCSSKIGMLSPKQFEYYSREKRAWESRGHSMSFTDLWGLIIEYFLNQEENPAK 474

Qy    254 LSDQREALSHGQNPLPIYCALNTKGQSLTTPEFGEWCEFSPYEVGPPKYGAFIPSELFGS 313
          ||| :|   : | | ||||  ::| | |||||| |||||| ||||||||||||||||||
Db    475 LSDQQETVSGQONPYPIYASINVH-KNISGDYFAEWCEFTPYEVGPPKYGAYVPTELFGS 533

Qy    314 EFFMQQLMKRLPESRICFLEGIWSNLYAANLQDSLYWASEPSQFWDRWVRNQANLDKEQV 373
          |:||  ::|  :::: ||||||| |:||| |||||||| || ||  ||| :| :
Db    534 EFFMGRLLHFWPEPRICYLQGMWGSAFAASLYEIFLKLGGLSLSFLDWHRGSVSV-TDDW 592

Qy    374 PLLKIEEPPSTAGRI------ABFFTDLLTWRPLAQATHNFLRGLHFHKDYFQHPHF-- 424
          | :||   | || |       :||||||| |:||  | | |:|  ||||||:|:|||
Db    593 PKLRKQDPTRLPTRLFTPMSSFSQAVLDIFTSRITCAQTFNFTRGLCMYKDYTARKDFVV 652

Qy    425 --STWKATTL---DGLPNQLTPSEPHLCLLDVGYLINTSCLPLLQPTRDVDLILSLDYNL 479
            :|||||    |||| ||| ||| ||  |||  |||| || ||||||||||||| |||
Db    653 SEDAWHSHNYGYPDACPNQLTPMKDFLSLVDGGFAINSPFPLVLQPQRAVDLIVSFDYSL 712

Qy    480 HGAFQOLQLLGRFCQEQGIPFPPISPSPEEQLQPRECHTFSDPTCPGAPAVLHF------ 533
          || | | : :|   | || ||| ||| |  :|  || ||| ||:|||||| :
Db    713 EGPFEVLQVTEKYCRDRGIPFPRIEVDPKDSEDPRECYLFAEAEDPCSPIVLHFPLVNRT 772

Qy    534 -----SSGV-RRTPEEAAAGEVNLSSSDSPYHYTKVTYSQEDVDKLLHLTHYNVCNNQEQ 587
               ::|  ||:|||||  ||| ||||| |||:  || ||||| |:| ||||| |: :
Db    773 FRTHLAPGVERQTAEEKAFGDFIINGPDTAYGMMDFTYEPKEFDRLVTLSRYNVLNNKET 832

Qy    588 LLEALRQAVQRRRQ 601
          |:|| | || :|
Db    833 IRHALQLALDRRRQ 846
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RESULT 12
US-10-380-873B-22
;    Sequence 22, Application US/10380873B
;    Publication No. US20040014089A1
;    GENERAL INFORMATION:
;    APPLICANT: Hiromasa MIYAJI, et al.
;    TITLE OF INVENTION: Polypeptide having phospholipase A2 activity
;    FILE REFERENCE: 2139.34
;    CURRENT APPLICATION NUMBER: US/10/380,873B
;    CURRENT FILING DATE: 2003-07-09
;    PRIOR APPLICATION NUMBER: JP 00/146466
;    PRIOR FILING DATE: 2000-09-19
;    PRIOR APPLICATION NUMBER: JP 01/284044
;    PRIOR FILING DATE: 2001-05-16
;    NUMBER OF SEQ ID NOS: 47
;    SOFTWARE: PatentIn Ver. 2.0
;    SEQ ID NO 22
;    LENGTH: 854
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;    TYPE: PRT
;    ORGANISM: Mus musculus
US-10-380-873B-22

Query Match     34.8%;    Score 1127;    DB 15;    Length 854;
Best Local Similarity   42.6%;    Pred. No. 7e-98;
Matches  231;  Conservative 100;  Mismatches 183;  Indels  28;  Gaps    7;

Qy     86 ELAVRLGFGPCAEEQAFLSRRKQVVAAALRQALQLDGDLQEDEIPVVAIMATGGIRAMT 145
          :: :|||  |||||| ||  |||  ||||||||||| | | |||||| ||||||||||
Db    308 DLDLRLGFDLCDGEQEFLDKRKQVASKALQRVMGLSEALHCDQVPVVAVLGSGGGTRAMT 367

Qy    146 SLYGQLAGLKELGLLDCVSYITGASGSTWALANLYEDPEWSQKDLAGPTELLKTQVTKNK 205
          |||| ||||:  :|||||  ||||||| |:|||||||||||||||||| ||  ||| |
Db    368 SLYGSLAGLQELGLLDAVTYLSVSGSSWCISTLYRDPSWSQKALQGPIKYASERVCSSK 427

Qy    206 LGVLAPSQLQRYRQELAERARLGYPSCFTNLWALINEALLHDEPHDHKLSDQREALSHGQ 265
          ||:|||| ||||||| :||||||| |||||||||||||||| |||| ||| :|   : |
Db    428 IGMLSPKQFEYYSREKRAWESRGHSMSFTDLWGLIIEYFLNQEENPAKLSDQQETVSGQQ 487

Qy    266 NPLPIYCALNTKGQSLTTPEFGEWCEFSPYEVGPPKYGAFIPSELFGSEFFMGQLMKRLP 325
          | | ||||  ::| | |||||| ||||| ||||||||| |||||||||:|||  ::|
Db    488 NPYPIYASINVH-KNISGDYFAEWCEFTPYEVGFPKYGVYVPTELFGSEFFMGRLLHFWP 546

Qy    326 ESRICFLEGIWSNLYAANLQDSLYWASEPSQFWDRWVRNQANLDKEQVPLLKIEEPPSTA 385
          :: ::  ||||| |:|||  ||||||| || ||  |||  :| |  | | :||   |
Db    547 EPRICYLQGMWGSAFAASLYEIFLKLGGLSLSFLDWHRGSVSV-TDDWPKLRKQDPTRLP 605

Qy    386 GRI------ABFFTDLLTWRPLAQATHNFLRGLHFHKDYFQHPHF----STWKATTL-- 432
          ||        :||||||| |:||  | | |:|  ||||||:|:||    :|||||
Db    606 TRLFTPMSSFSQAVLDIFTSRITCAQTFNFTRGLCMYKDYTARKDFVVSEDAWHSHNYGY 665

Qy    433 -DGLPNQLTPSEPHLCLLDVGYLINTSCLPLLQPTRDVDLILSLDYNLHGAFQQLQLLGR 491
           |||| ||| ||| ||  |||  |||| || |||||||||||| |||||| | | : :|
Db    666 PDACPNQLTPMKDFLSLVDGGFAINSPFPLVLQPQRAVDLIVSFDYSLEGPFEVLQVTEK 725

Qy    492 FCQEQGIPFPPISPSPEEQLQPRECHTFSDPTCPGAPAVLHF---------SSGV-RR 539
          |   | || ||| ||| |  :|  || ||| ||:||||||| :         ::|  ||
Db    726 YCRDRGIPFPRIEVDPKDSEDPRECYLFTEAADPCSPIVLHFPLVNRTFRTHLAPGVERQ 785

Qy    540 TPEEAAAGEVNLSSSDSPYHYTKVTYSQEDVDKLLHLTHYNVCNNQEQLLEALRQAVQRR 599
          |||||  ||| |||||| |||:  || |||||| |:| |||||| |: :|:|| | || :
Db    786 TAEEKAFGDFIINGPDTAYGMMDFTYEPKEFDRLVTLSRYNVLNNKETIRHALQLALDRR 845

Qy    600 RQ 601
          |
Db    846 RQ 847
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RESULT 13
US-10-332-426-3
;    Sequence 3, Application US/10332426
;    Publication No. US20040029136A1
;    GENERAL INFORMATION:
;    APPLICANT: INCYTE GENOMICS, INC.; TANG, Y. Tom;
;    APPLICANT: AZIMZAI, Yalda; DAS, Debopriya;
;    APPLICANT: THORNTON, Michael; LU, Dyung Aina M.;
;    APPLICANT: TRIBOULEY, Catherine M.; YUE, Henry;
;    APPLICANT: GANDHI, Ameena R.; CHAWLA, Narinder K.;
;    APPLICANT: KHAN, Farrah A.; LU, Yan;
;    APPLICANT: YAO, Monique G.; HAFALIA, April J. A.;
;    APPLICANT: ELLIOTT, Vicki S.; ARVIZU, Chandra S.;
;    APPLICANT: LAL, Preeti; RAMKUMAR, Jayalaxmi;
;    APPLICANT: NGUYEN, Danniel B.; BAUGHN, Mariah R.
;    TITLE OF INVENTION: LIPID METABOLISM MOLECULES
;    FILE REFERENCE: PI-0152 USN
;    CURRENT APPLICATION NUMBER: US/10/332,426
;    CURRENT FILING DATE: 2003-01-06
;    PRIOR APPLICATION NUMBER: US 60/216,803
;    PRIOR FILING DATE: 2000-07-07
;    PRIOR APPLICATION NUMBER: US 60/216,801
;    PRIOR FILING DATE: 2000-07-07
;    PRIOR APPLICATION NUMBER: US 60/218,233
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;  PRIOR FILING DATE: 2000-07-14
;  PRIOR APPLICATION NUMBER: US 60/220,046
;  PRIOR FILING DATE: 2000-07-21
;  PRIOR APPLICATION NUMBER: US 60/220,739
;  PRIOR FILING DATE: 2000-07-26
;  PRIOR APPLICATION NUMBER: US 60/222,824
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 16
;  SOFTWARE: PERL Program
;  SEQ ID NO 3
;  LENGTH: 848
;  TYPE: PRT
;  ORGANISM: Homo sapiens
;  FEATURE:
;  NAME/KEY: misc_feature
;  OTHER INFORMATION: Incyte ID No. US20040029136A1 1281946CD1
US-10-332-426-3

Query Match             34.4%;  Score 1112;  DB 12;  Length 848;
Best Local Similarity   41.2%;  Pred. No. 1.9e-96;
Matches   247;  Conservative   97;  Mismatches  211;  Indels   44;  Gaps   11;

Qy        43 MESLSVQAG------VQWRDLGS----LQPPPLGFKRPSC---------LSLPSSWDYR 83
                                                             :: ||
Db       250 MELLAAVQSGPSAELEAQTSKLGEGGILLSSLPLG-QBEQCSVALGEGEGVALSMTVEMS 308

Qy        84 LRELAVRLGFGPGPCAEEQAFLSRRKQVVAAALRQALQLDGDLQEDEIPVVAIMATGGGIRA 143
             | : :||||  |||||||||||||||||:::||: ||||||||||||:||
Db       309 SGDLDLRLGFDLSDGEQEFLDRRKQVVSKALQQVLGLSEALDSGQVPVVAVLGSGGGTRA 368

Qy       144 MTSLYGQLAGLKEIGLLDCVSYITGASGSTWALANLYEDPEWSQKDLAGPTELLKTQVTK 203
             :|:||||||||||:||||| :::: ||:|||||||||:|||::||:||
Db       369 MSSLYGSLAGLQEIGLLDTVTYLSGVSGSTWCISTLYRDPAWSQVALQGPIERAQVHVCS 428

Qy       204 NKLGVLAPSQLQRYRQELAERARLGYPSCFTNLWALINEALLHDEPHDHKLSDQREALSH 263
             : :| |||  ||:|| :| |::|| |||::||||||||||||||||:|||||::
Db       429 SKMGALSTERLQYYTQELGVRERSGHSVSLIDLWGLLVEYLLYQBENPAKLSDQQKAVRQ 488

Qy       264 GQNPLPIYCALNTKGQSLITFEFGEWCEFSPYEVGFPKYGAFIPSELFGSEFFMGQLMKR 323
             ||||| ::| ||||||||||||||||||||||||||||||||||||||||||||||||
Db       489 GQNPYPIYTSVNVR-TNLSGEDFA-WCEFTPYKVGFPKYGAYVPTELFGSELFMGRLLQL 546

Qy       324 LPESRICFLEGIWSNLYAANLQDSLYWASEPSQFWDRWVRNQANL-DKEQVPLLKIEEPP 382
             || || ||| ||  :::  ||||||||||||||||||||||||| ::|| :|||:::
Db       547 QPEPRICYLQGMWGSAFATSLDEIFLKTAGSGLLSFLEWYRGSVNITDDCQKP--QLHNPS 604

Qy       383 ------STAGRIAEFFTDLLTWRPLAQATHNFLRGLIHFHKDYFQHPFSTWKATTLDGL 435
                   :||  |:  :| ||||||||||||:| |::| |||| :::|:|||| |||
Db       605 RLRTRLLTPQGPFSQAVLDIFTSRFTSAQSFNFTRGLCLHKDYVAGREFVAWKDTHPDAF 664

Qy       436 PNQLTPSEPHLCLLDVGYLINTSCLPLLQPTRDVDLILSLDYNLHGAFQQLQLLGRFCQE 495
             |||||||||||||||||||||||| |||||||||||||||||||||:|||||||||||
Db       665 PNQLTPMRDCLYLVDGGFAINSPFPLALLPQRAVDLILSFDYSLEAPFEVLKMTEKYCLD 724

Qy       496 QGIPFPPISPSPEEQLQPRECHTFSDPTCPGAPAVLHF---------SSGV-RRTPEE 543
             :|| ||||| |||||||  |: ||| || ||:| |:||         |||| ||:||
Db       725 RGIPFPSIEVGPEDVEEARECYLFAKAEDDPRSPIVLHFPLVNRTFRTHLAPGVERQTAEE 784

Qy       544 AAAGEVNLSSSDSPYHYTKVTYSQEDVDKLLHLTHYNVCNNQEQLLEALRQAVQRRRQR 602
             ||:|:| ::|: || : : :  :| |||||||||||||||||||||||||||:|:
Db       785 KAFGDFVINRPDTPTVGMMNFTYEPQDFYRLIVALSRYNVLNNVETLKCALQLALDRHQAR 843
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;  TITLE OF INVENTION: Methods of Diagnosis of Angiogenesis, Compositions and
;  TITLE OF INVENTION: Methods of Screening for Angiogenesis Modulators
;  FILE REFERENCE: 018501-0062000US
;  CURRENT APPLICATION NUMBER: US/10/211,462
;  CURRENT FILING DATE: 2003-02-13
;  PRIOR APPLICATION NUMBER: US 09/784,356
;  PRIOR FILING DATE: 2001-02-14
;  PRIOR APPLICATION NUMBER: US 09/791,390
;  PRIOR FILING DATE: 2001-02-22
;  PRIOR APPLICATION NUMBER: US 60/310,025
;  PRIOR FILING DATE: 2001-08-03
;  PRIOR APPLICATION NUMBER: US 60/334,244
;  PRIOR FILING DATE: 2001-11-29
;  NUMBER OF SEQ ID NOS: 230
;  SOFTWARE: PatentIn Ver. 2.1
;  SEQ ID NO 50
;  LENGTH: 749
;  TYPE: PRT
;  ORGANISM: Homo sapiens
US-10-211-462-50

Query Match             19.1%;  Score 619;  DB 12;  Length 749;
Best Local Similarity   27.1%;  Pred. No. 1.9e-49;
Matches   174;  Conservative  125;  Mismatches  238;  Indels  106;  Gaps   22;

Qy        44 ESLSVAQAGVQWRDLGSLQPPPLGFKRFSCLSLPSSWDYRLRELA----VRLGFGPCAEE 99
                                                               :| ||||:
Db       100 ETLGTATFTVSSMKVGEKKEVPFIFNQVTEMVLEMS-----LEVCSCPDLRFSMALCDQE 154

Qy       100 QAFLSRRKQVVAAALRQAL--QLDGDLQEDEIPVVAIMATGGGIRAMTSLYGQLAGLKE 156
                |:  || | : ||:  |  ||| ||||||||||||||||||||||||||||||:
Db       155 KTFRQQRKEHIRESMKKLLGPKNSEGLHSARDVPVVAILGSGGGFRAMVGFSGVMKALYE 214

Qy       157 LGLLDCVSYITGASGSTWALANLYEDPEWSQKDLAGPTEL---LKTQVTKNKLGVLAPSQ 213
             ||||| :::: ||:|||||||||:|||::||:||  :    ||:|:|:|::| |||
Db       215 SGILDCATYVAGLSGSTWYMSTLYSHPDFPEK--GPEEINEELMKNVSHNPLLLLTPQK 271

Qy       214 LQRYRQELAERARLGYPSCFTNLWA-LINEALLHDEPHDHKLSDQREALSHGQNPLPIYC 272
             |||:|| :| |::|| |||::||||  ||:||||||:|||||||::    |||||:::|
Db       272 VKRYVESLWKKKSSGQPVTFDIFGMLIGETLIHNRMNT-TLSSLEKVNTAQCPLPLFT 330

Qy       273 ALNTKGQSLITFEFGEWCEFSPYEVGFPKYGAFIPSELFGSEFFMGQLMKRLPESRICFL 332
             ||||||||||||||||||||||||||||||||||||||||||||||||||::|| ||
Db       331 CLHVK-PDVSELMFADWVEFSPYEIGMAKYGTFMAPDLFGSKFFMGTVVKKYEENPLHFL 389

Qy       333 EGIWSNLYA-------------------ANLQDSLYWASEPSQFWDRWVRNQANLDKEQVPLL 376
             ::| ||                      |||:|||||||||||||||||||:||
Db       390 MGVWGSAFSILFNRVLGVSGSGQSRGSTMEEEL------ENITTKHIVSNDSDSDD---- 439

Qy       377 KIEEPPSTAGRIA--EFFTD--------------------ILTWRPLAQATHNFLRGLHFH 415
             ::  |::|: |    ||||                      ||||||||||||||| |: |
Db       440 ESHEPKGTENEDAGSDYQSDNQASWIHRMIMALVSDSALFNTREGRAGKVHNFMLGLNLN 499

Qy       416 KDYFQHP--HFSTWKATTLDGL---------------PNQ------LTPSEPHLCLLDVGYLINTSCL 460
             ||:| |   ||| |||| ||:                |        ||||||||||||||||||||
Db       500 TSYPLSPLSDFATQDSFDDELDAAVADPDFERIYEPLDVKSKKIHVVDSGLTFNLPYP 559

Qy       461 PLLQPTRDVDLILSLDYNLHGA------FQQLQLLGRFCQEQGIPFPPISPSPEEQLQPRE 515
             ||:|||:| |||||::|::|:|      | | : :| |: |:  || ||: || ||| |:
Db       560 LILRPQRGVDLIISFDFSARPSDSSPPFKELLLAEKWAKMNKLPFFKIDPYVFDRRGLKE 619

Qy       516 CHTFSDPTCP----GAPAVLHF-------------------SSGV-RRTPEEAAAGEVNL-SSSDSPY 558
             | : || |      ||| |:||                   |||| ||  || | |:|   ::: || :
Db       620 CYVFK-PKNPDMEKDCPTIHFVLANINFRKYKAPGVPRETEEEKEIADFDIFDDPESPF 678

Qy       559 HYTKVTYSQEDVDKLLHLTHYNVCNNQEQLLEALRQAVQRRRQ 601
             ||||||||| || || ||||||||||||||||||||| |:| |
Db       679 STFNFQYPNQAFKRLHDLMHFNTLNNIDVIKEAMVESIEYRRQ 721
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RESULT 15
US-10-157-898-2
;  Sequence 2, Application US/10157898
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RESULT 14
US-10-211-462-50
;  Sequence 50, Application US/10211462
;  Publication No. US20040033495A1
;  GENERAL INFORMATION:
;  APPLICANT: Murray, Richard
;  APPLICANT: Glynne, Richard
;  APPLICANT: Watson, Susan R.
;  APPLICANT: Aziz, Natasha
;  APPLICANT: Eos Biotechnology, Inc.
```

; Publication No. US2003022501A1
; GENERAL INFORMATION:
; APPLICANT: DAVID, Samuel
; APPLICANT: KALYVAS, Athena
; TITLE OF INVENTION: PHOSPHOLIPASE A2 EXPRESSION AND ACTIVITY AND USE THEREOF FOR DIAG
; TITLE OF INVENTION: PROGNOSTICATION, PREVENTION AND TREATMENT OF NEURAL INFLAMMATORY
; TITLE OF INVENTION: DEMYELINATING DISEASE
; FILE REFERENCE: 85827-36
; CURRENT APPLICATION NUMBER: US/10/157,898
; CURRENT FILING DATE: 2002-05-31
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn version 3.1
;
; SEQ ID NO 2
; LENGTH: 749
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-157-898-2

Query Match   19.1%;   Score 619;   DB 12;   Length 749;
Best Local Similarity 27.1%;   Pred. No. 1.9e-49;
Matches 174;   Conservative 125;   Mismatches 238;   Indels 106;   Gaps 22;

Qy   44 ESLSVAQAGVQWRDIGSLQPPPLGFKRFSCLSLPSSWDYRLRELA----VRLGFGPCAEE 99
              | :|:   :   : : :|:|
Db   100 ETLGTATFTVSSMKVGEKKEVPFIFNQVTEMVLEMS-----LEVCSCPDLRFSMALCDQE 154

Qy   100 QAFLSRRKQVVAALRQAL---QLDGDLQEDEIPVVAIMATGGIRAMTSLYGQLAGLKE 156
              | :|:   : :: |||||| :||||
Db   155 KTFRQQRKEHIRESMKKLLGPKNSEGLHSARDVPVVAILGSGGFRAMVGFSGVMKALYE 214

Qy   157 LGLLDCVSYITGASGSTWALANLYEDPEWSQKDLAGPTEL--LKTQVTKNKLGVLAPSQ 213
              | |||||| |||| | |: :| |: :| | : | ||||||
Db   215 SGILDCATYVAGLGSSTWYMSTLYSHPDFPEK---GPEEINEELMKNVSHNPLLLLTPQK 271

Qy   214 LQRYRQELAERARLGYPSCFTNLWA-LINEALLHDEPHDHKLSDQREALSHGQNPLPIYC 272
              :|: ||| :: ::| | : :| || :| | :||:
Db   272 VKRYVESLWKKKSSGQPVTFTDIFGMLIGETLIHNRMNT-TLSSLKEKVNTAQCPLPLFT 330

Qy   273 ALNTKGQSLTTFEFGEWCEFSPYEVGFPKYGAFIPSELFGSEFFMGQLMKRLPESRICFL 332
              || :||| | |: | ||||| : | : | :| ||||: ||| :
Db   331 CLHVK-PDVSELMFADWVEFSPYEIGMAKYGTFMAPDLFGSKFFMGTVVKKYEENPLHFL 389

Qy   333 EGIWSNLYA----------ANLQDSLYWASEPSQFWDRWVRNQANLDKEQVPLL 376
              |:| : :|: |
Db   390 MGVWGSAFSILFNRVLGVSGSQSRGSTMEEL-----ENITTKHIVSNDSDSDD---- 439

Qy   377 KIEEPPSTAGRIA--EFFTD----------------LLTWRPLAQATHNFLRGLHFH 415
              :   :|: | |: |::|||
Db   440 ESHEPKGTENEDAGSDYQSDNQASWIHRMIMALVSDSALFNTREGRAGKVHNFMLGLNLN 499

Qy   416 KDYFQHP--HPSTWKATTLDGL-------PNQ------LTPSEPHLCLLDVGYLINTSCL 460
              :| : | | :|:: | : || :||||:||:|
Db   500 TSYPLSPLSDFATQDSFDDELDAAVADPDEFERIYEPLDVKSKKIHVVDSGLTFNLPYP 559

Qy   461 PLLQPTRDVDLILSLDYNLHGA-----FQQLQLLGRFCQEQGIPFPPISPSPEEQLQPRE 515
              :|| : :|:|:: |: | :| :| :   : || ::|:
Db   560 LILRPQRGVDLIISFDSARPSDSSPPFKELLLAEKWAKMNKLPFPKIDPYVFDREGLKE 619

Qy   516 CHTFSDPTCP----GAPAVLHF-------SSGV-RRTPEAAAGEVNL-SSSDSPY 558
              |: | :| |: | :: | :| ||::|||
Db   620 CYVFK-PKNPDMEKDCPTIIHFVLANINFRKYKAPGVPRETEEEKEIADFDIFDDPESPF 678

Qy   559 HYTKVTYSQEDVDKLLHLTHYNVCNNQEQLLEALRQAVQRRRQ 601
              |: : | :| : | ::::: |||
Db   679 STFNFQYPNQAFKRLHDLMHFNTLNNIDVIKEAMVESIEYRRQ 721

Search completed: October 5, 2004, 19:41:16
Job time : 141.133 secs

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                    GenCore version 5.1.6
         Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on:    October  5, 2004, 19:21:45 ; Search time 41.14 Seconds
                                        (without alignments)
                                        1414.581 Million cell updates/sec

Title:          US-09-830-321A-2
Perfect score:  3235
Sequence:       1 MIFVELSPTLALCLERVASH........EQLLEALRQAVQRRRQRRPH 605

Scoring table:  BLOSUM62
                Gapop 10.0 , Gapext 0.5

Searched:       283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters:    283366

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :    PIR_78:*
              1: pir1:*
              2: pir2:*
              3: pir3:*
              4: pir4:*
```

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Match Length	DB	ID	Description
1	619	19.1	749	1	A39329	phospholipase A2
2	602	18.6	749	1	B39898	phospholipase A2 (
3	596	18.4	748	1	I50699	cytosolic phosphol
4	572	17.7	741	2	B54908	phospholipase A2 c
5	498.5	15.4	541	2	T13162	cytosolic phosphol
6	198	6.1	627	4	A40201	artifact-warning s
7	193.5	6.0	613	4	C40201	artifact-warning s
8	186	5.7	673	2	T50281	probable lysophosp
9	184	5.7	686	2	S66693	hypothetical prote
10	177	5.5	612	2	S29318	lysophospholipase
11	170	5.3	46	2	I54375	gene NF2 protein -
12	162	5.0	664	2	S53037	PLB1 protein - yea
13	160	5.0	39	2	I54374	gene NF2 protein -
14	159.5	4.9	623	2	T40991	probable lysophosp
15	159	4.9	624	2	T38006	probable lysophosp
16	158	4.9	53	2	A42442	integrin beta-1 ch
17	154	4.8	754	2	T18238	lysophospholipase
18	151	4.7	613	2	T38007	probable lysophosp
19	140	4.3	644	2	T37800	probable lysophosp
20	136	4.2	706	2	S53035	probable lysophosp
21	124	3.8	100	2	A46010	X-linked retinopat
22	122.5	3.8	673	4	F40201	artifact-warning s
23	122	3.8	536	2	S62110	lysophospholipase
24	118.5	3.7	1749	2	S75071	hypothetical prote
25	105	3.2	431	2	JC4805	core protein F - p
26	103.5	3.2	597	4	E40201	artifact-warning s
27	103	3.2	432	2	T10894	neuronal pentraxin
28	101.5	3.1	946	2	I38100	rho-GTPase-activat
29	101	3.1	372	2	T25621	hypothetical prote
30	101	3.1	1188	2	D86311	protein F1L3.20 [i
31	100.5	3.1	1461	2	B70588	probable polyketid
32	100	3.1	252	2	B82181	oxidoreductase, sh
33	99.5	3.1	1026	2	G81751	exodeoxyribonuclea
34	99.5	3.1	2611	2	T14591	actinomycin synthe
35	99	3.1	690	2	D75487	v-type ATP synthas
36	99	3.1	4687	1	A39638	plectin - rat
37	98.5	3.0	440	2	A26359	decay-accelerating
38	97	3.0	852	1	GNLJGA	pol polyprotein -
39	96	3.0	361	2	AD1079	Glucosamine-fructo
40	96	3.0	624	1	T39102	hypothetical prote
41	96	3.0	781	2	S37032	gene LL5 protein -
42	96	3.0	873	1	TVFVF	protein-tyrosine k
43	96	3.0	883	2	A49733	[heparan sulfate]-
44	95.5	3.0	569	2	C86934	probable membrane
45	95.5	3.0	613	2	AC2962	hypothetical prote

ALIGNMENTS

```
RESULT 1
A39329
phospholipase A2 (EC 3.1.1.4), cytosolic - human
C;Species: Homo sapiens (man)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 20-Apr-2000
C;Accession: A39329; A39898; A54198; S68898
R;Sharp, J.D.; White, D.L.; Chiou, X.G.; Goodson, T.; Gamboa, G.C.; McClure, D.; Burgett,
J. Biol. Chem. 266, 14850-14853, 1991
A;Title: Molecular cloning and expression of human Ca(2+)-sensitive cytosolic phospholipa
A;Reference number: A39329; MUID:91331987; PMID:1869522
A;Accession: A39329
A;Molecule type: mRNA
A;Residues: 1-749 <SHA>
A;Cross-references: GB:M68874; NID:g190003; PIDN:AAA60105.1; PID:g190004
A;Note: part of this sequence was confirmed by protein sequencing
R;Clark, J.D.; Lin, L.L.; Kriz, R.W.; Ramesha, C.S.; Sultzman, L.A.; Lin, A.Y.; Milona, N
Cell 65, 1043-1051, 1991
A;Title: A novel arachidonic acid-selective cytosolic PLA-2 contains a Ca(2+)-dependent t
A;Reference number: A39898; MUID:91256305; PMID:1904318
A;Accession: A39898
A;Molecule type: mRNA
A;Residues: 1-749 <CLA>
A;Cross-references: GB:M72393; NID:g190006; PIDN:AAB00789.1; PID:g190007
A;Note: part of this sequence was confirmed by protein sequencing
R;Li, B.; Copp, L.; Castelhano, A.L.; Feng, R.; Stahl, M.; Yuan, Z.; Krantz, A.
Biochemistry 33, 8594-8603, 1994
A;Title: Inactivation of a cytosolic phospholipase A-2 by thiol-modifying reagents: cyste
A;Reference number: A54198; MUID:94304876; PMID:8031794
A;Accession: A54198
A;Molecule type: protein
A;Residues: 319-338,'X',340-345,'X',347-358 <LIA>
A;Note: modification of preferred modification site Cys-324 abolished enzymatic activity
R;Gordon, R.D.; Leighton, I.A.; Campbell, D.G.; Cohen, P.; Creaney, A.; Wilton, D.C.; Mas
Eur. J. Biochem. 238, 690-697, 1996
A;Title: Cloning and expression of cytosolic phospholipase A(2) (cPLA(2)) and a naturall
esults in an increase in specific activity.
A;Reference number: S68897; MUID:96300233; PMID:8706669
A;Accession: S68898
A;Molecule type: protein
A;Residues: 497-507 <GOR>
C;Comment: This cytosolic phospholipase A2 translocates to membrane vesicles in response
C;Genetics:
A;Gene: GDB:PLA2G4A; PLA2G4
A;Cross-references: GDB:134687; OMIM:600522
A;Map position: 1q25-1q25
C;Superfamily: cytosolic phospholipase A2
C;Keywords: calcium; carboxylic ester hydrolase; cytosol; inflammation; phosphoprotein
F;505/Binding site: phosphate (Ser) (covalent) #status experimental

Query Match           19.1%;   Score 619; DB 1; Length 749;
Best Local Similarity 27.1%;   Pred. No. 1.1e-39;
Matches 174; Conservative 125; Mismatches 238; Indels 106; Gaps 22;
```

```
Qy    44 ESLSVAQAGVQWRDLGSLQPPPLGFKRFSCLSLPSSWDYRLRELA----VRLGFGPCAEE   99
         :|:  |  | |:| ::::  |||||||||||:: ::              :||:|||:::
Db   100 ETLGTATFTVSSMKVGEKKEVPFIFNQVTEMVLEMS-----LEVCSCPDLRFSMALCDQE  154

Qy   100 QAFLSRRKQVVAAALRQAL--QLDGDLQEDEIPVVAIMATGGIRAMTSLYGQLAGLKE    156
         :|| ||||: |:    |:|  :  :  ||  :|||||:|:|:|||| |:||:::|| ||
Db   155 KTFRQQRKEHIRESMKKLLGPKNSEGLHSARDVPVVAILGSGSGFRAMVGFSGVMKALYE  214

Qy   157 LGLLDCVSYITGASGSTWALANLYEDPEWSQKDLAGPTEL--LKTQVTKNKLGVLAPSQ   213
         :|:||||:||||:|||||::::||:||:|:|  |  | :|    ::::::::|:||: ||
Db   215 SGIILDCATYIAGLSGSTWYMSTLYSHPDFPEK---GPEEINEELMKNVSHNPLLLLTPQK 271

Qy   214 LQRYRQELAEBRARLGYPSCFTNLWA-LINEALLHDEPHDHKLSDQREALSHGQNPLPIYC  272
         :||| :||  :  ||   ::||: :: |:    |  : :::::: ::  :| |||||::::
Db   273 VKRYVESLMKKKSSGQPVTFTDIFGMLIGETLIHNRMNT-TLSSLKEKVNTAQCPLPLFT   330

Qy   273 ALNTKGQSLTTFEFGEWCEFSPYEVGFPKYGAFIPSELFGSEFFMGQLMKRLPESRICFL   332
         ||:::|||||| |||||||||||:|||:||||:||::|||| ||||:::::|||||||||
Db   331 CLHVK-PDVSELMFADWVEFSPYEIGMAKYGTFMAPDLFGSKFFMGTVVKKYEENPLHFL   389

Qy   333 EGIWSNLYA---------ANLQDSLYWASEPSQFWDRWVRNQANLDKEQVPLL          376
         ||:|:  :|         :|:::|:  :||:| ||||| |: |::
Db   390 MGVWGSAFSILFNRVLGVSGSGSRGSTMEEEL----ENITTKHIVSNDSSDSDD----    439

Qy   377 KIEEPPSTAGRIA-EFFTD---------LLTWRPLAQATHNFLRGLHFH             415
         ::|||||:||||  :||:|         ::||||| |::|:||||||||
Db   440 ESHEPKGTENEDAGSDYQSDNQASWIHRMIMALVSDSALFNTREGRAGKVHNFMLGLNLN  499

Qy   416 KDYFQHP-HFSTWKATTLDGL----PNQ------LTPSEPHLCLLDVGYLLINTSCL      460
          ||:::  |||||||||||||    |::      :||||||:|||||||||:||::||
Db   500 TSYPLSPLSDFATQDSFDDELDAAVADPDEFERIYEPLDVKSKKIHVDSGLTFNLPYP    559

Qy   461 PLLQPTRDVDLILSLDYNLHGA------FQQLQLLGRFCQEQGIPFPPISPSPEEQLQPRE  515
         :|:||:|||||||:|||:|||       |||||||:|:|:|||:||||||||||||||:
Db   560 LILRPQRGVDLIISFDFSARPSDSSPPFKELLLAEKWAKMNKLPFPKIDPYVFDREGLKE   619

Qy   516 CHTFSDPTCP----GAPAVLHF-------SSGV-RRTPEEAAAGEVNL-SSSDSPY       558
          || |:|::|    |:|:|:::       ||||  ||||||   |||:  |||||:
Db   620 CYVFK-PKNPDMEKDCPTIIHFVLANINFRKYKAPGVPRETEEEKEIADFDIFDDPESPF   678

Qy   559 HYTKVTYSQEDVDKLLHLTHYNVCNNQEQLLEALRQAVQRRRQ                   601
         :|:|||:|||||||||||||||||||||||||:|||||||||||
Db   679 STFNFQYPNQAFKRLHDLMHFNTLNNIDVIKEAMVESIEYRRRQ                  721
```

Query Match   18.6%; Score 602; DB 1; Length 749;
Best Local Similarity 27.1%; Pred. No. 2.3e-38;
Matches 172; Conservative 172; Mismatches 126; Indels 247; Gaps 21;

```
Db   155 KTFRQQRKENIKENMKKLLGPKKSEGLYSTRDVPVVAILGSGGGFRAMVGFSGVMKALYE  214

Qy   157 LGLLDCVSYITGASGSTWALANLYEDPEWSQKDLAGPTEL--LKTQVTKNKLGVLAPSQ   213

Db   215 SGIILDCATYIAGLSGSTWYMSTLYSHPDFPEK---GPEEINEELMKNVSHNPLLLLTPQK 271

Qy   214 LQRYRQELAEBRARLGYPSCFTNLWA-LINEALLHDEPHDHKLSDQREALSHGQNPLPIYC  272

Db   272 VKRYVESLWKKKSSGQPVTFTDIFGMLIGETLIQNR-MSMTLSSLKEKVNAARCPLPLFT   330

Qy   273 ALNTKGQSLTTFEFGEWCEFSPYEVGFPKYGAFIPSELFGSEFFMGQLMKRLPESRICFL   332

Db   331 CLHVK-PDVSELMFADWVEFSPYEIGMAKYGTFMAPDLFGSKFFMGTVVKKYEENPLHFL   389

Qy   333 EGIWSNLYA----------ANLQDSL--------YWASEPSQFWDRWVRNQANLDK       370

Db   390 MGVWGSAFSILFNRVLGVSGSGQNKGSTMEEELENITAKHIVSNDSSDDEAQGPKGTEN   449

Qy   371 EQVPLLKIEEPPSTAGRIAEFFTDLLTWRPL----AQATHNFLRGLHFHKDYFQHP-     422

Db   450 BEAE--KEYQSDNQASWVHRMLMALVSDSALFNTREGRAGKVHNFMLGLNNTSYPLSPL   507

Qy   423 -HFSTWKATTLDGL--------PNQ-----LTPSEPHLCLLDVGYLINTSCLPLLQPTRD  468

Db   508 RDFSSQDSFDDDELDAAVADPDEFERIYEPLDVKSKKIHVDSGLTFNLPYPLILRPQRG   567

Qy   469 VDLILSLDYNLHGA------FQQLQLLGRFCQEQGIPFPPISPSPEEQLQPRECHTFSDPT  523

Db   568 VDLIISFDFSARPSDTSPPFKELLLAEKWAKMNKLPFPKIDPYVFDREGLKECYVFK-PK  626

Qy   524 CP----GAPAVLHF--------SSGV-RRTPEEAAAGEVNL-SSSDSPYHYTKVTYS     566

Db   627 NPDVEKDCPTIIHFVLANINFRKYKAPGVLRETKEEKEIADFDIFDDPESPFSTFNFQYP  686

Qy   567 QEDVDKLLHLTHYNVCNNQEQLLEALRQAVQRRRQ                           601

Db   687 NQAFKRLHDLMYFNTLNNIDVIKDAIVESIEYRRRQ                          721
```

Query Match   18.4%; Score 596; DB 1; Length 748;
Best Local Similarity 25.9%; Pred. No. 6.8e-38;
Matches 166; Conservative 129; Mismatches 245; Indels 100; Gaps 20;

```
Qy    44 ESLSVAQAGVQWRDLGSLQPPPLGFKRFSCLSLPSSWDYRLRELAVRLGFGPCAEEQAFL  103

Db   100 ETLGMATFPISSLKLGEKKEVQLTFNNVTEMLELSLEV-CSSTDLRFSMALCDEEKKFR   158

Qy   104 SRRKQVVAAALRQALQLDGD--LQEDEIPVVAIMATGGIRAMTSLYGQLAGLKELGLL    160

Db   159 QQRKDNIMQSMKSFLGEENSKNLTTSRDVPVIAVLGSGGGFRAMVGFAGVMKALYESGVL  218

Qy   161 DCVSYITGASGSTWALANLYEDPEWSQKDLAGPTEL--LKTQVTKNKLGVLAPSQLQRY   217

Db   219 DCATYIAGLSGSTWYMSTLYSHPDFPEK---GPKEINQELMNSVSHNPLLLLTPQKVKRY  275
```

Db   373 VKQYENPLHFLMGVWGSAFSILFNRVLGVKETTSSSTMEEELEQIKPEHIVGDDSADNE 432
Qy   366 ANLDK--EQVPLLKIEEPPSTAGRIAEFFTDLL------TWRPLAQATHNFLRGLHFH   415
Db   433 EETQRGGTESADAEDERQRHAQASWVQRMLTSIMGDTTLFTTREGRAGKVHNFMLGLNLN 492
Qy   416 KDYFQHPHFSTWKATTLDGLPNQLT-PSE-----PHLCLLDVGYLINTSCLPL   462
Db   493 STLPFSPFSGITHQTSLEEEVDAVTDPDEFERIYEPLDVKSKKIHVVDSGLTFNLYPLI   552
Qy   463 LQPTRDVDLILSLDYNLHGA------FQQLQLLGRFCQEQGIPFPPISPSPEEQLQPRECH 517
Db   553 LRCQRGVDLIISFDFSARPSDSSPPFKEILLAEKWARMNKLPFPKIDSKVFDREGLKECY 612
Qy   518 TF----SDPTCPGAPAVLHF------SSGV-RRTPEEAAAGEVNL-SSSDSPYHY   560
Db   613 VFKPAKGDKNC---PTIIHFVLANINFRNFKAPGVPRDSDKDIEFGDFDIFDEPASPYST 669
Qy   561 TKVTYSQEDVDKLLHLTHYNVCNNQEQLLEALRQAVQRRRQ   601
Db   670 FNFKTNNQAFKRLHDLMEFNTLNNIEVIKEAIKDSLLRRE   710

RESULT 5
T13162
cytosolic phospholipase A2 gamma - human
N;Alternate names: protein DKFZp586C0423.1
C;Species: Homo sapiens (man)
C;Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 17-Nov-2000
A;Accession: T13162, T08799
R;Pickard, R.T.; Strifler, B.A.; Kramer, R.M.; Sharp, J.D.
J. Biol. Chem. 274, 8823-8831, 1999
A;Title: Molecular cloning of two new human paralogs of 85-kDa cytosolic phospholipase A2
A;Reference number: Z17618; MUID:99185108; PMID:10085124
A;Accession: T13162
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-541 <PIC>
A;Cross-references: EMBL:AF065214; NID:g3811344; PID:g3811345; PIDN:AAC78835.1
R;Ansorge, W.; Wirkner, U.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.
submitted to the Protein Sequence Database, May 1999
A;Reference number: Z16472
A;Accession: T08799
A;Molecule type: mRNA
A;Residues: 443-541 <ANS>
A;Cross-references: EMBL:AL050193
A;Experimental source: adult uterus; clone DKFZp586C0423
C;Genetics:
A;Gene: cPLA2 gamma
A;Map position: 19
A;Note: DKFZp586C0423.1

Query Match   15.4%; Score 498.5; DB 2;   Length 541;
Best Local Similarity   27.8%; Pred. No. 1.5e-30;
Matches 158; Conservative   86; Mismatches 190; Indels 135; Gaps   23;

Qy   98 EEQAFLSRRKQVVAAALRQALQLDGDLQEDEIPVVAIMATGGGIRAMTSLYGQLAGLKEL 157
Db   15 EEKAAVERRRLHVLKALKKL------RIEADEAPVVAVLGSGGGLRAHIACLGVLSEMKEQ 69
Qy   158 GLLDCVSYITGASGSTWALANLYE---DPEWSQKDLAGPTELLKTQVTKNKLGVLAPSQL 214
Db   70 GLLDAVTYIAGVSGSTWAISSLYTNDGDMEALEAD-----LKHRFTRQEW-----DL   116
Qy   215 QRYRQELAERARLGYPSCFTNLWA-LINEALLHDEPHDHKLSDQREALSHGQNPLPIYCA 273
Db   117 AKSLQKTIQAARSENYS-LTDFWAYMVISKQTRELPESH-LSNMKKPVEEGTLPYIFAA   174
Qy   274 ----LNTKGQSLITFEFGEWCEFSPYEVGFPKYGAFIPSELFGSEFFMGQLMKRLPESRI 329
Db   175 IDNDLQPSWQEARAPE--TWFEFTPHHAGFPALGAFVSITHFGSKFFKKGRLVRTHPERDL 232
Qy   330 CFLEGIWSN----------LYA--ANLQDSLY   349

Qy   218 RQELAERARLGYPSCFTNLWA-LINEALLHDEPHDHKLSDQRFALSHGQNPLPIYCALNT 276
Db   276 IEALWNKKSSGQPVTFDIFGMLIGETLIHNR-MDTTLSDMKEKVSEAQCALPLFTCLHV   334
Qy   277 KGQSLTTFEFGEWCEFSPYEVGFPKYGAFIPSELFGSEFFMGQLMKRLPESRICFLEGIW 336
Db   335 K-PDVSELMFADWVEFSPYEIGMAKYGTFMSPDLFGSKPFMGTVVKKYSENPLHFLMGVW 393
Qy   337 SNLYAANLQDSLYWASEPSQFWDRWVRNQANLDKEQVPLLKI----------EEP   381
Db   394 GSAPSILFNRVLGVSNS---------QNKGPTMEEELENIRLKHIVSNDSSDSEDESQHP 444
Qy   382 PSTAGRIA-------EFFTDLL------------TWRPLAQATHNFLRGLHFHKDYFQ   420
Db   445 KGTENSEANEEYQNSSQESWVQRMLMALVGDSALFNTREGRAGKVHNFMGLNLNSCYPL   504
Qy   421 HP-HFSTWKATTLDGL------PNQ----LTPSEPHLCLLDVGYLINTSCLPLLQP   465
Db   505 SPIADLLTQESVEEDELDAAVADPDEFERIYEPLDVKSKKIHIVDSGLTFNLYPLILRP   564
Qy   466 TRDVDLILSLDYNLHGA------FQQLQLLGRFCQEQGIPFPPISPSPEEQLQPRECHTP- 519
Db   565 QRGVDLIISFDFSARPSDSSPPFKEILLAEKWAKMNKLPFPKIDPNVFDREGLKECYVFK 624
Qy   520 ----SDPTCPGAPAVLHF------SSGV-RRTPEEAAAGEVNL-SSSDSPYHYT   561
Db   625 PKDTSSEKDC---PTIIHFVLANINFRKYKAPGLPRESKEEKDPADFDIFDDPNTPFSTF 681
Qy   562 KVTYSQEDVDKLLHLTHYNVCNNQEQLLEALRQAVQRRRQ   601
Db   682 NFQYPNEAFKRLHDLMEFNTLNNLDVIKQAMMBSIEYRKE   721

RESULT 4
B54908
phospholipase A2 cytosolic - zebra fish
C;Species: Brachydanio rerio (zebra fish)
C;Date: 07-Aug-1997 #sequence_revision 09-Aug-1997 #text_change 31-Oct-1997
C;Accession: B54908
R;Nalefski, E.A.; Sultzman, L.A.; Martin, D.M.; Kriz, R.W.; Towler, P.S.; Knopf, J.L.;
J. Biol. Chem. 269, 18239-18249, 1994
A;Title: Delineation of two functionally distinct domains of cytosolic phospholipase A2,
A;Reference number: A54908; MUID:94299545; PMID:8027085
A;Accession: B54908
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-741 <NAL2>
A;Cross-references: EMBL:U10329
C;Superfamily: cytosolic phospholipase A2

Query Match   17.7%; Score 572; DB 2;   Length 741;
Best Local Similarity   26.5%; Pred. No. 4.8e-36;
Matches 154; Conservative 115; Mismatches 236; Indels   76; Gaps   17;

Qy   89 VRLGFGPCAEEQAFLSRRKQVVAAALRQALQLDG----DLQEDEIPVVAIMATGGGIRAM 144
Db   138 LRFSMTLCDQEKLFMQTRDRVMLSIKKLLKMENPRFLPSSPREVPTIAILGSGGGFRAM   197
Qy   145 TSLYGQLAGLKELGLLDCVSYITGASGSTWALANLYE---LKTQV   201
Db   198 VGFSGVMKALYESGVFDCATYVAGLSGSTWYMSMLYSHPEFPAK---GPGDINKELMNRV 254
Qy   202 TKNKLGVLAPSQLQRYRQELAERARLGYPSCFTNLWA-LINEALLHDEPHDHKLSDQREA 260
Db   255 SNNPLKLLLPQNINRYVKALWKKSAGQPVTFDIFGMLIGETLIPGR-MNIKLSSLKGK   313
Qy   261 LSHGQNPLPIYCALNTKGQSLITTFEFGEWCEFSPYEVGFPKYGAFIPSELFGSEFFMGQL 320
Db   314 INEGQSPLPLFTCLHVK-PDVSELMFADWVEFSPYEIGMAKYGTFMSPGLFGSKFFMGSV 372
Qy   321 MKRLPESRICFLEGIWSNLY----------AANLQDSLYWASEPSQFWDRWVRNQ   365

```
Db  233  TFLRGLWGSALGNTEVIREYIFDQLRNLTLKGLWRRAVANAKSIGHLIFARLLRLQBSSQ  292

Qy  350  W------ASEPSQFW-----DRWVRNQANLDKEQVPLLKIEPPSTAGRIAEFF----  392
Db  293  GEHPPPEDEGGEPEHTWLTEMLENWTR--TSLEKQEQP---HEDPERKGSLSNLMDFVK  346

Qy  393  -TDLLTWRPLAQATHNFLRGLHFHKDYFQHPFSTWKATTLDGLPNQLTPSEPHLCLLDV  451
Db  347  KTGICASKWEWGTTHNFL--------YKH---------GGIRDKIMSSRKHLHLVDA  386

Qy  452  GYLINTSCLPLLQPTRDVDLILSLDYNLHGAFQQLLQLLGRFCQEQGIFPPPISPSPEEQL  511
Db  387  GLAINTPFPLVLPPTREVHLILSFDFSAGDPFETIRATTDYCRRHKIPFPQVE---EAEL  443

Qy  512  Q-----PRECHTFSDPTCPGAPAVLHFSSGVRRTP---BEAAAGEVNLSSSDSPYHYTKV  563
Db  444  DLWSKAPASCYILKGET---GPVVWHF------PLFNIDACGGDIEAWSDTYDTFKLAD  493

Qy  564  TYSOEDVDKLLHLTHYNVCNNQBQLLEAL  592
Db  494  TYTLDVVILLALAKKNVRENKKKILREL  522
```

RESULT 6
A40201
artifact-warning sequence (translated ALU class A) - human
C;Species: Homo sapiens (man)
C;Date: 31-Mar-1992 #sequence_revision 11-Aug-1995 #text_change 19-May-2000
C;Accession: A40201
R;Claverie, J.M.
personal communication, 1992
A;Reference number: A40201
A;Accession: A40201
A;Molecule type: DNA
A;Residues: 1-627 <CLA>
R;Claverie, J.M.
Genomics 12, 838-841, 1992
A;Title: Identifying coding exons by similarity search: Alu-derived and other potentiall
A;Reference number: A40200; MUID:92241891; PMID:1572661
A;Contents: annotation
C;Comment: This "warning" entry is a conceptual translation in all 6 reading frames of c
in-frame stop codons are shown as 'X'.
C;Comment: Any significant similarity of a predicted protein sequence to a portion of th

```
Query Match      6.1%; Score 198; DB 4; Length 627;
Best Local Similarity   80.9%; Pred. No. 3.4e-07;
Matches   38; Conservative   1; Mismatches   8; Indels   0; Gaps   0;

Qy   37  FFFFFEMESLSVAQAGVQWRDLGSLQPPPLGFKRFSCLSLPSSWDYR  83
         |||:||||||||||||||||||||||||||||||||||||||||||
Db  321  FLFFSETESRSVAKAGVQWRDLGSLQAPPPGFTPFSCLSLPSSWDYR  367
```

RESULT 7
C40201
artifact-warning sequence (translated ALU class C) - human
C;Species: Homo sapiens (man)
C;Date: 31-Mar-1992 #sequence_revision 11-Aug-1995 #text_change 19-May-2000
C;Accession: C40201
R;Claverie, J.M.
personal communication, 1992
A;Reference number: A40201
A;Accession: C40201
A;Molecule type: DNA
A;Residues: 1-613 <CLA>
R;Claverie, J.M.
Genomics 12, 838-841, 1992
A;Title: Identifying coding exons by similarity search: Alu-derived and other potentiall
A;Reference number: A40200; MUID:92241891; PMID:1572661
A;Contents: annotation
C;Comment: This "warning" entry is a conceptual translation in all 6 reading frames of d

in-frame stop codons are shown as 'X'.
C;Comment: Any significant similarity of a predicted protein sequence to a portion of th

```
Query Match      6.0%; Score 193.5; DB 4; Length 613;
Best Local Similarity   62.7%; Pred. No. 7.3e-07;
Matches   42; Conservative   1; Mismatches  17; Indels   7; Gaps   1;

Qy   37  FFFFFEMESLSVAQAGVQWRDLGSLQPPPLGFKRFSCLSLPSSWDYRLRELA------V  89
         |||||||||:||||||||||||||||||:||||||||||||||||||||  :|||||
Db  311  FFFFFETESHSVTQAGVQWRDLGSLQAPPPGFMPFSCLSLLRTWDYRRPHHAQLIFCIFS  370

Qy   90  RLGFGPC  96
         ||:|||
Db  371  RNGVLPC  377
```

RESULT 8
T50281
probable lysophospholipase (EC 3.1.1.5) precursor SPAC977.09c [similarity] - fission yea
C;Species: Schizosaccharomyces pombe
C;Date: 09-Jun-2000 #sequence_revision 09-Jun-2000 #text_change 19-Jan-2001
C;Accession: T50281; T42738
R;Zimmermann, W.; Wambutt, R.; McDougall, R.C.; Rajandream, M.A.; Barrell, B.G.
submitted to the EMBL Data Library, January 2000
A;Reference number: Z25053
A;Accession: T50281
A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-673 <ZIM>
A;Cross-references: EMBL:AL137130; NID:g6742151; PIDN:CAB69631.1; NID:g6742159; GSPDB:GN
A;Experimental source: strain 972h(-); cosmid c977
R;Yoshioka, S.; Kato, K.; Nakai, K.; Okayama, H.; Nojima, H.
DNA Res. 4, 363-369, 1997
A;Title: Identification of open reading frames in Schizosaccharomyces pombe cDNAs.
A;Reference number: Z17323; MUID:98162722; PMID:9501991
A;Accession: T42738
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 427-673 <YOS>
A;Cross-references: EMBL:D89183; NID:g1749573; PIDN:BAA13845.1; PID:g1749574
A;Experimental source: strain PR745
C;Genetics:
A;Gene: SPDB:SPAC977.09c
A;Map position: 1
A;Introns: 651/3
A;Function:
A;Description: catalyzes the hydolysis of 2-lysophosphatidylcholine to glycerophosphocho
C;Superfamily: yeast lysophospholipase
C;Keywords: carboxylic ester hydrolase

```
Query Match      5.7%; Score 186; DB 2; Length 673;
Best Local Similarity   21.1%; Pred. No. 3.2e-06;
Matches  148; Conservative  90; Mismatches  245; Indels  218; Gaps  35;

Qy    3  FVELSPTIALCLERV-ASHLTDTGLLVLFCPAPCPFFFFEMESLSVAQAGVQWRDLGSL  61
         ||:|||||:||:  |   |: ::  :|   |||||||||||||||||||||||
Db   11  FVQISLTLAYPPGRVEISEIYD------------FE-ESSSYKGQDIDTSVLYTL  52

Qy   62  -QPPPLGFKR----FSCLSLPSSWDYRLRELAVRLGFGPCAEEQAFLSRRKQVVAAALR  115
          |||||||:     |||||||||||  |:||   || ||  | |:|| :||:||
Db   53  SRKKPALVKRSTDASYAPFNVTCSNDNLLRPASEGLNEG---EQSYINKRISKVNSELR  108

Qy  116  QAL------QLDGDLQEDEIPVVAIMATGGIRAMTSLYGQLAGLKE------LGLL  160
          :||       |:   |  |:||  |  ||| |  | |:   | |         ||
Db  109  SFISKTGLNVDLDKVVNSSDGPRLGIAFSGGGLRAMVNGGAFNAFDSRFESDSPLSGIL  168

Qy  161  DCVSYITGASGSTWALANLYEDPEWSQKDLAGPTELLKTQVTKNKLGVLAP------SQL  214
          | |:   |:|:||| |  |   |      ||  ||:|| :|:  | |:|      :||
Db  169  QSAMYISGLSGGSWLVGSV-----AINNFTNIT-YLRDNVWNLEHSVFAPHGDNVIENL  221

Qy  215  QRY---RQELAEBRARLGYPSCFTNLWALINEALLIHDEPHDHKLSDQREA--------  260
          |||     | :   :|| | :|                |:  || :
```

```
Db  222  NYYNDLRKEIDQKKHAGFDCSLTDLW--GRAL------SRKLVDAERGGPGITYSSMRN  272
              :||:|:||:    |||:||||:
Qy  281  NLNATVF----EFNPFEMGSWDPSLNSFANVKYLGTNVSNGVPLERGKCTAGFDNAGFIM  336

Qy  261  --LSHGQNLPIYCA------LNTKGQSLTTFEFGEWCEFSPYEVGFPKYGAFI  306
              |  :|  :|| :::    ||||||||||||||||||||||||||||||
Db  334  GIWSNLYAANLQDSLYWASEPSQFWDRWVRNQANLDKEQVPLLKIEEP--PSTAGRIA--  389

Db  273  QSWFQNADYPYPIIVADSRLEEETAIPANTSIFEFTAYEFGTW------DNGIK---AFI  323
                                           |||||||||||:
Qy  337  GTSSTLF----------------------NQF--------------LLRINSTHLPSPITRLARH  365

Qy  307  PSELFGSEFFMGQLMKRLPESRIC-------FLEGIWSNLYAANLQDSLYWASEPSQFW  358
                   |:|:    :|:|||::|    |||||||||||||||||||||||||||||||
Db  390  ------EFFTDLLTWRPLAQATHNFLRGLHFHKDYFQHPHFSTWKATTLDGLPNQLTPSE  443

Db  324  PMEVVGT---HLLDGVPPDKSCIHNYDNAGFVMGTSATLFNSFLLD-------------W  367
                 ::|:|    | :|:|
Qy  359  DRWVRNQANLDKEQVPLLKIEEPSTAGRIAEFFTDLLTWRPLAQATHNFLRGLHFHKD--  417

Qy  368  NENVKKN----------------------DTYYDIL------HAILEDLSKHQDD  394
              :                       :||::|        ||:|:||::|:|
Db  444  PHLCLLDVGY-LINTSCLPLLQPTRDVDLILSLDYN--------LHGAFQQLQLL  489

Db  395  IAPYPNPYQNYTTSNTSVVNAF------EPYDTDLVDGGEDRENIPLWPLLHPQRFVD  447
                 :  :|  ||:||::|         |:     |: |
Qy  418  --YFQHPH--FSTWKATTLDGLPNQLTPSEPH--LCLLDVGY-LINTSCLPLLQPTRDVD  470

Qy  471  LILSLD--YNLHGAFQQLQLLGRFCQEQGIPFPPISPSPEEQLQPRECHTFSD----PTC  524
                ::|::|    |     :|| :|| :    :|:|:| :| :|:|||||||:
Db  490  GRFCQEQGIPFPPISPSPEEQLQPRECHTF------SDPTCPGA----------PAVL  531

Db  448  VVFAIDSTYN----------------DPYGWPLGSSIVATYERVVTFNANKSVDVRGFPYI  492
                 :: :|:||                |||||||||||::
Qy  471  ...
Qy  525  PGAPAVLHFSSSGVRRT------PEEAAAGEVNLSSSDSP------YHYTKVTYSQE  568
              |:  |:|:|:|::|:        ::|:|||:||:|:||       :||:||||:|:
Db  532  HFSSGVRRTPEEAAAGEVNLSSSDSPYHYTKVTYSQED----VDKLLHLTHYNVCNNQEQ  587

Db  493  PDENTIISLGLNTRPTFFGCDGKNTTAGNHDVDNNTPPLLIVYFPNYPWTYYSNISTFTMS  552
                  :|:|:
Qy  508  YLPN---------AEYSFNSNQSAF---KLSYSESQRRSMIQNGFEIATRNNFTDDPE  553

Qy  569  DVDKLLHLTHYNVC----NNQEQLLEALRQA-VQRRRQRR  603
              |||||||||||||     :||:|::||:|| :||||||
Db  588  LLEALRQAVQRRRQR  602

Db  553  MDDKWANGILENAFMSTTQNNNESFAVCLACAIIQRSLERK  593
                                    |:|| :||||||||
Qy  554  FMGCGVGCAIIRRKQQ  568
```

RESULT 9
S66693
hypothetical protein YOL011w - yeast (Saccharomyces cerevisiae)
N;Alternate names: hypothetical protein O2349
C;Species: Saccharomyces cerevisiae
C;Date: 12-Jul-1996 #sequence_revision 12-Jul-1996 #text_change 19-Apr-2002
C;Accession: S66693
R;Hughes, B.; Pohl, T.M.
submitted to the Protein Sequence Database, July 1996
A;Reference number: S66685
A;Accession: S66693
A;Molecule type: DNA
A;Residues: 1-686 <HUG>
A;Cross-references: EMBL:Z74753; NID:g1419780; PIDN:CAA99010.1; PID:g1419781; GSPDB:GN00
A;Experimental source: strain S288C
C;Genetics:
A;Gene: SGD:PLB3; MIPS:YOL011w
A;Cross-references: SGD:S0005371
A;Map position: 15L
C;Superfamily: yeast lysophospholipase

```
Query Match            5.7%;  Score 184;  DB 2;  Length 686;
Best Local Similarity  21.0%;  Pred. No. 4.7e-06;
Matches  129;  Conservative  80;  Mismatches  192;  Indels  214;  Gaps  31;

Qy   99  EQAFLSRRKQVVAALRQAL--------------------QLDGDLQEDEIPVVAIMATGGGIRA  143
              |:||||||:|| :|||:|                    |:| :|:|||||||:|||||||||
Db   57  ESAWLEKRNKVTSVALKDFLTRATANFSDSSEVLSKLFNDGNSENLPKIAVAVSGGGYRS  116

Qy  144  MTSLYGQLAGLKEL-----------------GLLDCVSYITGASGSTWALANL------  179
              ||||||:|||||||                 |||||||||||||||||||
Db  117  MLTGAGVLAAMDNRTEGAYEHGLGLGLLQSTTYLSGASGGNWLVGTLALNNWTSVQDILNN  176

Qy  180  --YEDPEWSQKD----LAGPTELLKTQVTKNKL-GVLAPSQLQRYRQELAE--RARLGYP  230
              |:||||:||     ||||:||||:|||:|| ||:|:||||:|||:|||  |||||:
Db  177  MQNDDSIWDLSDSIVTPGGINIFKTAKRWDHISNAVESKQNADYNTSLADIWGRA-LAY-  234

Qy  231  SCFTNLWALINE-----ALLHDEPHDHKLSDQREALSHGQNLPIYCA---LNTKGQ  279
              ||::||||:||      |||:|||:||||:|||:||||||||||||    |||||
Db  235  ---NFFPSLNRGGIGLTWSSIRDFP----------VFQNAEMPFPISVADGRYPGTKVI  280

Qy  280  SLTTFEFGEWCEFSPYEVGF--PKYGAFIPSELFGSEFFMGQLMKR------LPESRICFLE  333
```

RESULT 10
S29318
lysophospholipase (EC 3.1.1.5) precursor [validated] - Penicillium notatum (fragment)
C;Species: Penicillium notatum
C;Date: 10-Mar-1994 #sequence_revision 10-Mar-1994 #text_change 19-Jan-2001
C;Accession: S29318; S39981; S22045
R;Masuda, N.; Kitamura, N.; Saito, K.
Eur. J. Biochem. 202, 783-787, 1991
A;Title: Primary structure of protein moiety of Penicillium notatum phospholipase B deduc
A;Reference number: S29318; MUID:92111525; PMID:1722456
A;Accession: S29318
A;Molecule type: mRNA
A;Residues: 1-612 <MA1>
A;Cross-references: EMBL:X60348; NID:g3183; PIDN:CAA42906.1; PID:g3184
A;Accession: S39881
A;Molecule type: protein
A;Residues: 10-20;185-199 <MA2>
C;Superfamily: yeast lysophospholipase
C;Keywords: carboxylic ester hydrolase; glycoprotein
F;1-9/Domain: signal sequence (fragment) #status predicted <SIG>
F;10-612/Product: lysophospholipase #status experimental <MAT>
F;41,81,116,223,267,306,335,427,440,446,477,498,526,532,567,571/Binding site: carbohydrat

```
Query Match            5.5%;  Score 177;  DB 2;  Length 612;
Best Local Similarity  21.3%;  Pred. No. 1.4e-05;
Matches  108;  Conservative  60;  Mismatches  162;  Indels  178;  Gaps  23;

Qy   51  AGVQWRDLGSLQPPPLGFKRFSCLLSPSSWDYRLRELAVRLGFGPCAEEQAFLSRRKQVV  110
              ||||                                      :::||||||||||:||
Db    5  AGVQ---RALPNAPDGY---------VPTSVCPASRPTVRSAAKLSTNETSWLEVRRGKT  53

Qy  111  AAALRQ-------------------ALQLDGDL-QEDEIPVVAIMATGGGIRAMTSLYGQLAGLKEL  157
              |||||                     |:| ||| :|:||||||:||||||:|||||:|||||
Db   54  LSALKDFFGHVKVGDYDVGAYLDKHSGNSSSLPNIGIAVSGGGWRALMNGAGAVKAFDSR  113

Qy  158  -----------GLLDCVSYITGASGSTWALANLY  180
                         ||||||||||||||||||||||
Db  114  TDNATATGHLGGLLQSATYISGLSGSGSWLLGSSIYINNFTTVDKLQTHEAGSVWQFGNSII  173

Qy  181  EDPEWSQKDLAGPTELLKTQVTKNKLGVLAPSQLQRYRQELAE-----RARLGYPSCFTNL  236
              |||||:|||:||:|||||||||:|||:|||:|||:|||:||||     |||:|||||:||
Db  174  EGPD---------AGGIQLLDS-----------AGYYKDLADAVDVDGKKKAGFDTTLTDI  212

Qy  237  WALINEALLHDEPHD------HKLSDQREALSHGQNLPIYCALNTK------GQSLTTF  284
              ||||:||:||||||        :|:|:|||:|||||||:||:||:        |||:||
Db  237  ...
```

```
Db     213  WGRALSYQMFNASNGGLSYTWSSIADTPE-FQDGDYPMPFVVADGRNPGELVIGSNSTVY  271

Qy     285  EFGEWCEFSPYEVGPKYGAFIPSELFGSEFFMGQLMKRLPESRIC-------FLEGIW  336
                 ||:|| ||::.|  ||:|| |:|| .|:|:|                  |:.||
Db     272  EFNPW-EFGTFD---PTIFGFVPLEYLGSKPEGGS----LPSNESCIRGFDSAGFVIGTS  323

Qy     337  SNLYAANLQDSLYWASEPSQFWDRWVRNQANLDKEQVPLLKIEEPPSTAGRIAEPFTDLL  396
                 |:|:  ||:||||.|  |::.||| |    ||||:.||:
Db     324  SSLFNQFLL-QINTLSPSFIKDVFNGILFDLDKSQNDIASYDPNP-------------  368

Qy     397  TWRPLAQATHNFLRGLHFHKDYFCHPHFSTWKATTLDGLPNQLTPSEPHLC--LLDV--  451
                                         :|:                 ::|:
Db     369  -----------------------------------FYK-YNEH-----------  390

Qy     452  --GYLINTSCLPLLQPTRDVDLILSLD  476
               ||||||||||||||||| ||||||
Db     391  GEDGQ--NVPLHPLIQPERHVDVIFAVD  416
```

```
Query Match        5.3%;  Score 170;  DB 2;  Length 46;
Best Local Similarity   76.7%;  Pred. No. 1.2e-06;
Matches  33;  Conservative  0;  Mismatches 10;  Indels  0;  Gaps  0;

Qy      41  FEMESLSVAQGVQWRDLGSLQPPPLGFKRFSCLSLPSSWDYR  83
                ||||||||||||||||||||||||||||||
Db       4  FNCBSCCSVTLAGVQWRDLGLLQPLPPKFKRFSCLSFPSSWDYR  46
```

```
Query Match        5.0%;  Score 162;  DB 2;  Length 664;
Best Local Similarity   21.5%;  Pred. No. 0.00022;
Matches  96;  Conservative  64;  Mismatches 170;  Indels 116;  Gaps  20;

Qy      89  VRLGFGPCAEEQAFLSRR----KQVVAAALRQALQLDGDL------QEDEIPVVAIM  135
                |||| : .:                :|.:|                |:.|||.|
Db      43  VREASGLSDNETEWLKKRDAYTKEALHSFLNRATSNFSDTSLLSTLFGSNSSNMPKIAVA  102

Qy     136  ATGGGIRAMTSLYGQLAGLKEL---------GLLDCVSYTTGASGSTWALANLYEDPEW  185
                           ||:   |            ||  ::||                 |
Db     103  CSGGGYRAMLSGAGMLAAMDNRTDGANEHGLGGLLQGATYLAGLSGGNWLTSTLAWN-NW  161

Qy     186  SQKDLAGPTELLKTQVTKNKLGVLAPSQLQRYR--------QELAERARLGYPSCFTNL  236
                : .  . ||::|  ::                      ::  ::..  ||
Db     162  TSVQAIVDNTTESNSIWDISHSILTPDGINIFKTGSRWDDISDDVQDKKDAGFNISLADV  221

Qy     237  WALINEAL------LHDEPHDHKLSDQREA--LSHGQNPLPI-----YCALNTKGQSL  2B1
                : :|           :|||| ||:|          |  |||        .  |:|
Db     222  W---GRALAYNFWPSLHRGGVGYTWSLREADVFKNGEMPFPITVADGRYPGTTVINiNA  278

Qy     282  TTFBFGEWCEFSPYEVGF--PKYGAFIPSELFGSEFFMGQLMKRLPESRICFLEGIWSNL  339
                |:.   ||||:||||:     |:|||| :|||:|||| |:|:|:||:|:|   :|:.|
Db     279  TLF-------EFNPFEMGSWDPTLNAFTDVKYLGTNVTNGK-----PVNKGQCIAGFDNTG  327

Qy     340  YAANLQDSLYWASEPSQFWDRWVRNQANLDKEQVPLLKIEEPPSTAGRIAEFFTDLLTWR  399
                ::.                  :                     ||| |||:|:|||:|
Db     328  FITATSSTLF------NQF------------------LLRLNS-------TDLPSF-  352

Qy     400  PLAQATHNFLRGLHFHKD---------YFQHPHFSTWKATTLDGLPNQLTPSEPHLCLLDV  451
                :                        |||:|  :||     ||   |:|:|  |||:|||
Db     353  -IANLATDFLEDLSDNSDDIAYAPNPFKEANFLQKNAT-----SSIIESE-YLFLVDG  404

Qy     452  GY-LINTSCLPLLQPTRDVDLILSLD  476
                || ||||:||||||||||||||||||
Db     405  GEDNQNIPLVPLLQKERELDVIFALD  430
```

```
Query Match        4.9%;  Score 160;  DB 2;  Length 39;
Best Local Similarity   79.5%;  Pred. No. 5.4e-06;
Matches  31;  Conservative  0;  Mismatches  8;  Indels  0;  Gaps  0;

Qy      45  SLSVAQGVQWRDLGSLQPPPLGFKRFSCLSLPSSWDYR  83
                ||||||||||||||||||||||||||||||||
Db       1  SCSVTLAGVQWRDLGLLQPLPPKFKRFSCLSFPSSWDYR  39
```

```
RESULT 14
T40991
probable lysophospholipase precursor - fission yeast (Schizosaccharomyces pombe)
C;Species: Schizosaccharomyces pombe
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 21-Jan-2000
C;Accession: T40991
R;Lyne, M.; Rajandream, M.A.; Barrell, B.G.; Volckaert, G.
submitted to the EMBL Data Library, March 1999
A;Reference number: Z21962
A;Accession: T40991
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-623 <LYN>
A;Cross-references: EMBL:AL049559; PIDN:CAB40176.1; GSPDB:GN00068; SPDB:SPCC1450.09c
A;Experimental source: strain 972h-; cosmid c1450
C;Genetics:
A;Gene: SPDB:SPCC1450.09c
A;Map position: 3
C;Superfamily: yeast lysophospholipase

Query Match          4.9%;  Score 159.5; DB 2;  Length 623;
Best Local Similarity  21.3%;  Pred. No. 0.00032;
Matches  96;  Conservative  58;  Mismatches 149;  Indels 147;  Gaps  21;

Qy   99 EQAFLSRRKQVVAAAL----RQALQLD--GDLQEDEIPVVAIMATGGIRAMTSLYGQL 151
            |:| |||  ||:| : :||
Db   85 EQEFVDKRVSKVNSALESFISKTGLKIDTKSVLNDTDGPRLGIAISGGFPAMLTGAGAI 144

Qy  152 AGLKEL--------GLLDCVSYITGASGSTWALANLYEDPEWSQKDLAGPTELLKTQVTK 203
            ||:||        :|:|| ||| : : :|
Db  145 NAFDARNGNTTSLGGIIQGSSMYLTGLSGSWLVGSV-----AVNNFANIT-FLHDDVWN 197

Qy  204 NKIGVLAPSQ-------LQRYRQELAERARLGYPSCFTNLW----------- 237
            : :| :|:
Db  198 LDHSLFAPYDDAFENFYIYQEWFEQVLQKKNAGFNVSITDLWGRALALKLVNPLTGGANT 257

Qy  238 --ALINEALLHDEPHDHKLSDQREALSHGQNPLPIYCALNT-KGQSL-----TTFEFGE 288
             :|          |||  :|:|||
Db  258 TFSSVTNETWFQD------------------GEFPFPIIIADNVIEGETVIPLNDTVFEFTP 301

Qy  289 WCEFSPYEVGFPKYGAFIPSELFGSEFFMGQLMKRLPESRIC---------FLEGIWSNLY 340
            |||||||| :||||      ||||| |
Db  302 -IEFGTWDTGVE---SFIPMEYTGTHLING-----IPLNESCVRNFDNAGFLMGTSSNVF 352

Qy  341 AANLQDSLYWASEPSQFWDRWVRNQANLDKEQVPLLKIEEPPSTAGRIAEFFTDLLTWRP 400
            :
Db  353 SGIL-----------------------------PATNASLLTASNNT--------- 369

Qy  401 LAQATHNFLRGL--HFHKDYFQHPHFSTWKATTLDGLPNQLTPSEPH--LCLLDVGY-L 454
            |||  | ||       ||||    || :
Db  370 FNNAVLSFLEMLAEDQLDVGLYPNPYQGYGNASN---TTTNPLEPYPIIELIDGGSDS 425

Qy  455 INTSCLPLLQPTRDVDLILSLDYNLHGAFQ 484
            |||  || ||:|:||:::|
Db  426 EGIPFWPLLHPQRDVDVIFAID---GGYQ 451


RESULT 15
T38006
probable lysophospholipase precursor - fission yeast (Schizosaccharomyces pombe)
C;Species: Schizosaccharomyces pombe
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 21-Jan-2000
C;Accession: T38006
R;Churcher, C.M.
submitted to the EMBL Data Library, September 1997
A;Reference number: Z21761
A;Accession: T38006
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-624 <CHU>
A;Cross-references: EMBL:Z99258; PIDN:CAB16353.1; GSPDB:GN00066; SPDB:SPAC1A6.03c
```

```
A;Experimental source: strain 972h-; cosmid c1A6
C;Genetics:
A;Gene: SPDB:SPAC1A6.03c
A;Map position: 1
C;Superfamily: yeast lysophospholipase

Query Match          4.9%;  Score 159; DB 2;  Length 624;
Best Local Similarity  22.5%;  Pred. No. 0.00035;
Matches 112;  Conservative  69;  Mismatches 171;  Indels 146;  Gaps  29;

Qy   36 PFFFFFEMESLSVAQAGVQWRD-LGSLQPPLGFKRFSCLSLPSSWDYRLRELAVRLGFG 94
            :|:::  ||| |:|||
Db    9 PLSLMQKREALAIS--LSKRDSVGSYAP-----YNVTC---PS--DYMLRPASDGISSG 55

Qy   95 PCAEEQAFLSRRKQVVAAALRQALQ---LQGD---LQEDEIPVVAIMATGGIRAMTSL 147
         |
Db   56 ----EQSFIDKRIPKINTQMRSFISNTGLDVDVNSVINDSDGPRLGLAFSGGGLRAMVHG 111

Qy  148 YGQL--------AGLKELGLLDCVSYITGASGSTWALANLYEDPEWSQKDLAGPTELLKT 199
         :::   :
Db  112 GGVLNAFDSRNGNGSSLAGILQSAMYIAGLSGGSWLVGSV-----AVNNFANIT-YLRD 164

Qy  200 QVTKNKLGVLAP-------SQLQRY--RQELAERARLGYPSCFTNLW----------- 237
Db  165 NVWNLEHSVFAPHGDNVVENLAYYDDLDDEIDQKKDAGFDTSLTDLWGRALSRKLVDATQ 224

Qy  238 -----------ALINEALLH--DEPHDHKLSDQREALSHGQNPLPIYCALNTKGQSLITTFEFG 287
            :|
Db  225 GGPNITFSSIRNQTWFQNADYPYPIIISDSR--LEEEKAIP----ANTSIFEFTPYEFG 277

Qy  288 EWCEFSPYEVGFPKYGAFIPSELFGSEFFMGQLMKRLPESRIC----FLEGIWSNL 339
         :: |
Db  278 TW----DNGIK---AFLPMEYVGT-----HLKNGVPPDHKCIRNYDNAGFVMGTSATL 323

Qy  340 YAANLQDSLYWASEPSQFWDRWVRNQANLDKEQVPLLKIEPPSTAGRIAEFFTDLLTWR 399
Db  324 FNTFL---LEWSQEVTS-----NSTLYD---IIHKVFE-----KLSEDQNDI---A 360

Qy  400 PLAQATHNFLRGLHFHKDYFQHPHFSTWKATTLDGLPNQLTPSEPHLCLLDVGY-LINTS 458
         : :
Db  361 PYPNPYQNFTTTNTTVKNPFE--------RFDTID-----------LVDGGEDDENIP 399

Qy  459 CLPLLQPTRDVDLILSLD 476
         |||  || ||:||:::
Db  400 IWPLLHPQRFVDVIFAVD 417


Search completed: October  5, 2004, 19:36:29
Job time : 44.14 secs
```

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                    GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on:      October  5, 2004, 19:13:29 ; Search time 24.2 Seconds
                                          (without alignments)
                                          1301.754 Million cell updates/sec

Title:       US-09-830-321A-2
Perfect score: 3235
Sequence:    1 MIFVBLSPTLALCLERVASH.........EQLLEALRQAVQRRQRRPH 605

Scoring table: BLOSUM62
               Gapop 10.0 , Gapext 0.5

Searched:      141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters:     141681

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database  :  SwissProt_42:*

    Pred. No. is the number of results predicted by chance to have a
    score greater than or equal to the score of the result being printed,
    and is derived by analysis of the total score distribution.


                               SUMMARIES

                 *
Result     Query
No.   Score Match Length DB  ID              Description
----- ----- ----- ------ --  --              -----------
  1    619  19.1   749   1   PA24_HUMAN      P47712 homo sapien
  2   611.5 18.9   749   1   PA24_HORSE      O77793 equus cabal
  3   599.5 18.5   748   1   PA24_MOUSE      P47713 mus musculu
  4    596  18.4   748   1   PA24_CHICK      P49147 gallus gall
  5    594  18.4   752   1   PA24_RAT        P50393 rattus norv
  6    572  17.7   741   1   PA24_BRARE      P50392 brachydanio
  7   226.5  7.0   591   1   ALU8_HUMAN      P39195 homo sapien
  8   199.5  6.2   587   1   ALU2_HUMAN      P39189 homo sapien
  9   199.5  6.2   593   1   ALU7_HUMAN      P39194 homo sapien
 10    198   6.1   587   1   ALU3_HUMAN      P39190 homo sapien
 11   192.5  6.0   593   1   ALU6_HUMAN      P39193 homo sapien
 12    191   5.9   585   1   ALU5_HUMAN      P39192 homo sapien
 13    186   5.7   673   1   PLB3_SCHPO      Q9P327 schizosacch
 14    184   5.7   686   1   PLB3_YEAST      Q08108 saccharomyc
 15    182   5.6   591   1   ALU1_HUMAN      P39188 homo sapien
 16   177.5  5.5   649   1   PLB1_TORDE      Q11121 torulaspora
 17    177   5.5   612   1   PLB1_PENCH      P39457 penicillium
 18   172.5  5.3   659   1   PLB1_CANGA      Q8tg07 candida gla
 19   165.5  5.1   608   1   PLB2_CANAL      O93795 candida alb
 20    164   5.1   605   1   PLB1_CANAL      Q9uwf6 candida alb
 21    164   5.1   626   1   PLB_NEUCR       O42790 neurospora
 22    162   5.0   640   1   PLB_KLULA       O59863 kluyveromyc
 23    162   5.0   664   1   PLB1_YEAST      P39105 saccharomyc
 24   159.5  4.9   633   1   PLB5_SCHPO      Q9y7n6 schizosacch
 25    159   4.9   624   1   PLB2_SCHPO      O13857 schizosacch
 26    154   4.8   754   1   PLB3_CANAL      Q9uvxl candida alb
 27    151   4.7   613   1   PLB1_SCHPO      P78854 schizosacch
 28   146.5  4.5   695   1   PLB2_CANGA      Q8tg06 candida gla
 29   143.5  4.4   603   1   ALU4_HUMAN      P39191 homo sapien
 30    140   4.3   644   1   PLB6_SCHPO      Q9uth5 schizosacch
 31    136   4.2   706   1   PLB2_YEAST      Q03674 saccharomyc
 32    122   3.8   536   1   SPO1_YEAST      P53541 saccharomyc
 33    105   3.2   431   1   VGF_BPPHK       Q38041 bacteriopha
 34    103   3.2          1   NPX2_RAT        P97738 rattus norv
 35   101.5  3.1    946   1   RHG4_HUMAN      P98171 homo sapien
 36   100.5  3.1   1138   1   RDL3_ARATH      Q8w3k0 arabidopsis
 37   99.5   3.1    664   1   Y4FB_RHISN      P55440 rhizobium s
 38   99.5   3.1   1026   1   EX5B_CHLMU      Q9plt8 chlamydia m
 39    99    3.1    690   1   VATI_DEIRA      Q9rwh3 deinococcus
 40    99    3.1   4473   1   PLE1_CRIGR      Q9ji55 cricetulus
 41    99    3.1   4687   1   PLE1_RAT        P30427 rattus norv
 42   98.5   3.0   2208   1   POLN_MANCV      Q69014 manchester
 43    98    3.0    438   1   SGCE_HUMAN      O43556 homo sapien
 44    97    3.0    852   1   POL_BLVAU       P25059 bovine leuk
 45   96.5   3.0    772   1   LMBT_HUMAN      Q9y468 homo sapien
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ALIGNMENTS

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RESULT 1
PA24_HUMAN
ID   PA24_HUMAN          STANDARD;      PRT;    749 AA.
AC   P47712;
DT   01-FEB-1996 (Rel. 33, Created)
DT   01-FEB-1996 (Rel. 33, Last sequence update)
DT   10-OCT-2003 (Rel. 42, Last annotation update)
DE   Cytosolic phospholipase A2 (CPLA2) [Includes: Phospholipase A2
DE   (EC 3.1.1.4) (Phosphatidylcholine 2-acylhydrolase); Lysophospholipase
DE   (EC 3.1.1.5)].
GN   PLA2G4A OR PLA2G4 OR CPLA2.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A. AND PARTIAL SEQUENCE.
RX   MEDLINE=91256305; PubMed=1904318;
RA   Clark J.D., Lin L.-L., Kriz R.W., Ramesha C.S., Sultzman L.A.,
RA   Lin A.Y., Milona N., Knopf J.L.;
RT   "A novel arachidonic acid-selective cytosolic PLA2 contains a Ca(2+)-
RT   dependent translocation domain with homology to PKC and GAP.";
RL   Cell 65:1043-1051(1991).
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=91331987; PubMed=1869522;
RA   Sharp J., White D., Chiou G., Goodson T., Gamboa G., McClure D.,
RA   Burgett S., Hoskins J., Skatrud P., Sportsman J., Becker G., Kang L.,
RA   Roberts E., Kramer R.;
RT   "Molecular cloning and expression of human Ca(2+)-sensitive cytosolic
RT   phospholipase A2.";
RL   J. Biol. Chem. 266:14850-14853(1991).
RN   [3]
RP   SEQUENCE OF 1-186 FROM N.A.
RA   Howden P.;
RL   Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases.
RN   [4]
RP   MUTAGENESIS OF SER-505, AND PHOSPHORYLATION BY MAP KINASE.
RX   MEDLINE=93145328; PubMed=8381049;
RA   Lin L.-L., Wartmann M., Lin A.Y., Knopf J.L., Seth A., Davis R.J.;
RT   "cPLA2 is phosphorylated and activated by MAP kinase.";
RL   Cell 72:269-278(1993).
RN   [5]
RP   MUTAGENESIS OF SER-228.
RX   MEDLINE=94299545; PubMed=8027085;
RA   Sharp J.D.;
RL   Unpublished results, cited by:
RA   Nalefski E.A., Sultzman L.A., Martin D.M., Kriz R.W., Towler P.S.,
RA   Knopf J.L., Clark J.D.;
RL   J. Biol. Chem. 269:18239-18249(1994).
RN   [6]
RP   INTERACTION WITH HTATIP.
RX   MEDLINE=21309279; PubMed=11416127;
RA   Sheridan A.M., Force T., Yoon H.J., O'Leary E., Choukroun G.,
RA   Taheri M.R., Bonventre J.V.;
RT   "PLIP, a novel splice variant of Tip60, interacts with group IV
```

RT   cytosolic phospholipase A(2), induces apoptosis, and potentiates
RT   prostaglandin production.";
RL   Mol. Cell. Biol. 21:4470-4481(2001).
RN   [7]
RP   X-RAY CRYSTALLOGRAPHY (2.4 ANGSTROMS) OF 16-141.
RX   MEDLINE=98104145; PubMed=9430701;
RA   Perisic O., Fong S., Lynch D.E., Bycroft M., Williams R.L.;
RT   "Crystal structure of a calcium-phospholipid binding domain from
RT   cytosolic phospholipase A2.";
RL   J. Biol. Chem. 273:1596-1604(1998).
RN   [8]
RP   STRUCTURE BY NMR OF 1-138.
RX   MEDLINE=98332749; PubMed=9665851;
RA   Xu G.-Y., McDonagh T., Yu H.-A., Nalefski E.A., Clark J.D.,
RA   Cumming D.A.;
RT   "Solution structure and membrane interactions of the C2 domain of
RT   cytosolic phospholipase A2.";
RL   J. Mol. Biol. 280:485-500(1998).
CC   -!- FUNCTION: Selectively hydrolyzes arachidonyl phospholipids in the
CC   sn-2 position releasing arachidonic acid. Together with its
CC   lysophospholipid activity, it is implicated in the initiation of
CC   the inflammatory response.
CC   -!- CATALYTIC ACTIVITY: Phosphatidylcholine + H(2)O = 1-
CC   acylglycerophosphocholine + a fatty acid anion.
CC   -!- CATALYTIC ACTIVITY: 2-lysophosphatidylcholine + H(2)O =
CC   glycerophosphocholine + a fatty acid anion.
CC   -!- ENZYME REGULATION: Stimulated by agonists such as ATP, EGF,
CC   thrombin and bradykinin as well as by cytosolic Ca(2+).
CC   -!- SUBUNIT: Interacts with HTATIP.
CC   -!- SUBCELLULAR LOCATION: Cytoplasmic. Translocates to membrane
CC   vesicles in a calcium-dependent fashion.
CC   -!- TISSUE SPECIFICITY: Expressed in various tissues such as
CC   macrophages, platelets, neutrophils, fibroblasts and lung
CC   endothelium.
CC   -!- DOMAIN: The N-terminal C2 domain, by its association with lipid
CC   membranes, mediates the regulation of CPLA2 by presenting the
CC   active site to its substrate in response to elevations of
CC   cytosolic Ca(2+).
CC   -!- PTM: Activated by phosphorylation on a serine residue.
CC   -!- SIMILARITY: Contains 1 C2 domain.
CC   --
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CC   --
DR   EMBL; M72393; AAB00789.1; -.
DR   EMBL; M68874; AAA60105.1; -.
DR   EMBL; AL022147; CAB42689.1; -.
DR   PIR; A39329; A39329.
DR   PDB; 1RLW; 25-FEB-98.
DR   PDB; 1BCI; 13-JAN-99.
DR   PDB; 1CJY; 20-APR-00.
DR   Genew; HGNC:9035; PLA2G4A.
DR   MIM; 600522; -.
DR   GO; GO:0005829; C:cytosol; NAS.
DR   GO; GO:0016021; C:integral to membrane; NAS.
DR   GO; GO:0004623; F:phospholipase A2 activity; NAS.
DR   GO; GO:0006690; P:eicosanoid metabolism; NAS.
DR   GO; GO:0006663; P:platelet activating factor biosynthesis; NAS.
DR   InterPro; IPR000008; C2.
DR   InterPro; IPR008973; C2_CaLB.
DR   InterPro; IPR002642; PLAc.
DR   Pfam; PF00168; C2; 1.
DR   Pfam; PF01735; PLA2_B; 1.
DR   SMART; SM00239; PLAc; 1.
DR   SMART; SM00022; PLAc; 1.
DR   PROSITE; PS50004; C2_DOMAIN_2; 1.
KW   Hydrolase; Lipid degradation; Calcium; Phosphorylation; 3D-structure.
FT   DOMAIN   1   178   PHOSPHOLIPID BINDING (PROBABLE).
FT   DOMAIN   106   C2 DOMAIN.
FT   MOD_RES   505   PHOSPHORYLATION (BY MAPK).
FT   MUTAGEN   228   S ->A: ABOLISHES BOTH PHOSPHOLIPASE AND
FT   LYSOPHOSPHATASE ACTIVITY.
FT   MUTAGEN   505   505   S ->A: DECREASES AGONIST-STIMULATED
FT   RELEASE OF ARACHIDONIC ACID.
SQ   SEQUENCE   749 AA; 85210 MW; 9F9CDC5A98231C70 CRC64;

Query Match   19.1%; Score 619; DB 1; Length 749;
Best Local Similarity 27.1%; Pred. No. 4.4e-40;
Matches 174; Conservative 125; Mismatches 238; Indels 106; Gaps 22;

Qy   44 ESLSVAQAGVQWRDLGSLQPPLGFKRFSCLSLPSSWDYRLRELA----VRLGFGPCAEE   99
                 |:|:| ||:||| :|||:||:| |:|:| :|
Db   100 ETLGTATFTVSSMKVGEKKEVPFIFNQVTEMVLEMS-----LEVCSCPDLRFSMALCDQE 154

Qy   100 QAFLSRRKQVVAAALRQAL--QLDGDLQEDEIPVVAIMATGGGIRAMTSLYGQLAGLKE 156
                 :|| |:| ::| :   ::||||:|||| :|:||:
Db   155 KTFRQQRKEHIRESMKKLLGPKNSEGLHSARDVPVVAILGSGGGFRAMVGFSGVMKALYE 214

Qy   157 LGLLDCVSYITGASGSTWALANLYEDPEWSQKDLAGPTEL---LKTQVTKNKLGVLAPSQ 213
               |:||:|||||||||||:|||||:| | || ||:| ||:| |::|
Db   215 SGILDCATYVAGLSGSTWYMSTLYSHPDFPEK---GPEEINEELMKNVSHNPLLLLTPQK 271

Qy   214 LQRYRQELAERARLGYPSCFTNLWA-LINEALLHDEPHDHKLSDQREALSHGQNPLPIYC 272
               |:|:|:| |:||| ||: :| | | | :| || | : |||:| :|| :
Db   272 VKRYVESLWKKKSSQQPVFTDIFGMLIGETLIHNRMNT-TLSSLKEKVNTAQCPLPLFT 330

Qy   273 ALNTKGQSLTTFEFGEWCEFSPYEVGFPKYGAFIPSELFGSEFFMGQLMKRLPESRICFL 332
                |:| |:| | || | :|| | | | | :| ::| |:| :| | :|
Db   331 CLHVK-PDVSELMFADWVEFSPYEIGMAKYGTFMAPDLFGSKFMGTVVKKYEENPLHFL 389

Qy   333 EGIWSNLYA------------------ANLQDSLYWASEPSQFWDRWVRNQANLDKEQVPLL 376
               :|:|::| | :|:|: |: | :| | || :
Db   390 MGVWGSAFSIILFNRVLGVSGSQSRGSTMEEEL----------ENITTKHIVSNDSSDSDD----- 439

Qy   377 KIEEPPSTAGRIA--EFFTD--------------------LLTWRPLAQATHNFLRGLHFH 415
                   | | | | :| | | | ||| |::|
Db   440 ESHEPKGTENEDAGSDYQSDNQASWIHRMIMALVSDSALFNTREGRAGKVHNFMLGLNLN 499

Qy   416 KDYFQHP--HFSTWKATTLDGL------------PNQ-----------LTPSEPHLCLLDVGYLINTSCL 460
               ||:| | |:| ||| | || |:   :||:|||: : || |:| |
Db   500 TSYPLSPLSDFATQDSFDDELDAAVADPDEFERIYEPLDVKSKKIHVVDSGLTFNLPYP 559

Qy   461 PLLQPTRDVDLILSLDYNLHGA----FQQLQLLGRFCQEQGIPFPPISPSPEEQLQPRE 515
                |||| | |:||| |::| || || | | |: | | :| :|:
Db   560 LILRPQRGVDLIISFDFSARPSDSSPPFKEILLAEKWAKMNKLPFPKIDPYVFDREGLKE 619

Qy   516 CHTFSDPTCP----GAPAVLHF-------------SSGV-RRTPEEAAAGEVNL-SSSDSPY 558
               | | | ||| ||| ::| || | || | |:|
Db   620 CYVFK-PKNPDMEKDCPTIIHFVLANINFRKYKAPGVPRETEEKEIADFDIFDDPESPF 678

Qy   559 HYTKVTYSQEDVDKLLHLTHYNVCNNQEQLLEALRQAVQRRRQ 601
               | |:| || | |:|:| || | | |: ||||
Db   679 STFNFYQPNQAFKRLRLDLMHFNTLNNIDVIKEAMVESIEYRRQ 721

RESULT 2
PA24_HORSE
ID   PA24_HORSE   STANDARD;   PRT;   749 AA.
AC   O77793;
DT   15-JUL-1999 (Rel. 38, Created)
DT   15-JUL-1999 (Rel. 38, Last sequence update)
DT   28-FEB-2003 (Rel. 41, Last annotation update)
DE   Cytosolic phospholipase A2 (CPLA2) [Includes: Phospholipase A2
DE   (EC 3.1.1.4) (Phosphatidylcholine 2-acylhydrolase); Lysophospholipase
DE   (EC 3.1.1.5)].
GN   PLA2G4A OR PLA2G4 OR CPLA2.
OS   Equus caballus (Horse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
OX   NCBI_TaxID=9796;
RN   [1]

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Qy  322 KRLPESRICFLEGIWSNLYAANLQDSLYWASEPSQFWDRWTRWQANLDKEQVPLL----  376
            |: |.|||      ||| .|    ||   :    ::|.|| :::||:
Db  379 KKYEENPLHFLMGVWGSAFSILFNRVLGVSGS------------QNKGSTMEEELENITAKHI  429

Qy  377 ----------KIEEPPSTAGRIAE--FFTD-LLTW--RPL-----------AQAT  405
                      :|.|   ||.     :|| ||||  ||:
Db  430 VSNDSDSDDESQEPKGTENEDAERDYQNDNQASWVHRMLMALVSDSALFNTREGRAGKV  489

Qy  406 HNFLRGLHFHKDYFQHP--HFSTWKATTLDGL-------PNQ------LTPSEPHLCLLD  450
            ||||| | |   |    ||| :|| ||||:|          |||       |:|: :||| ||
Db  490 HNFMLGLNLNTSYPLSPLRNFTTQESLDDELDAAVADPDEFERIYEPLDVKSKKIHVVD  549

Qy  451 VGYLINTSCLPLLQPTRDVDLILSLDYNLHGA----FQQLQLLGRFCQEQGIPFPPISP  505
            ||  | || :| :|||| ||:|:|  ||.|||       ::||  |   | ||::||||||
Db  550 SGLTFNLPYPLILRFQRGVDLIISFDFSARPSDSSPPFKELLLAEKWAKMNKLPFPKIDP  609

Qy  506 SPEEQLQPRECHTFSDPTCP---GAPAVLHF--------SSGV-RRTPEEAAAGEV  549
             | :  ||   |:||     |:     |:|| |         | |  ||   |:|:
Db  610 YVFDRGLKECYVFK-PKNPDVEKDCPTIIHFVLANINFRKYKAPGVPRETKEKEELADF  668

Qy  550 NL-SSSDSPYHYTKVTYSQEDVDKLLHLTHYNVCNNQEQLLEALRQAVQRRRQ  601
            ||  :::|  ||   |  : |      |.  |||:    .:||| |  |  :|| |||
Db  669 DIFDDPESPPSTFNFQYPNQAFKRLHDLMHFNTLNNIDVIKNAMVESIEYRRQ  721
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RESULT 3
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PA24_MOUSE
ID   PA24_MOUSE    STANDARD;    PRT;    748 AA.
AC   P47713;
DT   01-FEB-1996 (Rel. 33, Created)
DT   01-FEB-1996 (Rel. 33, Last sequence update)
DT   10-OCT-2003 (Rel. 42, Last annotation update)
DE   Cytosolic phospholipase A2 (CPLA2) (Phospholipase A2)
DE   (EC 3.1.1.4) (Phosphatidylcholine 2-acylhydrolase); Lysophospholipase
DE   (EC 3.1.1.5)].
GN   PLA2G4A OR PLA2G4 OR CPLA2.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=91256305; PubMed=1904318;
RA   Clark J.D., Lin L.-L., Kriz R.W., Rameeha C.S., Sultzman L.A.,
RA   Lin A.Y., Miiona N., Knopf J.L.;
RT   "A novel arachidonic acid-selective cytosolic PlA2 contains a Ca(2+)-
RT   dependent translocation domain with homology to PKC and GAP.";
RL   Cell 65:1043-1051(1991).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Breast tumor;
RX   MEDLINE=22388257; PubMed=12477932;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length
RT   human and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC   -!- FUNCTION: Selectively hydrolyzes arachidonyl phospholipids in the
```

Second column:

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RP   SEQUENCE FROM N.A.
RC   TISSUE=Neutrophils;
RA   Larsson Forsell P.K.A., Lindberg A., Karlsson S., Lindgren J.A.,
RA   Claesson H.-E.;
RT   "Purification, characterization and cDNA sequencing of calcium-
RT   dependent cytosolic phospholipase A2 from equine neutrophils.";
RL   Submitted (SEP-1998) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: Selectively hydrolyzes arachidonyl phospholipids in the
CC       sn-2 position releasing arachidonic acid. Together with its
CC       lysophospholipid activity, it is implicated in the initiation of
CC       the inflammatory response.
CC   -!- CATALYTIC ACTIVITY: Phosphatidylcholine + H(2)O = 1-
CC       acylglycerophosphocholine + a fatty acid anion.
CC   -!- CATALYTIC ACTIVITY: 2-lysophosphatidylcholine + H(2)O =
CC       glycerophosphocholine + a fatty acid anion.
CC   -!- ENZYME REGULATION: Stimulated by agonists such as ATP, EGF,
CC       thrombin and bradykinin as well as by cytosolic Ca(2+) (By
CC       similarity).
CC   -!- SUBCELLULAR LOCATION: Cytoplasmic. Translocates to membrane
CC       vesicles in a calcium-dependent fashion (By similarity).
CC   -!- DOMAIN: The N-terminal C2 domain, by its association with lipid
CC       membranes, mediates the regulation of CPLA2 by presenting the
CC       active site to its substrate in response to elevations of
CC       cytosolic Ca(2+) (By similarity).
CC   -!- PTM: Activated by phosphorylation on a serine residue (By
CC       similarity).
CC   -!- SIMILARITY: Contains 1 C2 domain.
CC
CC   --------------------------------------------------------------------------
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CC   --------------------------------------------------------------------------
DR   EMBL; AF092539; AAC61774.1; -.
DR   HSSP; P47712; 1BCI.
DR   InterPro; IPR000008; C2.
DR   InterPro; IPR008973; C2_CaLB.
DR   InterPro; IPR002642; PLAc.
DR   Pfam; PF00168; C2; 1.
DR   Pfam; PF01735; PLA2_B; 1.
DR   SMART; SM00239; C2; 1.
DR   SMART; SM00022; PLAc; 1.
DR   PROSITE; PS50004; C2_DOMAIN_2; 1.
KW   Hydrolase; Lipid degradation; Calcium; Phosphorylation.
FT   DOMAIN        1    178       PHOSPHOLIPID BINDING (PROBABLE).
FT   DOMAIN        5    106       C2 DOMAIN.
FT   MOD_RES     505    505       PHOSPHORYLATION (BY MAPK) (BY
FT                                SIMILARITY).
SQ   SEQUENCE   749 AA;  85454 MW;  493A67DF28D50FE0 CRC64;
```

```
Query Match             18.9%;  Score 611.5;  DB 1;  Length 749;
Best Local Similarity   27.8%;  Pred. No. 1.7e-39;
Matches  165;  Conservative 121;  Mismatches 212;  Indels  95;  Gaps  21;

Qy   89 VRLGFGPCABEQAFLSRRKQVVAAALRQAL--QLDGDLQEDEIPVVAIMATGGGIRAMT  145
           |||:|         ::|:| .:  .:||     .|.:|||| :|::|||||  |||||
Db  144 LRFSMALCDQEKTFRQQRKENIKENMKLLGPKKSEGLYSTRDVPVVAILGSGGGFRAMV  203

Qy  146 SLYGQLAGLKELGLLDCVSYITGASGSTWALANLYEDPEWSQKDLAGPTEL--LKTQVT  202
           ||||        |: .|  |   ||.|| | |||.|||  ::|| |   |    ||||||:
Db  204 GFSGVMKALYESGILDCATYLAGLSGSSWYMSTLYSHPDFPEK--GPEEINKELMKNVS  260

Qy  203 KNKLGVLAPSQLQRYRQELAERARLGYPSCFTNLWA-LINEALLHDEPHDHKLSDQREAL  261
           ::|||:| |  ||||||:||:    |::|:|| | || :||:| ||||:||||:|| ::
Db  261 YDPLLLTPQKIKRYVBSLWKKKSSGQPVTFTDIFGMLIGETLIHNRMNT-TLSSLKEKV  319

Qy  262 SHGQNPLPIYCALNTKGQSLTTFEFGEWCBFSPYEVGPPKYGAFIPSELFGSEFFMGQLM  321
           :: ||||   | | .|| || :|| |||   ||||  || | |||||  |||::|||  ||:
Db  320 NTAQCPLPLFTCLHVK-PDVSELMFADWVEFSPYEIGMAKIYGTFMAPDLFGSKFFMGTVV  378
```

```
CC       sn-2 position releasing arachidonic acid. Together with its
CC       lysophospholipid activity, it is implicated in the initiation of
CC       the inflammatory response.
CC    -!- CATALYTIC ACTIVITY: Phosphatidylcholine + H(2)O = 1-
CC       acylglycerophosphocholine + a fatty acid anion.
CC    -!- CATALYTIC ACTIVITY: 2-lysophosphatidylcholine + H(2)O =
CC       glycerophosphocholine + a fatty acid anion.
CC    -!- ENZYME REGULATION: Stimulated by agonists such as ATP, EGF,
CC       thrombin and bradykinin as well as by cytosolic Ca(2+).
CC    -!- SUBCELLULAR LOCATION: Cytoplasmic. Translocates to membrane
CC       vesicles in a calcium-dependent fashion.
CC    -!- DOMAIN: The N-terminal C2 domain, by its association with lipid
CC       membranes, mediates the regulation of CPLA2 by presenting the
CC       active site to its substrate in response to elevations of
CC       cytosolic Ca(2+) (By similarity).
CC    -!- PTM: Activated by phosphorylation on a serine residue (By
CC       similarity).
CC    -!- SIMILARITY: Contains 1 C2 domain.
CC   --------------------------------------------------------------------------
CC       This SWISS-PROT entry is copyright. It is produced through a collaboration
CC       between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC       the European Bioinformatics Institute. There are no restrictions on its
CC       use by non-profit institutions as long as its content is in no way
CC       modified and this statement is not removed. Usage by and for commercial
CC       entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC       or send an email to license@isb-sib.ch).
CC   --------------------------------------------------------------------------
DR   EMBL; M72394; AAB00796.1; -.
DR   EMBL; BC003816; AAH03816.1; -.
DR   HSSP; P47712; 1BCI.
DR   MGD; MGI:1195256; Pla2g4a.
DR   InterPro; IPR000008; C2.
DR   InterPro; IPR008973; C2_CalB.
DR   InterPro; IPR002642; PlAc.
DR   Pfam; PF00168; C2; 1.
DR   Pfam; PF01735; PLA2_B; 1.
DR   SMART; SM00239; C2; 1.
DR   SMART; SM00022; PLAc; 1.
DR   PROSITE; PS50004; C2_DOMAIN_2; 1.
KW   Hydrolase; Lipid degradation; Calcium; Phospholipid binding; Phosphorylation.
FT   DOMAIN       1    178       C2.
FT   DOMAIN       5    106       PHOSPHOLIPID BINDING (PROBABLE).
FT   MOD_RES    505    505       PHOSPHORYLATION (BY MAPK) (BY
FT                               SIMILARITY).
SQ   SEQUENCE   748 AA;  85222 MW;  49D12BB2911492A CRC64;

Query Match             18.5%;  Score  599.5;  DB 1;  Length 748;
Best Local Similarity   26.9%;  Pred. No. 1.4e-31;
Matches  172;  Conservative 126;  Mismatches 242;  Indels  99;  Gaps  22;

Qy      44  ESLSVAQAGVQWRDIGSLQPPPLGPKRFSCLSLPSSWDYRLRELA----VRLGFGPCAEE  99
                   :|:   | : ||  |||| || ||||||  ::||||    :|
Db     100  ETLGTATFPVSSMKVGEKKEVPFIFNQVTEMILEMS-----LEVCSCPDLRFSMALCDQE  154

Qy     100  QAFLSRRKQVVAAALRQAL--QLDGDLQEDEIPVVAIMATGGIRAMTSLYGQLAGLKE    156
            :: ::|  : :|||| ::.   :||||| ||   |||| |||  :.  |
Db     155  KTFRQQRKENIKENMKKLLGPKKSEGLYSTRDVPVVAILGSGGGFRAMVGFSGVMKALYE  214

Qy     157  LGLLDCVSYITGASGSTWALANLYEDPEWSQKDLAGPTEL---LKTQVTKNKLGVLAPSQ  213
            : : |    | :  |  :|:  |:|| || :| :||  ||      :|| ||  :| :.
Db     215  SGIILDCATYIAGLSGSTWYMSTLYSHPDFPEK--GPEEINEELMKNVSHNPLLLLTPQK  271

Qy     214  LQRYRQELAERARLGYPSCFTNLWA-LINEALLHDEPHDHKLSDQRBALSHGQNPLPIYC  272
            |: ||: |   |  : ||  | :     ||| |     |
Db     272  VKRYVBSLWKKKSSQPVTFTDIFGMLIGETLIQNR-MSMTLSSLKEKVNAARCPLPLFT  330

Qy     273  ALNTKGQSLTTFEFGEWCEFSPYEVGFPKYGAFIPSELFGSEFFMGQLMKRLPESRICFL  332
                :: :|:. :|||||||      : | : |||  || ::||||  ::|| ||: :|||
Db     331  CLHVK-PDVSBLMFADWVEFSPYEIGMAKYGTFMAPDLFGSKFFMGTVVKKYEENPLHFL  389

Qy     333  EGIWSNLYA------------ANLQDSL------YWASEPSQFWDRWRVRNQANLDK  370
                 :  | |            :: :|||     ::: :|   | :|| ::| :|:
Db     390  MGVWGSAFSILFNRVLGVSGSGQNKGSTMEEELENITAKHIVSNDSDSDDEAQGPKGTEN  449
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```
Qy     371  EQVPLLKIEPPSTAGRIAEFFTDLLTWRPL-------AQATHNFLRGLHFHKDYFQHP-  422
            |:.                                  |||||| |||:|| |||::
Db     450  EEAE--KEYQSDNQASWVHRMLMALVSDSALFNTREGRAGKVHNFMLGLNLNTSYPLSPL  507

Qy     423  -HFSTWKATTLDGLPNQLTPS--------------EP-----HLCLLDVGYLINTSCLPLLQ  464
             :|: :|  : || |:   :               |:      :|| ||: ||||:||||||
Db     508  RDFS----SQDSFDELDAAVADPDEFRIYEPLDVKSKKIHVVDSGLIFNLPYPLILR  562

Qy     465  PTRDVDLILSLDYNLHGA------FQQLQLLGRFCQEQGIPFPPISPSPEEQLQPRECHTF  519
            |  ::||| :||| | |        : | :|:||:::| |  :|:::|::||    ||| |
Db     563  PQRGVDLIISFDFSARPSDTSPPFKELLLAEKWAKMNKLPFPKIDPYVFDREGLKECYVF  622

Qy     520  SDPTCP----GAPAVLHF-------SSGV-RRTPEEAAAGEVNL-SSSDSPYHYTK  562
            |:| |     :|| ::           ||  | |: ||: ::|  ||| |||:||
Db     623  K-PKNPDVEKDCPTIIHFVLANINFRKYKAPGVLRETKEKEIADFDIFDDPESPFSTFN  681

Qy     563  VTYSQEDVDKLLHLTHYNVCNNQEQLLEALRQAVQRRRQ  601
            | ||:|:|  ||: | :|| || :|  :|:::|:||||||
Db     682  FQYPNQAFKRLHDLMYFNTLNNIDVIKDAIVESIEYRRQ  720
```

```
RESULT 4
PA24_CHICK
ID   PA24_CHICK     STANDARD;      PRT;   748 AA.
AC   P49147;
DT   01-FEB-1996 (Rel. 33, Created)
DT   01-FEB-1996 (Rel. 33, Last sequence update)
DT   28-FEB-2003 (Rel. 41, Last annotation update)
DE   Cytosolic phospholipase A2 (CPLA2) (Includes: Phospholipase A2
DE   (EC 3.1.1.4) (Phosphatidylcholine 2-acylhydrolase); Lysophospholipase
DE   (EC 3.1.1.5)].
GN   PLA2G4A OR PLA2G4 OR CPIA2.
OS   Gallus gallus (Chicken).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC   Gallus.
OX   NCBI_TaxID=9031;
RN   [1]
RP   SEQUENCE FROM N.A., AND CHARACTERIZATION.
RX   MEDLINE=94299545; PubMed=8027085;
RA   Nalefski E.A., Sultzman L.A., Martin D.M., Kriz R.W., Towler P.S.,
RA   Knopf J.L., Clark J.D.;
RT   "Delineation of two functionally distinct domains of cytosolic
RT   phospholipase A2, a regulatory Ca(2+)-dependent lipid-binding domain
RT   and a Ca(2+)-independent catalytic domain.";
RL   J. Biol. Chem. 269:18239-18249(1994).
CC   -!- FUNCTION: Selectively hydrolyzes arachidonyl phospholipids in the
CC       sn-2 position releasing arachidonic acid. Together with its
CC       lysophospholipid activity, it is implicated in the initiation of
CC       the inflammatory response.
CC   -!- CATALYTIC ACTIVITY: Phosphatidylcholine + H(2)O = 1-
CC       acylglycerophosphocholine + a fatty acid anion.
CC   -!- CATALYTIC ACTIVITY: 2-lysophosphatidylcholine + H(2)O =
CC       glycerophosphocholine + a fatty acid anion.
CC   -!- ENZYME REGULATION: Stimulated by agonists such as ATP, EGF,
CC       thrombin and bradykinin as well as by cytosolic Ca(2+).
CC   -!- SUBCELLULAR LOCATION: Cytoplasmic. Translocates to membrane
CC       vesicles in a calcium-dependent fashion. (By similarity).
CC   -!- DOMAIN: The N-terminal C2 domain, by its association with lipid
CC       membranes, mediates the regulation of CPLA2 by presenting the
CC       active site to its substrate in response to elevations of
CC       cytosolic Ca(2+) (By similarity).
CC   -!- PTM: Activated by phosphorylation on a serine residue (By
CC       similarity).
CC   -!- SIMILARITY: Contains 1 C2 domain.
CC   --------------------------------------------------------------------------
CC       This SWISS-PROT entry is copyright. It is produced through a collaboration
CC       between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC       the European Bioinformatics Institute. There are no restrictions on its
CC       use by non-profit institutions as long as its content is in no way
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CC       entities requires a license agreement (See http://www.isb-sib.ch/announce/
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CC
CC       or send an email to license@isb-sib.ch).
DR   EMBL; U10329; AAA53228.1; -.
DR   PIR; I50699; I50699.
DR   HSSP; P47712; 1BCI.
DR   InterPro; IPR000008; C2.
DR   InterPro; IPR008973; C2_CaLB.
DR   InterPro; IPR002642; PLAc.
DR   Pfam; PF00168; C2; 1.
DR   Pfam; PF01735; PLA2_B; 1.
DR   SMART; SM00239; C2; 1.
DR   SMART; SM00022; PLAc; 1.
DR   PROSITE; PS50004; C2_DOMAIN_2; 1.
KW   Hydrolase; Lipid degradation; Calcium; Phosphorylation.
FT   DOMAIN        1    178       PHOSPHOLIPID BINDING.
FT   DOMAIN        5    106       C2 DOMAIN.
FT   MOD_RES     505    505       PHOSPHORYLATION (BY MAPK) (BY
FT                                SIMILARITY).
SQ   SEQUENCE   748 AA;  84978 MW;  996A5256CA032F75 CRC64;

Query Match             18.4%;  Score 596;  DB 1;  Length 748;
Best Local Similarity   25.9%;  Pred. No. 2.7e-38;
Matches  166;  Conservative 129;  Mismatches 245;  Indels 100;  Gaps  20;

Qy    44 ESLSVAQAGVQWRDLGSLQPPLGFKRFSCLSLPSSWDYRLRELAVRLGFGPCAEEQAFL 103
         :|::|| ||:|    |::||:  :||     :::|| |                   |:
Db   100 ETLGMATFPISSLKLGEKKEVQLTFNNVTEMTLELSLEV-CSSTDLRFSMALCDEEKKFR 158

Qy   104 SRRKQVVAAALRQALQLDGD--LQEDEIPVVAIMATGGIRAMTSLYGQLAGLKELGLL 160
         :     :: |   |::|     |:|:|:   ||  |     |    :    | : :|||
Db   159 QQRKDNIMQSMKSFLGEENSKNLTTSRDVPVIAVLGSSGGFRAMVGFAGVMKALYESGVL 218

Qy   161 DCVSYITGASGSTWALANLYEDPEWSQKDLAGPTEL---LKTQVTKNKLGVLAPSQLQRY 217
         |  || :||| ||      |  ||   | |::|           :|| ||: :| | |:|
Db   219 DCATYIAGLSGSTWYMSTLYSHPDFPEK---GPKEINQELMNSVSHNPLLLLTPQKVKRY 275

Qy   218 RQELAERARLGYPSCFTNLWA-LINEALLHDEPHDHKLSDQREALSHGQNPLPIYCALNT 276
         |||  :|||| |    |||:     |:| | ||    |            |:| | :|||
Db   276 IEALWNKKSSGQPVTFTDIPGMLIGETLIHNR-MDTTLSDMKEKVSEAQCALPLFTCLHV 334

Qy   277 KGQSLTTFEFGEWCEFSPYEVGFPKYGAFIPSELFGSEFFMGQLMKRLPESRICFLEGIW 336
         |  || ||  | |  ||  ||:| |      |::|   |   :|:|:|   :|   |:|
Db   335 K-PDVSELMFADWVEFSPYEIGMAKYGTFMSPDLFGSKFFMGTVVKKYSENPLHFLMGVW 393

Qy   337 SNLYAANLQDSLYWASEPSQFWDRWVRNQANLDKEQVPLLKI---------EEP 381
          :|      :|      |:    |    : |::|     | |         :::
Db   394 GSAFSILFNRVLGVSNS-------QNKGPTMEEELENIRLKHLVSNDSSDSEDESQHP 444

Qy   382 PSTAGRIA--------EFFTDLL-------------TWRPLAQATHNFLRGLHFHKDYFQ 420
         |: | :::        ::|        ||  |       |                |:
Db   445 KGTENSEANEEYQNSSQESWVQRMLMALVGDSALFNTREGRAGKVHNFMLGLNLNSCYPL 504

Qy   421 HP--HFSTWKATTLDGL-------PNQ------LTPSEPHLCLLDVGYLINTSCLPLLQP 465
            :|::::  :::|:        |::       |      |::|   :|:::  | :|
Db   505 SPLADLLTQESVEEDELDAAVADPDEFERIYEPLDVKSKKIHIVDSGLTFNLPYPLIIRP 564

Qy   466 TRDVDLILSLDYNLHGA---FQQLQLLGRFCQEQGIPFPPISPSPEEQLQPRECHTF- 519
         ||  |:  ||| ||:||     :| :|  |  |||||  |:|  |||| |:| | :
Db   565 QRGVDLIISFDFSARPSDSSPPFKEILLAEKNAKMNKLPFFPKIDPNVFDREGLKECVVFK 624

Qy   520 -----SDPTCPGAPAVLHF--------SSGV-RRTPEEAAAGEVNL-SSSDSPYHYT 561
              ||:|   | |::||         :::|   :      | :::  ::::|: ||:
Db   625 PKDTSSEKDC---PTIIHFVLANINFRKYKAPGLPRESKEEKDFADFIFDDPNTPFSTF 681

Qy   562 KVTYSQEDVDKLLIHLTHYNVCNNQEQLLEALRQAVQRRRQ 601
         |  |    | |:  |:  |:|:      |:  |:| |:||:|
Db   682 NFQYPNEAFKRLRHDLMEFNTLNNLDVIKQAMMESIEYRKE 721
```

RESULT 5
PA24_RAT
ID   PA24_RAT   STANDARD;   PRT;   752 AA.
AC   P50393;

```
DT   01-OCT-1996 (Rel. 34, Created)
DT   01-OCT-1996 (Rel. 34, Last sequence update)
DT   28-FEB-2003 (Rel. 41, Last annotation update)
DE   Cytosolic phospholipase A2 (CPLA2) (Includes: Phospholipase A2
DE   (EC 3.1.1.4) (Phosphatidylcholine 2-acylhydrolase); Lysophospholipase
DE   (EC 3.1.1.5)].
GN   PLA2G4A OR PLA2G4 OR CPLA2.
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Brain;
RA   Owada Y., Tominaga T., Yoshimoto T., Kondo H.;
RT   "Molecular cloning of rat cDNA for cytosolic phospholipase A2 and the
RT   increased gene expression in the dentate gyrus following transient
RT   forebrain ischemia.";
RL   Brain Res. Mol. Brain Res. 25:364-368(1994).
RN   [2]
RP   ERRATUM.
RX   MEDLINE=95206125; PubMed=7898324;
RA   Owada Y., Tominaga T., Yoshimoto T., Kondo H.;
RL   Brain Res. Mol. Brain Res. 27:355-355(1994).
RN   [3]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Sprague-Dawley; TISSUE=Pancreatic islets;
RX   MEDLINE=9823459; PubMed=9555100;
RA   Ma Z., Ramanadham S., Hu Z., Turk J.;
RT   "Cloning and expression of a group IV cytosolic Ca2+-dependent
RT   phospholipase A2 from rat pancreatic islets. Comparison of the
RT   expressed activity with that of an islet group VI cytosolic Ca2+-
RT   independent phospholipase A2.";
RL   Biochim. Biophys. Acta 1391:384-400(1998).
CC   -!- FUNCTION: Selectively hydrolyzes arachidonyl phospholipids in the
CC       sn-2 position releasing arachidonic acid. Together with its
CC       lysophospholipid activity, it is implicated in the initiation of
CC       the inflammatory response.
CC   -!- CATALYTIC ACTIVITY: Phosphatidylcholine + H(2)O = 1-
CC       acylglycerophosphocholine + a fatty acid anion.
CC   -!- CATALYTIC ACTIVITY: 2-lysophosphatidylcholine + H(2)O =
CC       glycerophosphocholine + a fatty acid anion.
CC   -!- ENZYME REGULATION: Stimulated by agonists such as ATP, EGF,
CC       thrombin and bradykinin as well as by cytosolic Ca(2+).
CC   -!- SUBCELLULAR LOCATION: Cytoplasmic. Translocates to membrane
CC       vesicles in a calcium-dependent fashion (By similarity).
CC   -!- TISSUE SPECIFICITY: In brain tissue, expressed in low levels in
CC       olfactory mitral and granule cells, in hippocampal pyramidal
CC       cells and in dentate and cerebellar granule cells.
CC   -!- INDUCTION: Levels of rat CPLA2 are increased in dentate granule
CC       cells during ischemia.
CC   -!- DOMAIN: The N-terminal C2 domain, by its association with lipid
CC       membranes, mediates the regulation of CPLA2 by presenting the
CC       active site to its substrate in response to elevations of
CC       cytosolic Ca(2+) (By similarity).
CC   -!- PTM: Activated by phosphorylation on a serine residue (By
CC       similarity).
CC   -!- SIMILARITY: Contains 1 C2 domain.
CC   --------------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   --------------------------------------------------------------------------
DR   EMBL; S77829; AAB33847.1; -.
DR   EMBL; U38376; AAC15911.1; -.
DR   HSSP; P47712; 1BCI.
DR   InterPro; IPR000008; C2.
DR   InterPro; IPR008973; C2_CaLB.
DR   InterPro; IPR002642; PLAc.
```

DR   Pfam; PF00168; C2; 1.
DR   Pfam; PF01735; PLA2_B; 1.
DR   SMART; SM00239; C2; 1.
DR   SMART; SM00022; PLAc; 1.
DR   PROSITE; PS50004; C2_DOMAIN_2; 1.
KW   Hydrolase; Lipid degradation; Calcium; Phosphorylation.
FT   DOMAIN   1   178   PHOSPHOLIPID BINDING (PROBABLE).
FT   DOMAIN   5   106   C2 DOMAIN.
FT   MOD_RES   505   505   PHOSPHORYLATION (BY MAPK) (BY
FT   SIMILARITY).
FT   CONFLICT   139   139   C -> S (IN REF. 3).
FT   CONFLICT   159   159   R -> Q (IN REF. 3).
FT   CONFLICT   287   287   Q -> L (IN REF. 3).
FT   CONFLICT   308   310   MST -> IVP (IN REF. 3).
FT   CONFLICT   410   410   S -> L (IN REF. 3).
FT   CONFLICT   489   489   B -> V (IN REF. 3).
FT   CONFLICT   635   635   P -> T (IN REF. 3).
SQ   SEQUENCE   752 AA; 85706 MW; C68F71BB05FBF732 CRC64;

Query Match   18.4%; Score 594; DB 1; Length 752;
Best Local Similarity   26.9%; Pred. No. 3.8e-23;
Matches 171; Conservative 125; Mismatches 249; Indels 90; Gaps 21;

Qy   44 ESLSVAQGAVQWRDLGSLQPPLGFKRFSCLSLPSSWDYRLRELA----VRLGFGFGPCAEE 99
                 |:| |::| ||| :   :| |||:| :|:|
Db   100 ETLGTATFPVSSMKVGEKKEVPFIFNQVTEMILEMS-----LBVCSCPDLRFSMALCDQE 154

Qy   100 QAFLSRRKQVVAAALRQAL--QLDGDLQEDEIPVVAIMATGGIRAMTSLYGQLAGLKE 156
                ::||| :   ::|: ::: ||||| :||:|| |||
Db   155 KTFRRQRKENIKENMKKLLGPKKSEGLYSTRDVPVVALLGSGGGFRAMVGFSGVMKALYE 214

Qy   157 LGLLDCVSYITGASGSTWALANLYEDPEWSQKDLAGPTEL---LKTQVTKNKLGVLIAPSQ 213
                ||| || || ::||| ||: ||| ::||| | ||
Db   215 SGIIDCATTVAGLSGSTWYMSTLYSHPDFPEK---GPEEINEELMKNVSHNPLLLLTPQK 271

Qy   214 LQRYRQELAERARLGYPSCFTNLWA-LINEALLHDEPHDHKLSDQREALSHGQNLPIYC 272
                 ::|| :|| :|| | |:| |:::|:|: || :||: |||:||
Db   272 VKRYVESLWKKKSSGQPVTFTDIFGMLIGETLIQNR-MSTTLSSLKEKVSAARCPLPLFT 330

Qy   273 ALNTKGQSLTTFEFGEWCESPSPYEVGFPKYGAFIPSELFGSEFPMGQLMKRLPESRICFL 332
                :| || ||::| |:|||| ||::|:|:||:|: |::: |: | :
Db   331 CLHVK--PDVSELMFADWVEFSPYEIGMAKYGTFWTPDLFGSKFPMGTVVKKYENPLHFL 389

Qy   333 EGIWSNLYA-----------ANLQDSL------YWASEPSQFWDRWVRNQANLDK 370
                |||| | |:| ||:|:||:||| :| |
Db   390 MGVWGSAFSILFNRVLGVSGSQNKGSTMEEELENITAKHIVSNDSSDSDDEAQGPKGTEN 449

Qy   371 EQVPLLKIEPPSTAGRIAEFFTDLLTWRPL--------AQATHNFLRGLHFHKDYFQHP- 422
                ||: | :|| :||| | || | :|| ::|:|||||:|
Db   450 EDAE--REYQNDNQASWVHRMLMALVSDSALFNTREGRAGKEHNFMLGLNLNTSYPLSPL 507

Qy   423 -HFSTWKATTLDGL----------PNQ------LTPSEPHLCLLDVGVLINTSCLPLLQPTRD 468
                :| |::   :|| :|:: | ||:
Db   508 RDFSPQDSFDDELDAAVADPDEFFRIYEPLDVKSKKIHVVDSGLTFNLPYPLLIRPQRG 567

Qy   469 VDLILSLDYNLHGA-----FQQLQLGRFCQEQGIPFPPISPSPEEQLQPRECHTFSDPT 523
                ||:| :||| || :| :|:|| :|:   ::| | :|
Db   568 VDLIISFDFSARPSDTSPPFKELLLAEKWAKMNKLPFPKIDPYVFDREGLKBCYVFK-PK 626

Qy   524 CP---GAPAVLHF----------SSGV-RRTPEEAAAGEVNL-SSSDSPYHYTKVTYS 566
                || |:| :|| ::   :| :: | |
Db   627 NPDVEKDCPTIIHFVLANINFRKYKAPGVLRETKEKEIADFDIFDDPESPFSTFNFQYP 686

Qy   567 QEDVDKLLLHLTHYNVCNNQEQLLEALRQAVQRRRQ 601
                :|:| || :::|| :|::|:: |:||
Db   687 NQAFKRLHDLMYFNTLNNIDVIKDAIVESIEYRRQ 721

RESULT 6
PA24_BRARE   STANDARD;   PRT;   741 AA.
ID   PA24_BRARE
AC   P50392;
DT   01-OCT-1996 (Rel. 34, Created)

DT   01-OCT-1996 (Rel. 34, Last sequence update)
DT   15-MAR-2004 (Rel. 43, Last annotation update)
DE   Cytosolic phospholipase A2 (CPLA2) [Includes: Phospholipase A2
DE   (EC 3.1.1.4) (Phosphatidylcholine 2-acylhydrolase); Lysophospholipase
DE   (EC 3.1.1.5)].
GN   PLA2G4A OR PLA2G4 OR CPLA2.
OS   Brachydanio rerio (Zebrafish) (Danio rerio).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC   Cyprinidae; Danio.
OX   NCBI_TaxID=7955;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Embryo;
RX   MEDLINE=94299545; PubMed=8027085;
RA   Nalefski E.A., Sultzman L.A., Martin D.M., Kriz R.W., Towler P.S.,
RA   Knopf J.L., Clark J.D.;
RT   "Delineation of two functionally distinct domains of cytosolic
RT   phospholipase A2, a regulatory Ca(2+)-dependent lipid-binding domain
RT   and a Ca(2+)-independent catalytic domain.";
RL   J. Biol. Chem. 269:18239-18249(1994).
CC   -!- FUNCTION: selectively hydrolyzes arachidonyl phospholipids in the
CC   sn-2 position releasing arachidonic acid. Together with its
CC   lysophospholipid activity, it is implicated in the initiation of
CC   the inflammatory response.
CC   -!- CATALYTIC ACTIVITY: Phosphatidylcholine + H(2)O = 1-
CC   acylglycerophosphocholine + a fatty acid anion.
CC   -!- CATALYTIC ACTIVITY: 2-lysophosphatidylcholine + H(2)O =
CC   glycerophosphocholine + a fatty acid anion.
CC   -!- ENZYME REGULATION: Stimulated by agonists such as ATP, EGF,
CC   thrombin and bradykinin as well as by cytosolic Ca(2+).
CC   -!- SUBCELLULAR LOCATION: Cytoplasmic. Translocates to membrane
CC   vesicles in a calcium-dependent fashion (By similarity).
CC   -!- DOMAIN: The N-terminal C2 domain, by its association with lipid
CC   membranes, mediates the regulation of CPLA2 by presenting the
CC   active site to its substrate in response to elevations of
CC   cytosolic Ca(2+) (By similarity).
CC   -!- PTM: Activated by phosphorylation on a serine residue (By
CC   similarity).
CC   -!- SIMILARITY: Contains 1 C2 domain.
CC   --
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   --
DR   EMBL; U10330; AAA53229.1; -.
DR   PIR; B54908; B54908.
DR   HSSP; P47712; 1BCI.
DR   ZFIN; ZDB-GENE-990415-45; cpla2.
DR   InterPro; IPR000008; C2.
DR   InterPro; IPR008973; C2_CaLB.
DR   InterPro; IPR002642; PLAc.
DR   Pfam; PF00168; C2; 1.
DR   Pfam; PF01735; PLA2_B; 1.
DR   SMART; SM00239; C2; 1.
DR   SMART; SM00022; PLAc; 1.
DR   PROSITE; PS50004; C2_DOMAIN_2; 1.
KW   Hydrolase; Lipid degradation; Calcium; Phosphorylation.
FT   DOMAIN   1   172   PHOSPHOLIPID BINDING (PROBABLE).
FT   DOMAIN   1   100   C2 DOMAIN.
FT   MOD_RES   498   498   PHOSPHORYLATION (BY MAPK) (BY
FT   SIMILARITY).
SQ   SEQUENCE   741 AA; 83809 MW; 34896B1A8364A9D4 CRC64;

Query Match   17.7%;   Score 572; DB 1; Length 741;
Best Local Similarity   26.5%;   Pred. No. 1.9e-36;
Matches 154; Conservative 115; Mismatches 236; Indels 76; Gaps 144;

Qy   89 VRLGFGFGPCAEEQAFLSRRKQVVAAALRQALQLDG----DLQEDEIPVVAIMATGGGIRAM 144

```
Db   138 LRFSMTLCDQEKLFMQTRRDRVMLSIKKLLKMENPRFLPSSPREVPTAILGSGGFRAM 197
             :  |: |.:   |   |  |: .|::  |||:|::  |   :::: |||| |||
Qy   145 TSLYGQAGLKELGLLDCVSYITGASGSTWALANLYEDPEWSQKDLAGPTEL---LKTQV 201

Db   198 VGFSGVMKALYESGVFDCATYVAGLSGSTWYMSMLYSHPEFPAK---GPGDINKELMNRV 254
             : | : |||  ::| ||| | ||||||| :: | ::: |  |      :  : :|
Qy   202 TKNKLGVLAPSQLQRYRQELAERARLGYPSCFTNLWA-LINEALLHDEPHDHKLSDQREA 260

Db   255 SNNPLKLLLPQNINRYVKALWKKKSAGQPVTFTDIFGMLJIGETLIPGR-MNIKLSSLKGK 313
             :  |  ||: |:  ::   |:      |  || ||| :|:|  |||| ||:|: |||||
Qy   261 LSHGQNPLPIYCALNTKGQSLTTPEFGEWCEFSPYEVGPPKYGAFIPSELFGSRFFMGQL 320

Db   314 INEGQSPLPLFTCLHVK-PDVSELMFADWVEFSPYEIGMAKYGTFMSPGLFGSKFFMGSV 372
            :|||:::|||       :     ||:   ||||||:|   |||| |||||||:|||||:
Qy   321 MKRLPESRICFLEGIWSNLY---------------AANLQDSLYWASEPSQFWDRWVRNQ 365

Db   373 VKQYEENPLHFLMGVWGSAFSILFNRVLGVKETTSSSTMEEELEQIKPEHIVGDDSADNE 432
             :|: |: ||.|||:| ||||| ||:  |:   | || |::::::|   ::|  ::::
Qy   366 ANLDK---EQVPLLKIEEPPSTAGRIAEFFTDLL-------TWRPLAQATHNFLRGLHFH 415

Db   433 EETQRGGTESADAEDERQRHAQASWVQRMLTSIMGDTTLFTTREGRAGKVHNFMLGLNLN 492
            :: || :  :  || |   :    :    ::.:  |:  ||:  | |:|:|||:|:|:|:
Qy   416 KDYFQHPHFSTWKATTLDGLPNQLT-PSE--------PHLCLLDVGYLINTSCLPL 462

Db   493 STLPFSPFSGITHQTSLBEEVDAVTDPDEFERIYEPLDVKSKKIHVVDSGLITFNLPYPLI 552
             :| |: | :  |:|:|       :|| ||| | ||| ::|| ::::|: |||||| ||:
Qy   463 LQPTRDVDLILSLDYNLHGA-----FQQLQLLGRFCQEQGIFPPPISPSPEEQLQPRECH 517

Db   553 LRCQRGVDLIISDFSARPSDSSPPFKELLLAEKWARMNKLPFPKIDSKVFDREGLKECY 612
              | :  :: ::::|:: |||:|||:|::|   :: :: | |::  ::  |: .|::|
Qy   518 TF---SDPTCPGAPAVLHF-------SSGV-RRTPEBAAAGEVNL-SSSDSPYHY 560

Db   613 VFKPAKGDKNC---PTIIHFVLANINPRNFKAPGVPRDSDKDIEFGDFDIFDEPASPYST 669
            |:| |   ||     || ||: ||:|||||  |::   |::||  ::| :|  || ||||
Qy   561 TKVTYSQEDVDKLLHLTHYNVCNNQEQLLEALRQAVQRRRQ 601

Db   670 FNFKYNNQAFKRIHDLMEFNTLNNIEVIKEAIKDSILLRRE 710
```

RESULT 7
ALU8_HUMAN
```
ID   ALU8_HUMAN     STANDARD;      PRT;   591 AA.
AC   P39195;
DT   01-FEB-1995 (Rel. 31, Created)
DT   01-FEB-1995 (Rel. 31, Last sequence update)
DT   10-OCT-2003 (Rel. 42, Last annotation update)
DE   Alu subfamily SX sequence contamination warning entry.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=95021758; PubMed=7935834;
RA   Claverie J.-M., Makalowski W.;
RT   "Alu alert.";
RL   Nature 371:752-752 (1994).
RN   [2]
RP   CONCEPT.
RX   MEDLINE=92241891; PubMed=1572661;
RA   Claverie J.-M.;
RT   "Identifying coding exons by similarity search: alu-derived and other
RT   potentially misleading protein sequences.";
RL   Genomics 12:838-841 (1992).
RN   [3]
RP   ALU FAMILIES CLASSIFICATION.
RX   MEDLINE=88333009; PubMed=3138422;
RA   Quentin Y.;
RT   "The Alu family developed through successive waves of fixation
RT   closely connected with primate lineage history.";
RL   J. Mol. Evol. 27:194-202 (1988).
RN   [4]
RP   ALU FAMILIES CLASSIFICATION.
RX   MEDLINE=91178815; PubMed=1706781;
RA   Jurka J., Milosavljevic A.;
RT   "Reconstruction and analysis of human Alu genes.";
RL   J. Mol. Evol. 32:105-121(1991).
CC   -!- MISCELLANEOUS: VARIOUS ANALYSES (SEE REF.3 AND REF.4) INDICATE
CC       THAT ALU REPEATS FALL INTO 8 SUBFAMILIES. THEREFORE, 8 ALU WARNING
CC       CONSENSUS SEQUENCES HAVE BEEN CONSTITUTED THAT CONTAIN ALL SIX
CC       FRAMES CONCEPTUAL TRANSLATIONS OF EACH OF THESE CLASSES OF ALU
CC       REPEATS.
CC   -!- MISCELLANEOUS: ISOLATED 'X' INDICATES THE PRESENCE OF A STOP
CC       CODON. 'XXX' IS USED TO SEPARATE THE VARIOUS TRANSLATION PHASES.
CC   -!- CAUTION: This Alu entry is provided in order to avoid the further
CC       pollution of protein sequence databases with Alu-derived amino
CC       acid sequences.
CC   -!- CAUTION: Alu repetitive sequences are interspersed in human and
CC       primate genomes with an average spacing of 4 kb. Some of them are
CC       actively transcribed by pol III. Normal transcripts may contain
CC       Alu-derived sequences in 5' or 3' untranslated regions. However,
CC       cDNA libraries also contain partial and/or rearranged cDNAs
CC       ligated with Alu-derived sequence in any orientation. Although Alu
CC       elements (especially situated on the complementary strand) have a
CC       great potential to create additional/alternative exons,
CC       consideration should be given to the possibility that the presence
CC       of an Alu in an open reading frame may have resulted from a
CC       cloning artifact or may be due to misinterpretation of sequencing
CC       data. This point has been overlooked on several occasions, with
CC       the consequence of erroneous Alu-derived amino acid sequences
CC       being reported.
CC   -!- CAUTION: Any significant similarity of a putative protein sequence
CC       with an Alu-translated entry must be taken as a warning that a
CC       part of Alu repeat may have been artifactually included in the
CC       coding nucleotide sequence.
```

```
DR   EMBL; U14574; -; NOT_ANNOTATED_CDS.
KW   Hypothetical protein.
FT   DOMAIN        1     96       FRAME-1.
FT   DOMAIN      100    195       FRAME-2.
FT   DOMAIN      199    294       FRAME-3.
FT   DOMAIN      298    393       FRAME-4.
FT   DOMAIN      397    492       FRAME-5.
FT   DOMAIN      496    591       FRAME-6.
SQ   SEQUENCE   591 AA;  64395 MW;  AC8154AD8A6BB280 CRC64;

Query Match             7.0%;  Score 226.5;  DB 1;  Length 591;
Best Local Similarity  65.3%;  Pred. No. 8.8e-10;
Matches  47;  Conservative   1;  Mismatches  17;  Indels   7;  Gaps   1;

Qy     32 PAPCPFFFFEMESLSVAQAGVQWRDLGSLQPPPLGFKRFSCLSLPSSWDYRLRE---- 86
          |                       ||||||||||||||||||||||||||||
Db    488 PASARXXXFFETESRSVAQAGVQWRDLGSLQPPPGFKRFSCLSLPSSWDYRRAPPRPAN 547

Qy     87 --LAVRLGFGPC 96
            ||  |  | |
Db    548 FCIFSRDGVSPC 559
```

RESULT 8
ALU2_HUMAN
```
ID   ALU2_HUMAN     STANDARD;      PRT;   587 AA.
AC   P39189;
DT   01-FEB-1995 (Rel. 31, Created)
DT   01-FEB-1995 (Rel. 31, Last sequence update)
DT   10-OCT-2003 (Rel. 42, Last annotation update)
DE   Alu subfamily SB sequence contamination warning entry.
```

OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=95021758; PubMed=7935834;
RA   Claverie J.-M., Makalowski W.;
RT   "Alu alert.";
RL   Nature 371:752-752 (1994).
RN   [2]
RP   CONCEPT.
RX   MEDLINE=92241891; PubMed=1572661;
RA   Claverie J.-M.;
RT   "Identifying coding exons by similarity search: alu-derived and other
RT   potentially misleading protein sequences.";
RL   Genomics 12:838-841(1992).
RN   [3]
RP   ALU FAMILIES CLASSIFICATION.
RX   MEDLINE=88333009; PubMed=3138422;
RA   Quentin Y.;
RT   "The Alu family developed through successive waves of fixation
RT   closely connected with primate lineage history.";
RL   J. Mol. Evol. 27:194-202 (1988).
RN   [4]
RP   ALU FAMILIES CLASSIFICATION.
RX   MEDLINE=91178815; PubMed=1706781;
RA   Jurka J., Milosavljevic A.;
RT   "Reconstruction and analysis of human Alu genes.";
RL   J. Mol. Evol. 32:105-121(1991).
CC   -!- MISCELLANEOUS: VARIOUS ANALYSES (SEE REF.3 AND REF.4) INDICATE
CC   THAT ALU REPEATS FALL INTO 8 SUBFAMILIES. THEREFORE, 8 ALU WARNING
CC   CONSENSUS SEQUENCES HAVE BEEN CONSTITUTED THAT CONTAIN ALL SIX
CC   FRAMES CONCEPTUAL TRANSLATIONS OF EACH OF THESE CLASSES OF ALU
CC   REPEATS.
CC   -!- MISCELLANEOUS: ISOLATED 'X' INDICATES THE PRESENCE OF A STOP
CC   CODON, 'XXX' IS USED TO SEPARATE THE VARIOUS TRANSLATION PHASES.
CC   -!- CAUTION: This Alu entry is provided in order to avoid the further
CC   pollution of protein sequence databases with Alu-derived amino
CC   acid sequences.
CC   -!- CAUTION: Alu repetitive sequences are interspersed in human and
CC   primate genomes with an average spacing of 4 kb. Some of them are
CC   actively transcribed by pol III. Normal transcripts may contain
CC   Alu-derived sequences in 5' or 3', untranslated regions. However,
CC   cDNA libraries also contain partial and/or rearranged cDNAs
CC   ligated with Alu-derived sequence in any orientation. Although Alu
CC   elements (especially situated on the complementary strand) have a
CC   great potential to create additional/alternative exons,
CC   consideration should be given to the possibility that the presence
CC   of an Alu in an open reading frame may have resulted from a
CC   cloning artifact or may be due to misinterpretation of sequencing
CC   data. This point has been overlooked on several occasions, with
CC   the consequence of erroneous Alu-derived amino acid sequences
CC   being reported.
CC   -!- CAUTION: Any significant similarity of a putative protein sequence
CC   with an Alu-translated entry must be taken as a warning that a
CC   part of Alu repeat may have been artifactually included in the
CC   coding nucleotide sequence.
CC   ---
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---
DR   EMBL; U14568; -; NOT_ANNOTATED_CDS.
KW   Hypothetical protein.
FT   DOMAIN   1   96   FRAME-1.
FT   DOMAIN   100   194   FRAME-2.
FT   DOMAIN   198   292   FRAME-3.
FT   DOMAIN   296   391   FRAME-4.
FT   DOMAIN   395   489   FRAME-5.
FT   DOMAIN   493   587   FRAME-6.
SQ   SEQUENCE   587 AA;   63703 MW; 3EAAB3E3E3929203 CRC64;

Query Match   6.2%; Score 199.5; DB 1; Length 587;
Best Local Similarity 65.6%; Pred. No. 1.1e-07;
Matches   42; Conservative   1; Mismatches   14; Indels   7; Gaps   1;

Qy   40 FFEMESLSVAQAGVQWRDLGSLQPPLGFKRFSCLSLPSSWDYRLRE------LAVRLG 92
            |||||||||||||||||||||||||||||||||||||||||||||| : ||
Db   493 FFETESRSVAQAGVQWRDLGSLQAPPGFTPFSCLSLPSSWDYRRPPRPANFCIFSRDG 552

Qy   93 FGPC 96
            ||
Db   553 VSPC 556

RESULT 9
ALU7_HUMAN
ID   ALU7_HUMAN   STANDARD;   PRT;   593 AA.
AC   P39194;
DT   01-FEB-1995 (Rel. 31, Created)
DT   01-FEB-1995 (Rel. 31, Last sequence update)
DT   10-OCT-2003 (Rel. 42, Last annotation update)
DE   Alu subfamily SQ sequence contamination warning entry.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=95021758; PubMed=7935834;
RA   Claverie J.-M., Makalowski W.;
RT   "Alu alert.";
RL   Nature 371:752-752(1994).
RN   [2]
RP   CONCEPT.
RX   MEDLINE=92241891; PubMed=1572661;
RA   Claverie J.-M.;
RT   "Identifying coding exons by similarity search: alu-derived and other
RT   potentially misleading protein sequences.";
RL   Genomics 12:838-841(1992).
RN   [3]
RP   ALU FAMILIES CLASSIFICATION.
RX   MEDLINE=88333009; PubMed=3138422;
RA   Quentin Y.;
RT   "The Alu family developed through successive waves of fixation
RT   closely connected with primate lineage history.";
RL   J. Mol. Evol. 27:194-202(1988).
RN   [4]
RP   ALU FAMILIES CLASSIFICATION.
RX   MEDLINE=91178815; PubMed=1706781;
RA   Jurka J., Milosavljevic A.;
RT   "Reconstruction and analysis of human Alu genes.";
RL   J. Mol. Evol. 32:105-121(1991).
CC   -!- MISCELLANEOUS: VARIOUS ANALYSES (SEE REF.3 AND REF.4) INDICATE
CC   THAT ALU REPEATS FALL INTO 8 SUBFAMILIES. THEREFORE, 8 ALU WARNING
CC   CONSENSUS SEQUENCES HAVE BEEN CONSTITUTED THAT CONTAIN ALL SIX
CC   FRAMES CONCEPTUAL TRANSLATIONS OF EACH OF THESE CLASSES OF ALU
CC   REPEATS.
CC   -!- MISCELLANEOUS: ISOLATED 'X' INDICATES THE PRESENCE OF A STOP
CC   CODON, 'XXX' IS USED TO SEPARATE THE VARIOUS TRANSLATION PHASES.
CC   -!- CAUTION: This Alu entry is provided in order to avoid the further
CC   pollution of protein sequence databases with Alu-derived amino
CC   acid sequences.
CC   -!- CAUTION: Alu repetitive sequences are interspersed in human and
CC   primate genomes with an average spacing of 4 kb. Some of them are
CC   actively transcribed by pol III. Normal transcripts may contain
CC   Alu-derived sequences in 5' or 3', untranslated regions. However,
CC   cDNA libraries also contain partial and/or rearranged cDNAs
CC   ligated with Alu-derived sequence in any orientation. Although Alu
CC   elements (especially situated on the complementary strand) have a
CC   great potential to create additional/alternative exons,

RL   J. Mol. Evol. 27:194-202 (1988).
RN   [4]
RP   ALU FAMILIES CLASSIFICATION.
RX   MEDLINE=91178815; PubMed=1706781;
RA   Jurka J., Milosavljevic A.;
RT   "Reconstruction and analysis of human Alu genes.";
RL   J. Mol. Evol. 32:105-121(1991).
CC   -!- MISCELLANEOUS: VARIOUS ANALYSES (SEE REF.3 AND REF.4) INDICATE
CC   THAT ALU REPEATS FALL INTO 8 SUBFAMILIES. THEREFORE, 8 ALU WARNING
CC   CONSENSUS SEQUENCES HAVE BEEN CONSTITUTED THAT CONTAIN ALL SIX
CC   FRAMES CONCEPTUAL TRANSLATIONS OF EACH OF THESE CLASSES OF ALU
CC   REPEATS.
CC   -!- MISCELLANEOUS: ISOLATED 'X' INDICATES THE PRESENCE OF A STOP
CC   CODON. 'XXX' IS USED TO SEPARATE THE VARIOUS TRANSLATION PHASES.
CC   -!- CAUTION: This Alu entry is provided in order to avoid the further
CC   pollution of protein sequence databases with Alu-derived amino
CC   acid sequences.
CC   -!- CAUTION: Alu repetitive sequences are interspersed in human and
CC   primate genomes with an average spacing of 4 kb. Some of them are
CC   actively transcribed by pol III. Normal transcripts may contain
CC   Alu-derived sequences in 5' or 3' untranslated regions. However,
CC   cDNA libraries also contain partial and/or rearranged cDNAs
CC   ligated with Alu-derived sequence in any orientation. Although Alu
CC   elements (especially situated on the complementary strand) have a
CC   great potential to create additional/alternative exons,
CC   consideration should be given to the possibility that the presence
CC   of an Alu in an open reading frame may have resulted from a
CC   cloning artifact or may be due to misinterpretation of sequencing
CC   data. This point has been overlooked on several occasions, with
CC   the consequence of erroneous Alu-derived amino acid sequences
CC   being reported.
CC   -!- CAUTION: Any significant similarity of a putative protein sequence
CC   with an Alu-translated entry must be taken as a warning that a
CC   part of Alu repeat may have been artifactually included in the
CC   coding nucleotide sequence.

DR   EMBL; U14569; -; NOT_ANNOTATED_CDS.
KW   Hypothetical protein.
FT   DOMAIN   1   96   FRAME-1.
FT   DOMAIN   100   194   FRAME-2.
FT   DOMAIN   198   292   FRAME-3.
FT   DOMAIN   296   391   FRAME-4.
FT   DOMAIN   395   489   FRAME-5.
FT   DOMAIN   493   587   FRAME-6.
SQ   SEQUENCE   587 AA; 63573 MW; B5C415726DEF235 CRC64;

Query Match   6.1%; Score 198; DB 1; Length 587;
Best Local Similarity 86.4%; Pred. No. 1.4e-07;
Matches   38; Conservative   0; Mismatches   6; Indels   0; Gaps   0;

Qy   40 FFEMESLSVAQAGVQWRDLGSLQPPPLGFKRFSCLSLPSSWDYR 83
               |||:|| ||||||||||||||||||| || ||||||||||||||
Db   493 FFETESRSVAQAGVQWRDLGSLQAPPGFTPFSCLSLPSSWDYR 536

RESULT 11
ALU6_HUMAN
ID   ALU6_HUMAN   STANDARD;   PRT;   593 AA.
AC   P39193;
DT   01-FEB-1995 (Rel. 31, Created)
DT   01-FEB-1995 (Rel. 31, Last sequence update)
DT   10-OCT-2003 (Rel. 42, Last annotation update)
DE   Alu subfamily SP sequence contamination warning entry.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

CC   consideration should be given to the possibility that the presence
CC   of an Alu in an open reading frame may have resulted from a
CC   cloning artifact or may be due to misinterpretation of sequencing
CC   data. This point has been overlooked on several occasions, with
CC   the consequence of erroneous Alu-derived amino acid sequences
CC   being reported.
CC   -!- CAUTION: Any significant similarity of a putative protein sequence
CC   with an Alu-translated entry must be taken as a warning that a
CC   part of Alu repeat may have been artifactually included in the
CC   coding nucleotide sequence.

DR   EMBL; U14573; -; NOT_ANNOTATED_CDS.
KW   Hypothetical protein.
FT   DOMAIN   1   97   FRAME-1.
FT   DOMAIN   101   196   FRAME-2.
FT   DOMAIN   200   295   FRAME-3.
FT   DOMAIN   299   395   FRAME-4.
FT   DOMAIN   399   494   FRAME-5.
FT   DOMAIN   498   593   FRAME-6.
SQ   SEQUENCE   593 AA; 64417 MW; 54A4F50F33A6089F CRC64;

Query Match   6.2%; Score 199.5; DB 1; Length 593;
Best Local Similarity 63.1%; Pred. No. 1.1e-07;
Matches   41; Conservative   1; Mismatches   16; Indels   7; Gaps   1;

Qy   39 FFFEMESLSVAQAGVQWRDLGSLQPPPLGFKRFSCLSLPSSWDYRLRE-----LAVRL 91
               |||||||||||||||||||||||||||| ||||||||||||| :   :
Db   299 FFLRRSFALVAQAGVQWRDLGSLQPPPGFKRFSCLSLPSSWDYRRPPRPANFCIFSRD 358

Qy   92 GFGPC 96
Db   359 GVSPC 363

RESULT 10
ALU3_HUMAN
ID   ALU3_HUMAN   STANDARD;   PRT;   587 AA.
AC   P39190;
DT   01-FEB-1995 (Rel. 31, Created)
DT   01-FEB-1995 (Rel. 31, Last sequence update)
DT   10-OCT-2003 (Rel. 42, Last annotation update)
DE   Alu subfamily SB1 sequence contamination warning entry.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=95021758; PubMed=7935834;
RA   Claverie J.-M., Makalowski W.;
RT   "Alu alert.";
RL   Nature 371:752-752(1994).
RN   [2]
RP   CONCEPT.
RX   MEDLINE=92241891; PubMed=1572661;
RA   Claverie J.-M.;
RT   "Identifying coding exons by similarity search: alu-derived and other
RT   potentially misleading protein sequences.";
RL   Genomics 12:838-841(1992).
RN   [3]
RP   ALU FAMILIES CLASSIFICATION.
RX   MEDLINE=88333009; PubMed=3138422;
RA   Quentin Y.;
RT   "The Alu family developed through successive waves of fixation
RT   closely connected with primate lineage history.";

```
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=95021758; PubMed=7935834;
RA   Claverie J.-M., Makalowski W.;
RT   "Alu alert.";
RL   Nature 371:752-752(1994).
RN   [2]
RP   CONCEPT.
RX   MEDLINE=92241891; PubMed=1572661;
RA   Claverie J.-M.;
RT   "Identifying coding exons by similarity search: alu-derived and other
RT   potentially misleading protein sequences.";
RL   Genomics 12:838-841(1992).
RN   [3]
RP   ALU FAMILIES CLASSIFICATION.
RX   MEDLINE=88333009; PubMed=3138422;
RA   Quentin Y.;
RT   "The Alu family developed through successive waves of fixation
RT   closely connected with primate lineage history.";
RL   J. Mol. Evol. 27:194-202(1988).
RN   [4]
RP   ALU FAMILIES CLASSIFICATION.
RX   MEDLINE=91178815; PubMed=1706781;
RA   Jurka J., Milosavljevic A.;
RT   "Reconstruction and analysis of human Alu genes.";
RL   J. Mol. Evol. 32:105-121(1991).
CC   -!- MISCELLANEOUS: VARIOUS ANALYSES (SEE REF.3 AND REF.4) INDICATE
CC       THAT ALU REPEATS FALL INTO 8 SUBFAMILIES. THEREFORE, 8 ALU WARNING
CC       CONSENSUS SEQUENCES HAVE BEEN CONSTITUTED THAT CONTAIN ALL SIX
CC       FRAMES CONCEPTUAL TRANSLATIONS OF EACH OF THESE CLASSES OF ALU
CC       REPEATS.
CC   -!- MISCELLANEOUS: ISOLATED 'X' INDICATES THE PRESENCE OF A STOP
CC       CODON. 'XXX' IS USED TO SEPARATE THE VARIOUS TRANSLATION PHASES.
CC   -!- CAUTION: This Alu entry is provided in order to avoid the further
CC       pollution of protein sequence databases with Alu-derived amino
CC       acid sequences.
CC   -!- CAUTION: Alu repetitive sequences are interspersed in human and
CC       primate genomes with an average spacing of 4 kb. Some of them are
CC       actively transcribed by pol III. Normal transcripts may contain
CC       Alu-derived sequences in 5' or 3' untranslated regions. However,
CC       cDNA libraries also contain partial and/or rearranged cDNAs
CC       ligated with Alu-derived sequence in any orientation. Although Alu
CC       elements (especially situated on the complementary strand) have a
CC       great potential to create additional/alternative exons,
CC       consideration should be given to the possibility that the presence
CC       of an Alu in an open reading frame may have resulted from a
CC       cloning artifact or may be due to misinterpretation of sequencing
CC       data. This point has been overlooked on several occasions, with
CC       the consequence of erroneous Alu-derived amino acid sequences
CC       being reported.
CC   -!- CAUTION: Any significant similarity of a putative protein sequence
CC       with an Alu-translated entry must be taken as a warning that a
CC       part of Alu repeat may have been artifactually included in the
CC       coding nucleotide sequence.
CC   --------------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   --------------------------------------------------------------------------
DR   EMBL; U14572; -; NOT_ANNOTATED_CDS.
KW   Hypothetical protein.
FT   DOMAIN         1     97       FRAME-1.
FT   DOMAIN       101    196       FRAME-2.
FT   DOMAIN       200    295       FRAME-3.
FT   DOMAIN       299    395       FRAME-4.
FT   DOMAIN       399    494       FRAME-5.
FT   DOMAIN       498    593       FRAME-6.
```

```
SQ   SEQUENCE   593 AA;   64603 MW;   136EF344AACD12A2 CRC64;

     Query Match             6.0%;
     Best Local Similarity  61.5%;   Score 192.5;   DB 1;   Length 593;
     Matches   40;   Conservative    1;   Mismatches   17;   Indels    7;   Gaps    1;

Qy     39  FFFEMESLSVAQAGVQWRDLGSLQPPPLGFKRFSCLSLPSSWDYLRLE------LAVRL  91
                ||||||||| ||||||||||||  |||||||||||||||||||||      : |||||
Db    299  FFLRRSFALVAQAGVQWRDLGSPQPPPGFKRFSCLSLPSSWDYRHAPPRPANFCIFSRD 358

Qy     92  GFGPC  96
               |||||
Db    359  GVSPC 363
```

```
RESULT 12
ALU5_HUMAN
ID   ALU5_HUMAN    STANDARD;    PRT;    585 AA.
AC   P39192;
DT   01-FEB-1995 (Rel. 31, Created)
DT   01-FEB-1995 (Rel. 31, Last sequence update)
DT   10-OCT-2003 (Rel. 42, Last annotation update)
DE   Alu subfamily SC sequence contamination warning entry.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=9021758; PubMed=7935834;
RA   Claverie J.-M., Makalowski W.;
RT   "Alu alert.";
RL   Nature 371:752-752(1994).
RN   [2]
RP   CONCEPT.
RX   MEDLINE=92241891; PubMed=1572661;
RA   Claverie J.-M.;
RT   "Identifying coding exons by similarity search: alu-derived and other
RT   potentially misleading protein sequences.";
RL   Genomics 12:838-841(1992).
RN   [3]
RP   ALU FAMILIES CLASSIFICATION.
RX   MEDLINE=88333009; PubMed=3138422;
RA   Quentin Y.;
RT   "The Alu family developed through successive waves of fixation
RT   closely connected with primate lineage history.";
RL   J. Mol. Evol. 27:194-202(1988).
RN   [4]
RP   ALU FAMILIES CLASSIFICATION.
RX   MEDLINE=91178815; PubMed=1706781;
RA   Jurka J., Milosavljevic A.;
RT   "Reconstruction and analysis of human Alu genes.";
RL   J. Mol. Evol. 32:105-121(1991).
CC   -!- MISCELLANEOUS: VARIOUS ANALYSES (SEE REF.3 AND REF.4) INDICATE
CC       THAT ALU REPEATS FALL INTO 8 SUBFAMILIES. THEREFORE, 8 ALU WARNING
CC       CONSENSUS SEQUENCES HAVE BEEN CONSTITUTED THAT CONTAIN ALL SIX
CC       FRAMES CONCEPTUAL TRANSLATIONS OF EACH OF THESE CLASSES OF ALU
CC       REPEATS.
CC   -!- MISCELLANEOUS: ISOLATED 'X' INDICATES THE PRESENCE OF A STOP
CC       CODON, 'XXX' IS USED TO SEPARATE THE VARIOUS TRANSLATION PHASES.
CC   -!- CAUTION: This Alu entry is provided in order to avoid the further
CC       pollution of protein sequence databases with Alu-derived amino
CC       acid sequences.
CC   -!- CAUTION: Alu repetitive sequences are interspersed in human and
CC       primate genomes with an average spacing of 4 kb. Some of them are
CC       actively transcribed by pol III. Normal transcripts may contain
CC       Alu-derived sequences in 5' or 3' untranslated regions. However,
CC       cDNA libraries also contain partial and/or rearranged cDNAs
CC       ligated with Alu-derived sequence in any orientation. Although Alu
CC       elements (especially situated on the complementary strand) have a
CC       great potential to create additional/alternative exons,
CC       consideration should be given to the possibility that the presence
CC       of an Alu in an open reading frame may have resulted from a
```

```
CC    cloning artifact or may be due to misinterpretation of sequencing
CC    data. This point has been overlooked on several occasions, with
CC    the consequence of erroneous Alu-derived amino acid sequences
CC    being reported.
CC -!- CAUTION: Any significant similarity of a putative protein sequence
CC    with an Alu-translated entry must be taken as a warning that a
CC    part of Alu repeat may have been artifactually included in the
CC    coding nucleotide sequence.
CC    --------------------------------------------------------------------------
CC    This SWISS-PROT entry is copyright. It is produced through a collaboration
CC    between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC    the European Bioinformatics Institute. There are no restrictions on its
CC    use by non-profit institutions as long as its content is in no way
CC    modified and this statement is not removed. Usage by and for commercial
CC    entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC    or send an email to license@isb-sib.ch).
CC    --------------------------------------------------------------------------
DR    EMBL; U14571; -; NOT_ANNOTATED_CDS.
KW    Hypothetical protein.
FT    DOMAIN      1     95       FRAME-1.
FT    DOMAIN     99    193       FRAME-2.
FT    DOMAIN    197    291       FRAME-3.
FT    DOMAIN    295    389       FRAME-4.
FT    DOMAIN    393    487       FRAME-5.
FT    DOMAIN    491    585       FRAME-6.
SQ    SEQUENCE  585 AA;  63957 MW;  46EEBC4F493650A7 CRC64;

Query Match             5.9%;  Score 191;  DB 1;  Length 585;
Best Local Similarity  31.7%;  Pred. No. 4.9e-07;
Matches   71;  Conservative   20;  Mismatches   63;  Indels   70;  Gaps   10;

Qy     39 FFFEMESLSVAQAGVQWRDLGSLQPPPLGFKRFSCLSLPSSWDYRLRE------LAVRL 91
          ||| ||||||||||||||||||||||||||||||||||||||        ||||
Db    393 FFXDGVSL-CRQAGVQWRDLGSLQPPPGFKRFSCLSLPSSWDYRRAPPRPANFCIFSRD 451

Qy     92 GFGPCAEEQAFLSRRKQVVAAALRQALQLQGDIPVVAIMATGGIRAMTSLYGQL 151
          |   |                 ||  |  ||   |            ||||
Db    452 GVSPCWP----------------GWSRSLDLVIRPPRPPKVL-----GLQAXATAPGXX 489

Qy    152 AGL----KELGLLDCVSVITGASGSTWALANL---YEDPEWSQKDLAGPTE------- 195
          |||         |  |   |                        | :|
Db    490 XFFETESRSVARLEC------SGAISAHCNLRLPGSSDSPASASRVAGTTGARHHAQLI 542

Qy    196 ---LLKT--QVTKNKLGVLAPSQLQRYRQELAERARLGYPSCF 233
          |      |   :| : | :| |           :|
Db    543 FVFLVETGFHHVGQDGLDLLT----------SXSARLGLPKCW 575

RESULT 13
PLB4_SCHPO
ID    PLB4_SCHPO     STANDARD;      PRT;   673 AA.
AC    Q9P327;
DT    10-OCT-2003 (Rel. 42, Created)
DT    10-OCT-2003 (Rel. 42, Last sequence update)
DT    10-OCT-2003 (Rel. 42, Last annotation update)
DE    Putative lysophospholipase C977.09c precursor (EC 3.1.1.5)
DE    (Phospholipase B).
GN    SPAC977.09C OR SPAC1348.10C.
OS    Schizosaccharomyces pombe (Fission yeast).
OC    Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
OC    Schizosaccharomycetales; Schizosaccharomycetaceae;
OC    Schizosaccharomyces.
OX    NCBI_TaxID=4896;
RN    [1]
RP    SEQUENCE FROM N.A.
RC    STRAIN=972;
RX    MEDLINE=21848401; PubMed=11859360;
RA    Wood V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,
RA    Sgouros J., Peat N., Hayles J., Baker S., Basham D., Bowman S.,
RA    Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,
RA    Collins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A.,
RA    Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,
RA    Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,
RA    James K., Jones L., Jones M., Leather S., McDonald S., McLean J.,
RA    Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,
RA    Oliver K., O'Neil S., Pearson D., Quail M.A., Rabbinowitsch E.,
RA    Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,
RA    Skelton J., Simmonds M., Squares R., Squares S., Stevens K.,
RA    Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,
RA    Woodward J., Volckaert G., Aert R., Robben J., Grymonprez B.,
RA    Weltjens I., Vanstreels E., Rieger M., Schaefer M., Mueller-Auer S.,
RA    Gabel C., Fuchs M., Fritzc C., Holzer E., Moestl D., Hilbert H.,
RA    Borzym K., Langer I., Beck A., Lehrach H., Reinhardt R., Pohl T.M.,
RA    Eger P., Zimmermann W., Wedler H., Wambutt R., Purnelle B.,
RA    Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S.,
RA    Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
RA    Lucas M., Rochet M., Gaillardin C., Tallada V.A., Garzon A., Thode G.,
RA    Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,
RA    Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L.,
RA    Cerrutti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J.,
RA    Shpakovski G.V., Ussery D., Barrell B.G., Nurse P.;
RT    "The genome sequence of Schizosaccharomyces pombe.";
RL    Nature 415:871-880(2002).
CC -!- FUNCTION: Catalyzes the release of fatty acids from
CC    lysophospholipids (By similarity).
CC -!- CATALYTIC ACTIVITY: 2-lysophosphatidylcholine + H(2)O =
CC    glycerophosphocholine + a fatty acid anion.
CC -!- SUBCELLULAR LOCATION: Secreted (Probable).
CC -!- SIMILARITY: Belongs to the lysophospholipase family.
CC    --------------------------------------------------------------------------
CC    This SWISS-PROT entry is copyright. It is produced through a collaboration
CC    between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC    the European Bioinformatics Institute. There are no restrictions on its
CC    use by non-profit institutions as long as its content is in no way
CC    modified and this statement is not removed. Usage by and for commercial
CC    entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC    or send an email to license@isb-sib.ch).
CC    --------------------------------------------------------------------------
DR    EMBL; AL358912; CAB94277.1; -.
DR    EMBL; AL137130; CAB69631.1; -.
DR    PIR; T50281; T50281.
DR    GeneDB_SPombe; SPAC977.09C; -.
DR    InterPro; IPR001179; FKBP_PPIase.
DR    InterPro; IPR002642; PLAC.
DR    Pfam; PF01735; PLA2_B; 1.
DR    SMART; SM00022; PLAc; 1.
KW    Hypothetical protein; Lipid degradation; Hydrolase; Glycoprotein;
KW    signal.
FT    SIGNAL        1     19       POTENTIAL.
FT    CHAIN        20    673       PUTATIVE LYSOPHOSPHOLIPASE C977.09C.
FT    CARBOHYD     72     72       N-LINKED (GLCNAC...)  (POTENTIAL).
FT    CARBOHYD    125    125       N-LINKED (GLCNAC...)  (POTENTIAL).
FT    CARBOHYD    191    191       N-LINKED (GLCNAC...)  (POTENTIAL).
FT    CARBOHYD    194    194       N-LINKED (GLCNAC...)  (POTENTIAL).
FT    CARBOHYD    272    272       N-LINKED (GLCNAC...)  (POTENTIAL).
FT    CARBOHYD    301    301       N-LINKED (GLCNAC...)  (POTENTIAL).
FT    CARBOHYD    374    374       N-LINKED (GLCNAC...)  (POTENTIAL).
FT    CARBOHYD    404    404       N-LINKED (GLCNAC...)  (POTENTIAL).
FT    CARBOHYD    409    409       N-LINKED (GLCNAC...)  (POTENTIAL).
FT    CARBOHYD    481    481       N-LINKED (GLCNAC...)  (POTENTIAL).
FT    CARBOHYD    516    516       N-LINKED (GLCNAC...)  (POTENTIAL).
FT    CARBOHYD    545    545       N-LINKED (GLCNAC...)  (POTENTIAL).
FT    CARBOHYD    574    574       N-LINKED (GLCNAC...)  (POTENTIAL).
SQ    SEQUENCE  673 AA;  74595 MW;  B39A773E76CD694B CRC64;

Query Match             5.7%;  Score 186;  DB 1;  Length 673;
Best Local Similarity  21.1%;  Pred. No. 1.5e-06;
Matches  148;  Conservative   90;  Mismatches  245;  Indels  218;  Gaps   35;

Qy      3 FVELSPTLALCLERV-ASHLTDTGLLVLFCPAPCPFFFFEMESLSVAQAGVQWRDLGSL 61
          |  ||||| || |         |  |                 || |
Db     11 FVQISLTLAYPPGRVEISEIYD------FE-ESSSYKGQDIDTSVLYTL          52

Qy     62 -QPPPLGFKR----FSCLSLPSSWDYRLRELAVRLGFGPCAEEQAFLSRRKQVVAAALR 115
          :   : :      :                       :   | : | :|    :| |
Db     53 SRKRKPALVKRSTDASYAPFNVTCSNDLLRPASEGLNEG----EQSYINKRISKVNSELR 108
```

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Qy  116 QAL------QLDGDLQEDEIPVAIMATGGGIRAMTSLYGQLAGLKE------LGLL 160
             :|:|           ||||:|||  : :|||:||| : :|            ||||
Db  109 SFISKTGLNVDLDKVVNSSDGPRLGIAFSGGGLRAMVNGGAFNAFDSRFESDSPLSGLL 168

Qy  161 DCVSYITGASGSTWALANLYEDPEWSQKDLAGPTELLKTQVTKNKLGVLAP------SQL 214
             |::|:||:|||||              :|:
Db  169 QSAMYISGLSGGSWLVGSV------AINNFTNIT-YLRDNVWNLEHSVFAPHGDNVIENL 221

Qy  215 QRY--RQELARARLGYPSCFTNLWALINEALLHDEPHDHKLSDQREA--------- 260
             |||     :         ||              :|      |||
Db  222 NYYNDLRKEIDQKKHAGFDCSLITDLW--GRAL-----SRKIVDAERGGPGITYSSMRN 272

Qy  261 --LSHGQNPLPIYCA------------LNTKGQSLTTFEFGEWCEFSPYEVGFPKYGAFI 306
               :                      |||| ||:|:||:|          :    |||
Db  273 QSWFQNADYPYPIIVADSRLEEETAIPANTSIFEFTAYEFGTW------DNGIK--AFI 323

Qy  307 PSELFGSEFFMGQLMKRLPESRIC------------FLEGIWSNLYAANLQDSLYWASEPSQFW 358
             |  : |                             | |   |   :  :|
Db  324 PMEYVGI------HLLDGVPPDKSCIIHNYDNAGFVMGTSATLFNSFLLD------W 367

Qy  359 DRWVRNQANLDKEQVPLLKIEEPPSTAGRIAEFFTDLLTWRPLAQATHNFLRGLHFHKD- 417
                     :     |    :                 |:
Db  368 NENVKKN----------------------DTYYDIL------HAILEDLSKHQDD 394

Qy  418 --YFQHPH-FSTWKATTLDGLENQLTPSEPH-LCLLDVGY-LINTSCLPLLQPTRDVD 470
                :|:|:       :| |: :          :|:||:|  |||   : |:|
Db  395 IAPYPNPYQNYTTSNTSVVNAF------EPYDTIDLVDGGEDRENIPLWPLLHPQRFVD 447

Qy  471 LILSLD--YNLHGAFQQLLGRFCQEQGIPFPPISPSPEEQLQPRECHTFSD----PTC 524
             ::|:|:  |||                |:      ::|:
Db  448 VVFAIDSTYN----------------DPYGWPLGSSIVATYERVVTFNANKSVDVRGFPYI 492

Qy  525 PGAPAVLHFSSGVVRRT-----PEEAAAGEVNLSSSDSP---------YHYTKVTYSQE 568
             |          |        ||:                     :|  : |::
Db  493 PDENTIISIGLNTRPTFFGCDGKNTTAGNHDVDNNTPPLLVYFNYPWTYYSNISTFTMS 552

Qy  569 DVDKLLHLTHYNVC------NNQEQLLEALRQA-VQRRRQRR 603
             :    |:|:|       |::|:  |:
Db  553 MDDKMANGILENAFMSTTQNNNESFAVCLACAIIQRSLERK 593
```

RESULT 14
PLB3_YEAST

```
ID   PLB3_YEAST     STANDARD;      PRT;   686 AA.
AC   Q08108;
DT   01-NOV-1997 (Rel. 35, Created)
DT   01-NOV-1997 (Rel. 35, Last sequence update)
DT   10-OCT-2003 (Rel. 42, Last annotation update)
DE   Lysophospholipase 3 precursor (EC 3.1.1.5) (Phospholipase B 3).
GN   PLB3 OR YOL011W.
OS   Saccharomyces cerevisiae (Baker's yeast).
OC   Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC   Saccharomycetales; Saccharomycetaceae; Saccharomyces.
OX   NCBI_TaxID=4932;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Hughes B., Pohl T.M.;
RL   Submitted (JUL-1996) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: Catalyzes the release of fatty acids from
CC       lysophospholipids.
CC   -!- CATALYTIC ACTIVITY: 2-lysophosphatidylcholine + H(2)O =
CC       glycerophosphocholine + a fatty acid anion.
CC   -!- SUBCELLULAR LOCATION: Secreted (Potential).
CC   -!- SIMILARITY: Belongs to the lysophospholipase family.
```

```
CC
DR   EMBL; Z74753; CAA99010.1; -.
DR   PIR; S66693; S66693.
DR   GermOnline; 143433; -.
DR   SGD; S0005371; PLB3.
DR   GO; GO:0005615; C:extracellular space; IDA.
DR   GO; GO:0004622; F:lysophospholipase activity; IMP.
DR   GO; GO:0006660; P:phosphatidylserine catabolism; IDA.
DR   GO; GO:0030384; P:phosphoinositide metabolism; IDA.
DR   InterPro; IPR002642; PLAc.
DR   Pfam; PF01735; PLA2_B; 1.
DR   SMART; SM00022; PLAc; 1.
KW   Lipid degradation; Hydrolase; Glycoprotein; Signal.
FT   SIGNAL      1     26       POTENTIAL.
FT   CHAIN      27    686       LYSOPHOSPHOLIPASE 3.
FT   DOMAIN    627    643       POLY-SER.
FT   CARBOHYD   56     56       N-LINKED (GLCNAC...)    (POTENTIAL).
FT   CARBOHYD   82     82       N-LINKED (GLCNAC...)    (POTENTIAL).
FT   CARBOHYD  129    129       N-LINKED (GLCNAC...)    (POTENTIAL).
FT   CARBOHYD  166    166       N-LINKED (GLCNAC...)    (POTENTIAL).
FT   CARBOHYD  221    221       N-LINKED (GLCNAC...)    (POTENTIAL).
FT   CARBOHYD  283    283       N-LINKED (GLCNAC...)    (POTENTIAL).
FT   CARBOHYD  313    313       N-LINKED (GLCNAC...)    (POTENTIAL).
FT   CARBOHYD  351    351       N-LINKED (GLCNAC...)    (POTENTIAL).
FT   CARBOHYD  495    495       N-LINKED (GLCNAC...)    (POTENTIAL).
FT   CARBOHYD  519    519       N-LINKED (GLCNAC...)    (POTENTIAL).
FT   CARBOHYD  547    547       N-LINKED (GLCNAC...)    (POTENTIAL).
FT   CARBOHYD  571    571       N-LINKED (GLCNAC...)    (POTENTIAL).
FT   CARBOHYD  588    588       N-LINKED (GLCNAC...)    (POTENTIAL).
FT   CARBOHYD  614    614       N-LINKED (GLCNAC...)    (POTENTIAL).
SQ   SEQUENCE   686 AA;  75076 MW;  9SA2DBF41BF13E20F CRC64;
```

Query Match 5.7%; Score 184; DB 1; Length 686;
Best Local Similarity 21.0%; Pred. No. 2.1e-06;
Matches 129; Conservative 80; Mismatches 192; Indels 214; Gaps 31;

```
Qy   99 EQAFLSRRKQVVAALRQAL------------QLDGDLQEDEIPVAIMATGGGIRA 143
            : | ::  |  :||||              |||:||||||||:||||||:
Db   57 ESAWLEKRNKVTSVALKDFLTRATANFSDSSEVLSKLFNDGNSENLPKIAVVSGGGYRS 116

Qy  144 MTSLYGQLAGLKEL------------------GLLDCVSYITGASGSTWALANL---- 179
            | : |:|:| :                   |||| : |||:|| ||:|
Db  117 MLTGAGVLAAMDNRTEGAYEHGLGGLLQSTTYLSGASGNWLVGTLALNNWTSVQDILNN 176

Qy  180 --YEDPEWSQKD---LAGPTELLKTQVTKNKL-GVLAPSQLQRYRQELAE---RARLGYP 230
              |::       |  |  :: |  :  :  |  | | |: | |:|||    | |:|
Db  177 MQNDDSIWDLSDSIVTPGGINIFKTAKRWDHISNAVESKQNADYNTSLADIWGRA-LAY- 234

Qy  231 SCFTNLWALINE------ALLHDEPHDHKLSDQREALSHGQNPLPIYCA--LNTKGQ 279
            |  |:|::|       ||:|: |::|  |:  |||  |:|:|||   |:|:|
Db  235 ---NFPPSLNRGGIGLTWSSIRDFP------------VFQNAEMPFFISVADGRYPGTKVI 280

Qy  280 SLTTFEFGEWCEFSPYEVGF--PKYGAFIPSELFGSEFFMGQLMKR---LPESRICFLE 333
            ||:| |   |  |::|||: |  || | ||:|||| ||||| |:|      |||::|||
Db  281 NLNATVF----EFNPFEMGSWDPSLNSFANVKYLGTNVSNGVPLERGKCTAGFDNAGFIM 336

Qy  334 GIWSNLYAANLQDSLYWASEPSQFWDRWVRNQANLDKEQVPLLKIEEP--PSTAGRIA-- 389
             |::|||  ||||:||||:||:|   | |:   |  ||:|| |::|       ||:  |:|
Db  337 GTSSTLF-------------------------NQF----------------LLRINSTHLPSFITRLARH 365

Qy  390 ------EPFTDLLTWRPLAQATHNFLRGLHFHKDYFQHPHFSTWKATTLDGLPNQLTPSE 443
Db  366 FLKDLSQDFNDIAVYSPNPFKDTKFL------DSDY------------SIVDSD 403

Qy  444 PHLCLLDVGY-LINTSCLPLLQPTRDVDLILSLDYN------------------ 489
Db  404 -SLFLVDGGEDDENVPVLPLIQKERDVDIIFAVDNSADMRLAWPDGSSIVHTYERQFVKQ 462

Qy  490 GRFCQEQGIPFPPISPSPEEQLQPRECHTF------SDPTCPGA------------PAVL 531
Db  463 G------QGMSFPVVP------------DTNTFVNLGLNKPTFFGCDANNLTDLQYIPLLVV 507

Qy  532 HFSSGVRRTPEEAAAGEVNLSSSDSPYHYTKVTYSQED---VDKLLHLTHYNVCNNQEQ 587
```

```
Db        508 YLPN---------AEYSFNSNQSAF---KLSYSESQRRSMIQNGFEIATRNNFTDDPE 553
              :     :     |::::|:|: |:  |::|:
Qy        588 LLEALRQAVQRRRQR 602
              :    :|:|:||:
Db        554 FMGCVGCAIIRRKQQ 568
```

RESULT 15
```
ALU1_HUMAN
ID   ALU1_HUMAN      STANDARD;     PRT;    591 AA.
AC   P39188;
DT   01-FEB-1995 (Rel. 31, Created)
DT   01-FEB-1995 (Rel. 31, Last sequence update)
DT   10-OCT-2003 (Rel. 42, Last annotation update)
DE   Alu subfamily J sequence contamination warning entry.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=95021758; PubMed=7935834;
RA   Claverie J.-M., Makalowski W.;
RT   "Alu alert.";
RL   Nature 371:752-752(1994).
RN   [2]
RP   CONCEPT.
RX   MEDLINE=92241891; PubMed=1572661;
RA   Claverie J.-M.;
RT   "Identifying coding exons by similarity search: alu-derived and other
RT   potentially misleading protein sequences.";
RL   Genomics 12:838-841(1992).
RN   [3]
RP   ALU FAMILIES CLASSIFICATION.
RX   MEDLINE=88333009; PubMed=3138422;
RA   Quentin Y.;
RT   "The Alu family developed through successive waves of fixation
RT   closely connected with primate lineage history.";
RL   J. Mol. Evol. 27:194-202(1988).
RN   [4]
RP   ALU FAMILIES CLASSIFICATION.
RX   MEDLINE=91178815; PubMed=1706781;
RA   Jurka J., Milosavljevic A.;
RT   "Reconstruction and analysis of human Alu genes.";
RL   J. Mol. Evol. 32:105-121(1991).
CC   -!- MISCELLANEOUS: VARIOUS ANALYSES (SEE REF.3 AND REF.4) INDICATE
CC       THAT ALU REPEATS FALL INTO 8 SUBFAMILIES. THEREFORE, 8 ALU WARNING
CC       CONSENSUS SEQUENCES HAVE BEEN CONSTITUTED THAT CONTAIN ALL SIX
CC       FRAMES CONCEPTUAL TRANSLATIONS OF EACH OF THESE CLASSES OF ALU
CC       REPEATS.
CC   -!- MISCELLANEOUS: ISOLATED 'X' INDICATES THE PRESENCE OF A STOP
CC       CODON, 'XXX' IS USED TO SEPARATE THE VARIOUS TRANSLATION PHASES.
CC   -!- CAUTION: This Alu entry is provided in order to avoid the further
CC       pollution of protein sequence databases with Alu-derived amino
CC       acid sequences.
CC   -!- CAUTION: Alu repetitive sequences are interspersed in human and
CC       primate genomes with an average spacing of 4 kb. Some of them are
CC       actively transcribed by pol III. Normal transcripts may contain
CC       Alu-derived sequences in 5' or 3' untranslated regions. However,
CC       cDNA libraries also contain partial and/or rearranged cDNAs
CC       ligated with Alu-derived sequence in any orientation. Although Alu
CC       elements (especially situated on the complementary strand) have a
CC       great potential to create additional/alternative exons,
CC       consideration should be given to the possibility that the presence
CC       of an Alu in an open reading frame may have resulted from a
CC       cloning artifact or may be due to misinterpretation of sequencing
CC       data. This point has been overlooked on several occasions, with
CC       the consequence of erroneous Alu-derived amino acid sequences
CC       being reported.
CC   -!- CAUTION: Any significant similarity of a putative protein sequence
CC       with an Alu-translated entry must be taken as a warning that a
CC       part of Alu repeat may have been artifactually included in the
```

(continued)

```
CC       coding nucleotide sequence.
CC   -----------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics  and the  EMBL outstation -
CC   the European Bioinformatics Institute.  There are no restrictions on its
CC   use by non-profit institutions as long  as its content is in no way
CC   modified and this statement is not removed.  Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   -----------------------------------------------------------------------
DR   EMBL; U14567; -; NOT_ANNOTATED_CDS.
KW   Hypothetical protein.
FT   DOMAIN        1     96       FRAME-1.
FT   DOMAIN      100    195       FRAME-2.
FT   DOMAIN      199    294       FRAME-3.
FT   DOMAIN      298    393       FRAME-4.
FT   DOMAIN      397    492       FRAME-5.
FT   DOMAIN      496    591       FRAME-6.
SQ   SEQUENCE   591 AA;  63790 MW;  665D395735519D95 CRC64;
```

Query Match   5.6%; Score 182; DB 1; Length 591;
Best Local Similarity   81.8%; Pred. No. 2.5e-06;
Matches   36; Conservative   0; Mismatches   8; Indels   0; Gaps   0;

```
Qy    40 FFEMESLSVAQAGVQWRDLGSLQPPLGFKRFSCLSLPSSWDYR 83
         ||| |||||||||||||||| ||||| || |||||||||||||
Db   496 FFETGSRSVAQAGVQWRDHGSLQPRPPGLKRSSCLSLPSSWDYR 539
```

Search completed: October 5, 2004, 19:25:33
Job time : 27.2 secs

This Page Blank (uspto)

```
          GenCore version 5.1.6
          Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on:    October  5, 2004, 18:51:24 ; Search time 120.193 Seconds
                                         (without alignments)
                                         1588.179 Million cell updates/sec

Title:          US-09-830-321A-2
Perfect score:  3235
Sequence:       1 MIFVELSPTLALCLERVASH.........EQLLEALRQAVQRRRQRRPH 605

Scoring table:  BLOSUM62
                Gapop 10.0 , Gapext 0.5

Searched:       1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters:    1017041

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :      SPTREMBL_25:*
            1:  sp_archea:*
            2:  sp_bacteria:*
            3:  sp_fungi:*
            4:  sp_human:*
            5:  sp_invertebrate:*
            6:  sp_mammal:*
            7:  sp_mhc:*
            8:  sp_organelle:*
            9:  sp_phage:*
           10:  sp_plant:*
           11:  sp_rodent:*
           12:  sp_virus:*
           13:  sp_vertebrate:*
           14:  sp_unclassified:*
           15:  sp_rvirus:*
           16:  sp_bacteriap:*
           17:  sp_archeap:*
```

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the total score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB	ID	Description
1	2767.5	85.5	1012	4	Q9UKV7	Q9ukv7 homo sapien
2	2767.5	85.5	1012	4	O95712	O95712 homo sapien
3	1931.5	59.7	439	11	Q80VV8	Q80vv8 mus musculu
4	1492	46.1	818	4	Q86XP0	Q86xp0 homo sapien
5	1141.5	35.3	845	4	Q8IUP3	Q8iup3 homo sapien
6	1127	34.8	841	11	Q80VV9	Q80vv9 mus musculu
7	708	21.9	356	11	Q8BX44	Q8bx44 mus musculu
8	685	21.2	372	11	Q80VQ8	Q80vq8 mus musculu
9	639.5	19.8	748	6	Q9TT38	Q9tt38 oryctolagus
10	622	19.2	749	13	Q7T0T9	Q7t0t9 xenopus lae
11	599.5	18.5	740	11	Q9DBX5	Q9dbx5 mus musculu
12	498.5	15.4	541	4	Q9UP65	Q9up65 homo sapien
13	490.5	15.2	541	4	O75457	O75457 homo sapien
14	397.5	12.3	216	4	Q8N176	Q8n176 homo sapien
15	371.5	11.5	530	11	Q7TN01	Q7tn01 mus musculu
16	239	7.4	634	3	Q9P8L1	Q9p8l1 cryptococcu
17	227.5	7.0	637	3	Q9P8P2	Q9p8p2 cryptococcu
18	227	7.0	634	3	Q8X0Z4	Q8x0z4 cryptococcu
19	225	6.8	199	4	Q8WWC5	Q8wwc5 homo sapien
20	221	6.8	634	3	Q96WX0	Q96wx0 cryptococcu
21	211	6.5	157	4	Q8N845	Q8n845 homo sapien
22	205	6.3	163	4	Q96MM0	Q96mm0 homo sapien
23	200	6.2	135	6	Q95KE1	Q95ke1 macaca fasc
24	199	6.2	158	4	Q8NAL9	Q8nal9 homo sapien
25	198	6.1	61	10	Q9UI48	Q9ui48 homo sapien
26	196.5	6.1	138	4	Q8N874	Q8n874 homo sapien
27	194.5	6.0	162	4	Q9H5D5	Q9h5d5 homo sapien
28	194	6.0	86	4	Q8N5B5	Q8n5b5 homo sapien
29	192	5.9	122	6	Q9BGW3	Q9bgw3 macaca fasc
30	192	5.9	152	4	Q9NX85	Q9nx85 homo sapien
31	190.5	5.9	151	4	Q9HA67	Q9ha67 homo sapien
32	187	5.8	208	4	Q9NWI4	Q9nwi4 homo sapien
33	185	5.7	101	4	Q7Z4P3	Q7z4p3 homo sapien
34	185	5.7	375	4	O60448	O60448 homo sapien
35	184.5	5.7	180	4	Q8N7M7	Q8n7m7 homo sapien
36	183	5.7	643	3	Q7Z8L3	Q7z8l3 pichia jadi
37	182	5.6	162	4	Q9BYA5	Q9bya5 homo sapien
38	178.5	5.5	66	4	Q96HL9	Q96hl9 homo sapien
39	177	5.5	125	4	Q9H842	Q9h842 homo sapien
40	176	5.4	118	4	Q9H387	Q9h387 homo sapien
41	175.5	5.4	164	4	Q9UQD6	Q9uqd6 homo sapien
42	175	5.4	244	4	Q9H700	Q9h700 homo sapien
43	175	5.4	434	4	Q8N2I3	Q8n2i3 homo sapien
44	175	5.4	506	4	Q9H6L7	Q9h6l7 homo sapien
45	174	5.4	126	4	Q8N1G7	Q8n1g7 homo sapien

ALIGNMENTS

```
RESULT 1
Q9UKV7
ID    Q9UKV7;                    PRELIMINARY;        PRT;   1012 AA.
AC    Q9UKV7;
DT    01-MAY-2000 (TrEMBLrel. 13, Created)
DT    01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT    01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE    Cytosolic phospholipase A2 beta.
OS    Homo sapiens (Human).
OC    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC    Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX    NCBI_TaxID=9606;
RN    [1]
RP    SEQUENCE FROM N.A.
RX    MEDLINE=99287906; PubMed=10358058;
RA    Song C., Chang X.J., Bean K.M., Proia M.S., Knopf J.L., Kriz R.W.;
RT    "Molecular characterization of cytosolic phospholipase A2-beta.";
RL    J. Biol. Chem. 274:17063-17067(1999).
CC   -!- SIMILARITY: CONTAINS 1 C2 DOMAIN.
DR    EMBL; AF121908; AAD32135.1; -.
DR    HSSP; P04410; 1A25.
DR    GO; GO:0004620; F:phospholipase activity; IEA.
DR    GO; GO:0003395; P:phospholipid catabolism; IEA.
DR    InterPro; IPR000008; C2.
DR    InterPro; IPR008973; C2_CaLB.
DR    InterPro; IPR002642; PLAc.
DR    InterPro; IPR003347; TF_JmjC.
DR    Pfam; PF00168; C2; 1.
DR    Pfam; PF01735; PLA2_B; 1.
DR    SMART; SM00239; C2; 1.
DR    SMART; SM00558; JmjC; 1.
DR    SMART; SM00022; PLAc; 1.
DR    PROSITE; PS50004; C2_DOMAIN 2; 1.
SQ    SEQUENCE 1012 AA;  114154 MW;  1A9D3269B4A57797 CRC64;

Query Match             85.5%;      Score 2767.5;  DB 4;  Length 1012;
Best Local Similarity   87.6%;      Pred. No. 6.4e-231;
Matches  537;  Conservative  5;  Mismatches  22;  Indels  49;  Gaps  6;
```

Left column (RESULT 2 — O95712):

```
Qy    24 TGLLVLFCPAPCPFFFFEMESLSVAQAGVQWRDLGSLQPPLGFKRFSCLSLPSSWDYR  83
            :|:|  |||  ||  : |||:  :|:||
Db   418 TGTFRFHCPA-C-----WEQE-LSI------------RLQDAPEEQLKAPLSALPSGQVVR 459

Qy    84 -------------LRELAVRLGFGPCAEEQAFLSRRKQVVAAALRQALQLDGD 123
                         |||||||||||||||||||||||||||||||||||||
Db   460 LVFPTSQEPLMRVELKKEAGLRELAVRLGFGPCAEEQAFLSRRKQVVAAALRQALQLDGD 519

Qy   124 LQEDEIPVVAIMATGGIRAMTSLYGQLAGLKELGLLDCVSYITGASGSTWALANLYEDP 183
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   520 LQEDEIPVVAIMATGGIRAMTSLYGQLAGLKELGLLDCVSYITGASGSTWALANLYEDP 579

Qy   184 EWSQKDLAGPTELLKTQVTKNKLGVLAPSQLQRYRQELAERARLGYPSCFTNLWALINEA 243
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   580 EWSQKDLAGPTELLKTQVTKNKLGVLAPSQLQRYRQELAERARLGYPSCFTNLWALINEA 639

Qy   244 LLHDEPHDHKLSDQREALSHGQNPLPIYCALNTKGQSLTTFEFGEWCEFSPYEVGFPKYG 303
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   640 LLHDEPHDHKLSDQREALSHGQNPLPIYCALNTKGQSLTTFEFGEWCEFSPYEVGFPKYG 699

Qy   304 AFIPSELFGSEFFMGQLMKRLPESRICFLEGIWSNLYAANLQDSLYWASEPSQFWDRWVR 363
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   700 AFIPSELFGSEFFMGQLMKRLPESRICFLEGIWSNLYAANLQDSLYWASEPSQFWDRWVR 759

Qy   364 NQANLDKEQVPLLKIEEPPSTAGRIAEFFTDLLTWRPLAQATHNFLRGLHFHKDYFQHPH 423
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   760 NQANLDKEQVPLLKIEEPPSTAGRIAEFFTDLLTWRPLAQATHNFLRGLHFHKDYFQHPH 819

Qy   424 FSTWKATTLDGLPNQLTPSEPHLCLLDVGYLINTSCLPLLQPTRDVDLILSLDYNLHGAF 483
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   820 FSTWKATTLDGLPNQLTPSEPHLCLLDVGYLINTSCLPLLQPTRDVDLILSLDYNLHGAF 879

Qy   484 QQLQLLGRFCQEQGIPFPPISPSPEEQLQPRECHTFSDPTCPGAPAVLHF----------- 533
            ||||||||||||||||||||||||||||||| |||||||||||||||||
Db   880 QQLQLLGRFCQEQGIPFPPISPSPEEQLQPRRCHTFSDPTCPGAPAVLHFTHYNVCNNQEQLLEAL 939

Qy   534 -SSGVRRTPEEAAAGEVNLSSSDSPYHYTKVTYSQEDVDKLLHLTHYNVCNNQEQLLEAL 592
             | |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   940 SAPGVRRTPEEAAAGEVNLSSSDSPYHYTKVTYSQEDVDKLLHLTHYNVCNNQEQLLEAL 999

Qy   593 RQAVQRRRQRRPH 605
            |||||||||||||
Db  1000 RQAVQRRRQRRPH 1012
```

RESULT 2
O95712

ID   O95712   PRELIMINARY;   PRT;   1012 AA.
AC   O95712;
DT   01-MAY-1999 (TrEMBLrel. 10, Created)
DT   01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Cytosolic phospholipase A2 beta.
GN   CPLA2 BETA.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=9185108; PubMed=10085124;
RA   Pickard R.T., Strifler B.A., Kramer R.M., Sharp J.D.;
RT   "Molecular cloning of two new human paralogs of 85-kDa cytosolic
RT   phospholipase A2.";
RL   J. Biol. Chem. 274:8823-8831(1999).
CC   -!- SIMILARITY: CONTAINS 1 C2 DOMAIN.
DR   EMBL; AF065215; AAC78836.1; -.
DR   HSSP; P04410; 1A25.
DR   Genew; HGNC:9036; PLA2G4B.
DR   GO; GO:0004627; F:calcium-dependent cytosolic phospholipase A. . .; TAS.
DR   InterPro; IPR000008; C2.
DR   InterPro; IPR008973; C2_CaLB.
DR   InterPro; IPR002642; PLAc.

Right column (continuation of O95712 record and RESULT 3 — Q80VV8):

DR   InterPro; IPR003347; TF_JmjC.
DR   Pfam; PF00168; C2; 1.
DR   Pfam; PF01735; PLA2_B; 1.
DR   SMART; SM00239; C2; 1.
DR   SMART; SM00558; JmjC; 1.
DR   SMART; SM00022; PLAc; 1.
DR   PROSITE; PS50004; C2_DOMAIN_2; 1.
SQ   SEQUENCE 1012 AA; 114120 MW; 989EDB4AD3CF19DD CRC64;

Query Match   85.5%; Score 2767.5; DB 4; Length 1012;
Best Local Similarity   87.6%;
Matches 537; Conservative   5; Mismatches   22; Indels   49; Gaps   6;
Pred. No. 6.4e-231;

```
Qy    24 TGLLVLFCPAPCPFFFFEMESLSVAQAGVQWRDLGSLQPPLGFKRFSCLSLPSSWDYR  83
            :|:|  |||  ||  : |||:  :|:||
Db   418 TGTFRFHCPA-C-----WEQE-LSI------------RLQDAPEEQLKAPLSALPSGQVVR 459

Qy    84 -------------LRELAVRLGFGPCAEEQAFLSRRKQVVAAALRQALQLDGD 123
                         |||||||||||||||||||||||||||||||||||||
Db   460 LVFPTSQEPLMRVELKKEAGLRELAVRLGFGPCAEEQAFLSRRKQVVAAALRQALQLDGD 519

Qy   124 LQEDEIPVVAIMATGGIRAMTSLYGQLAGLKELGLLDCVSYITGASGSTWALANLYEDP 183
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   520 LQEDEIPVVAIMATGGIRAMTSLYGQLAGLKELGLLDCVSYITGASGSTWALANLYEDP 579

Qy   184 EWSQKDLAGPTELLKTQVTKNKLGVLAPSQLQRYRQELAERARLGYPSCFTNLWALINEA 243
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   580 EWSQKDLAGPTELLKTQVTKNKLGVLAPSQLQRYRQELAERARLGYPSCFTNLWALINEA 639

Qy   244 LLHDEPHDHKLSDQREALSHGQNPLPIYCALNTKGQSLTTFEFGEWCEFSPYEVGFPKYG 303
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   640 LLHDEPHDHKLSDQREALSHGQNPLPIYCALNTKGQSLTTFEFGEWCEFSPYEVGFPKYG 699

Qy   304 AFIPSELFGSEFFMGQLMKRLPESRICFLEGIWSNLYAANLQDSLYWASEPSQFWDRWVR 363
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   700 AFIPSELFGSEFFMGQLMKRLPESRICFLEGIWSNLYAANLQDSLYWASEPSQFWDRWVR 759

Qy   364 NQANLDKEQVPLLKIEEPPSTAGRIAEFFTDLLTWRPLAQATHNFLRGLHFHKDYFQHPH 423
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   760 NQANLDKEQVPLLKIEEPPSTAGRIAEFFTDLLTWRPLAQATHNFLRGLHFHKDYFQHPH 819

Qy   424 FSTWKATTLDGLPNQLTPSEPHLCLLDVGYLINTSCLPLLQPTRDVDLILSLDYNLHGAF 483
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   820 FSTWKATTLDGLPNQLTPSEPHLCLLDVGYLINTSCLPLLQPTRDVDLILSLDYNLHGAF 879

Qy   484 QQLQLLGRFCQEQGIPFPPISPSPEEQLQPRECHTFSDPTCPGAPAVLHF----------- 533
            ||||||||||||||||||||||||||||||| |||||||||||||||||
Db   880 QQLQLLGRFCQEQGIPFPPISPSPEEQLQPRRCHTFSDPTCPGAPAVLHFTHYNVCNNQEQLLEAL 939

Qy   534 -SSGVRRTPEEAAAGEVNLSSSDSPYHYTKVTYSQEDVDKLLHLTHYNVCNNQEQLLEAL 592
             | |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   940 SAPGVRRTPEEAAAGEVNLSSSDSPYHYTKVTYSQEDVDKLLHLTHYNVCNNQEQLLEAL 999

Qy   593 RQAVQRRRQRRPH 605
            |||||||||||||
Db  1000 RQAVQRRRQRRPH 1012
```

RESULT 3
Q80VV8

ID   Q80VV8   PRELIMINARY;   PRT;   439 AA.
AC   Q80VV8;
DT   01-JUN-2003 (TrEMBLrel. 24, Created)
DT   01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Similar to phospholipase A2, group IVB (Cytosolic) (Fragment).
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=FVB/N; TISSUE=Salivary gland;

RA   Strausberg R.;
RL   Submitted (JAN-2003) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC042758; AAH42758.1; -.
DR   PIR; PT0721; PT0721.
DR   GO; GO:0004620; F:phospholipase activity; IEA.
DR   GO; GO:0009395; P:phospholipid catabolism; IEA.
DR   InterPro; IPR002642; PLAc.
DR   Pfam; PF01735; PLA2_B; 1.
FT   NON_TER   1   1
SQ   SEQUENCE   439 AA; 50464 MW; EA9041FA820F5F10 CRC64;

Query Match   59.7%; Score 1931.5; DB 11; Length 439;
Best Local Similarity   82.5%; Pred. No. 6.9e-159;
Matches 358; Conservative 30; Mismatches 35; Indels 11; Gaps 1;

Qy   181 EDPEWSQKDLAGPTELLKTQVTKNKLGVLAPSQLQRYRQELAERARLGYPSCFTNLWALI 240
         ||||||||||||||| ||||||| ||| ||||||| |||||||||||||| |||||||||
Db   1 EDPEWSQKDLAGPTEVLKTQVTKSKLGLAAPSQLWRYRQELAERARLGHPTCFTNLWALI 60

Qy   241 NEALLHDEPHDHKLSDQREALSHGQNPLPIYCALNTKGQSLTTFEFGEWCEFSPYEVGFP 300
         ||||||| ||| ||||||||| |||||||||| ||| |||| : |||||||||||||||
Db   61 NEALLHDKPHEHKLSDQREALSRGQNPLPIYCALNSKEQLSTFDFGEWCEFSPYEVGFP 120

Qy   301 KYGAFIPSELFGSEFFMGQLMKRLPESRICFLEGIWSNLYAANLQDSLYWASEPSQFWDR 360
         ||||||:||||||||||| : ||||||||||||||||| ||| ||||||| |||||||
Db   121 KYGAFISSELFGSEFFMGRLVKQLPESRICFLEGIWSNLFAASLQDSLYWSSEPSQFWDR 180

Qy   361 WVRNQANLDKEQVPLLKIEEPPSTAGRIAEFFTDLLTWRPLAQATHNFLRGLHFHKDYFQ 420
         | :| ||||||||| | ||||||||||||||||||||| ||| | |||| ||||||||||
Db   181 WAQDQANLDKEQVPHLKTAEPPTMAGRIAELFTDLLTKRPLAHATHNFTRGLHFHKDYFQ 240

Qy   421 HPHFSTWKATTLDGLPNQLTPSEPHLCLLDVGYLINTSCLPLLQPTRDVDLIILSLDYNLH 480
         | :|: |: : : |||||| |||||||||||| ||||: ||||||||||||||||||||:
Db   241 NSHFSAWKASKLDRLPNQLTPAEPHLCLLDVGYFINTSCPPLLQPTRDVDKLLRLLTHYNI 300

Qy   481 GAFQQLQLLGRFCQEQGIPFPPISPSPEEQLQPRECHTFSDPTCPGAPAVLHF------- 533
         |||||||||||||||||||||:||||||||||||:|||||||::|:|:|||
Db   301 GAFQQLQLLSRFCQEQGIPFPPISPSPEEQRQPQECHLFCDPAQPEAPAVLHFPLVNDSF 360

Qy   534 ----SSGVRRTPEEAAAGEVNLSSSDSPYHYTKVTYSQEDVDKLLHLTHYNVCNNQEQLL 589
             ||:||:::||:||||||||||||||||||||||||||||:||::||||:|:|::
Db   361 QDYSAPGVPRTSEKAAGEVNLSSSDSPYHYTKVTYSQEDVDKLRLLTHYNICNNQDRLR 420

Qy   590 EALRQAVQRRRQRR 603
         ||::|||||| ||
Db   421 EAMHQAVQRRRRKRK 434

RESULT 4
Q86XP0
ID   Q86XP0;
AC   Q86XP0;
DT   01-JUN-2003 (TrEMBLrel. 24, Created)
DT   01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Cytosolic phospholipase A2 delta.
DE   CPLA2 DELTA.
GN   Homo sapiens (Human).
OS   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Imai Y., Chiba H.;
RT   "cytosolic phospholipase A2 homolog(cPLA2delta).";
RL   Submitted (AUG-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AB090876; BAC67158.1; -.
DR   GO; GO:0004620; F:phospholipase activity; IEA.
DR   GO; GO:0009395; P:phospholipid catabolism; IEA.
DR   InterPro; IPR000008; C2.
DR   InterPro; IPR008973; C2_CaLB.
DR   InterPro; IPR002642; PLAc.
DR   Pfam; PF00168; C2; 1.

Q86XP0   PRELIMINARY;   PRT;   818 AA.

DR   Pfam; PF01735; PLA2_B; 1.
DR   SMART; SM00239; C2; 1.
DR   SMART; SM00022; PLAc; 1.
DR   PROSITE; PS50004; C2 DOMAIN 2; 1.
SQ   SEQUENCE   818 AA; 91955 MW; E5ADF3478FDAB1B0 CRC64;

Query Match   46.1%; Score 1492; DB 4; Length 818;
Best Local Similarity   51.6%; Pred. No. 2.6e-120;
Matches 296; Conservative 92; Mismatches 152; Indels 34; Gaps 8;

Qy   61 LQPPPLGFKRFSCLSLPSSWDYRLR-------ELAVRLGFGPCAEEQAFLSRRKQVVAA 112
         | :| :|:|| :   : | :   ELAV LGF CAEEQAFLSRRKQVVA
Db   244 LRPLTIGKEVTMDVPAPNAPGVRLQLKAEGCPEELAVHLGFNLCAEEQAFLSRRKQVVAK 303

Qy   113 ALRQAIQLDGDLQEDRIPVVAIMATGGIRAMTSLYGQLAGLKELGLLDCVSYITGASGS 172
         || ||||| ||||| :|||.||||||| ||||||| | | :||||||||:|::|:|||
Db   304 ALKQAIQLDRDLQEDEVPVVGIMATGGARAMTSLYGHLLALQKLGLLDCVTYFSGISGS 363

Qy   173 TWALANLYEDPEWSQKDLAGPTELLKTQVTKNKLGVLAPSQLQRYRQELAERARLGYPSC 232
         || : :||.|||||::||.|| : : : ||| | | :| |: || :| |:|
Db   364 TWTMAHLYGDPEWSQRDLEGPIRYAREHLAKSKLEVFSPERLASYRRELELRAEQGHPTT 423

Qy   233 FTNLWALINEALLHDEPHDHKLSDQREALSHGQNPLPIYCALNTKGQSLTTFEFGEWCEF 292
         | :|||: :: :|| :: | ||| : |||.:||:|||| |: :. : |: |:||.||
Db   424 FVDLWALVLESMLHGQVMDQKLSGQRAALERGQNPLPYLSLNVKENNLETLDFKEWVEF 483

Qy   293 SPYEVGFPKYGAFIPSELFGSEFFMGQLMKRLPESRICFLEGIWSNLYAANLQDSLYWAS 352
         |||||||:||||::| |||||||||| ||:| ||.|||||| |||| :: || | ||:
Db   484 SPYEVGFLKYGAFVPPELFGSEFFMGRLMRRIPEPRICFLEAIWSNIFSLNLLDAWYDLT 543

Qy   353 EPSQFWDRWVRNQA-NLDKEQVPLL-------KIEE--PPSTAGRIAEFFTDLLTWRPLA 402
          :: : : :: : | : | | | . |: :: : | : |||
Db   544 SSGGSSWKQHIKDKTRSLEKE--PLITSGTSSRLEASWLQPGTA--LAQAFKGFLTGRPLH 599

Qy   403 QATHNFLRGLHFHKDYFQHPHFSTWKATTLDGLPNQLTPSEPHLCLLDVGYLINTSCLPL 462
         | : |||:|| :.|| .| :||| | ||| |||| ||:|:||:|:| | |||| ||
Db   600 QRSPNFLQGLQLHQDYCSHKDFSTWADYQLDSMPSQLTPKEPRLCLVDAAYFINTSSPSM 659

Qy   463 LQPTRDVDLIILSLDYNLHGAFQQLQLLGRFCQEQGIPFPPISPSPEEQLQPRECHTFSDP 522
          :| ||:||||| ||| ||| ||| || ::||| |||||:|.||| | | |||||:||||
Db   660 FRPGRRLDLILSFDYSLSAPFEALQQTELYCRARGLPFPRVEPSPQDHQPRECHLFSDP 719

Qy   523 TCPGAPAVLHF----------------SSGVRRTPEEAAAGEVNLSSSDSPYHYTKVTYSQEDVD 571
          || ||::|| : | : :: .: :||:|| | | : : :
Db   720 ACPEAPILLHFPLVNASFKDHSAPGVQRSPAELQGGQVDLTGATCPYTLSNMTYKEEDFE 779

Qy   572 KLLHLTHYNVCNNQEQLLEALRQAVQRRR-QRRP 604
         :|| |: ||| : | :||| |:::: | ::
Db   780 RLLRLSDYNVQTSQGAIIQALRTALKHRTLEARP 813

RESULT 5
Q8IUP3
ID   Q8IUP3;
AC   Q8IUP3;
DT   01-MAR-2003 (TrEMBLrel. 23, Created)
DT   01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Similar to phospholipase A2, group IVB (Cytosolic) (Fragment).
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Brain;
RA   Strausberg R.;
RL   Submitted (JUL-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC035335; AAH35335.1; -.
DR   GO; GO:0004620; F:phospholipase activity; IEA.
DR   GO; GO:0009395; P:phospholipid catabolism; IEA.
DR   InterPro; IPR000008; C2.
DR   InterPro; IPR008973; C2_CaLB.

Q8IUP3   PRELIMINARY;   PRT;   845 AA.

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DR   InterPro; IPR002642; PLAc.
DR   Pfam; PF00168; C2; 1.
DR   Pfam; PF01735; PLA2_B; 1.
DR   SMART; SM00239; C2; 1.
DR   SMART; SM00022; PLAc; 1.
DR   PROSITE; PS50004; C2_DOMAIN_2; 1.
FT   NON_TER    1    1
SQ   SEQUENCE   845 AA;  93280 MW;  32FEBBB34FF96D53 CRC64;

Query Match             35.3%;  Score 1141.5;  DB 4;  Length 845;
Best Local Similarity   41.1%;  Pred. No. 7.4e-90;
Matches  258;  Conservative   95;  Mismatches  220;  Indels   55;  Gaps   11;

Qy    2 IFVELSPTLALC--------LERVASHLTDTGLLVLFCPAPCPFFFFEMESLSVAQAGVQ   54
          :||||    |  |   :|:                            ||
Db  241 LHVELMEVLAAVQSGPSAELEAQTSKLGEGGILLSSLP------LGQEEQCSVA-------  288

Qy   55 WRDIGSLQPPPLGFKRFSCLSLPSSWDYRLRELAVRLGFGPCAEEQAFLSRRKQVVAAAL  114
          :|  |  |      :|   ||||
Db  289 ---LGEGQEVALSMK----VEMSSG------DLDLRLGFDLSDGEQEFLDRRKQVVSKAL  335

Qy  115 RQAIQLDGDLQEDEIPVVAIMATGGGIRAMTSLYGQLAGLKELGLLDCVSYITGASGSTW  174
        :|:||||| |||||||||||||||||||| ||:|||||||||||||| |||||:||||||
Db  336 QQVIGLSEALDSGQVPVVAVLGSGGGTRAMSSLYGSLAGLQELGLLDAVTYLSGVSGSTW  395

Qy  175 ALANLYEDPEWSQKDLAGPTELLKTQVTKNKLGVLAPSQLQRYRQELAERARLGYPSCFT  234
         ||||||||||||:::|||| :|||||| ||||||| :|||||||||||||||||||||||
Db  396 CISTLYRDPAWSQVALQGPIERAQVHVCSSKMGALSTERLQYTQELGVRERSCHSVSLI   455

Qy  235 NLWALINEALLHDEPHDHKLSDQREALSHGQNPLPIYCALNTKGQSLITFEFGEWCEFSP  294
        ||:|||||| |||||||||||| :| :|| ||||||||||||||||||||||||||| :|
Db  456 DLWGLLVEYLLYQEENPAKLSDQQEAVRQGQNPYPIYTSVNVR-TNLSGEDFAEWCEFTP  514

Qy  295 YEVGFPKYGAFIPSELFGSEFFMGQLMKRLLPESRICFLEGIWSNLYAANLQDSLYWASEP  354
        ||||||||||  |||||| |||:|  :|||| :|:| : |    :    ::    |
Db  515 YEVGFPKYGAYVPTELFGSELFMGRLLQLQPEPRICYLQGMWGSAFATSLDEIFLKTAGS  574

Qy  355 SQFWDRWRNQANL-DKEQVPLLKIEEPP-------STAGRIAEFFTDLLTWRPLAQATH   406
            |:  ||  |    ||   |::|
Db  575 GLSFLEWYRGSVNITDDCQKP--QLHNPSRLRTRLLTPQQPFSQAVLDIFTSRFTSAQSF  632

Qy  407 NFLRGLHFHKDYFQHPHFSTWKATTLDGLPNQLTPSEPHLCLLDVGYLINTSCLPLLQPT  466
        ||:|||| || |  |||||||||| |||   ::||| ::|| ||| |||  ||||||||
Db  633 NFTRGLCLHKDYVAGREFVAWKDTHPDAFPNQLTPMRDCLYLVDGGFAINSPFPIALLPQ  692

Qy  467 RDVDLILSLDYNLHGAFQQLQLLGRFCQEQGIPFPPISPSPEEQLQPRECHTFSDPTCPG  526
         :| |||||||||| :||||||||||| ||||||||||||||||||||:||||||| ||
Db  693 RAVDLIILSFDYSLEAPFEVLKMTEKYCLDRGIPFPPSIEVGPEDVEEARECYLFAKAEDPR  752

Qy  527 APAVLHF--------SSGV-RRTPEERAAGEVNLSSSDSPYHYTKVTYSQEDVDKLL   574
          |:|||         |:    :  :| :||:|||| ::||:||:||| :|::| :|
Db  753 SPIVLHFPLVNRTFRTHLAPGVERQTAEEKAFGDFVINRPDTPYGMMNFTYEPQDFYRLV  812

Qy  575 HLTHYNVCNNQEQLLEALRQAVQRRRRQR  602
           :|||:|||:| ||:|| :::
Db  813 ALSRYNVLNNVETLKCALQLALDRHQAR  840
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RESULT 6
Q80VV9
ID   Q80VV9        PRELIMINARY;    PRT;   841 AA.
AC   Q80VV9;
DT   01-JUN-2003 (TrEMBLrel. 24, Created)
DT   01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Similar to phospholipase A2, group IVB (Cytosolic) (Fragment).
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=FVB/N; TISSUE=Salivary gland;
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RA   Strausberg R.;
RL   Submitted (NOV-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC039947; AAH39947.1; -.
DR   GO; GO:0004620; F:phospholipase activity; IEA.
DR   GO; GO:0003395; P:phospholipid catabolism; IEA.
DR   InterPro; IPR000008; C2.
DR   InterPro; IPR008973; C2_CaLB.
DR   InterPro; IPR002642; PLAc.
DR   Pfam; PF00168; C2; 1.
DR   Pfam; PF01735; PLA2_B; 1.
DR   SMART; SM00239; C2; 1.
DR   SMART; SM00022; PLAc; 1.
DR   PROSITE; PS50004; C2_DOMAIN_2; 1.
FT   NON_TER    1    1
SQ   SEQUENCE   841 AA;  95063 MW;  D03F239BECA2BBE4 CRC64;

Query Match             34.8%;  Score 1127;  DB 11;  Length 841;
Best Local Similarity   42.6%;  Pred. No. 1.3e-88;
Matches  231;  Conservative  100;  Mismatches  183;  Indels   28;  Gaps    7;

Qy   86 ELAVRLGFGPCAEEQAFLSRRKQVVAAALRQALQLDGDLQEDEIPVVAIMATGGGIRAMT  145
        :|:|||||  |:|||||:|||||||:|||:||:|:|| | |||:|||||:|:||||:||||
Db  295 DLDLRLGFDLCDGQEFLDKRKQVASKALQRVMGLSEALHCDQVPVVAVLGSGGGTRAMT  354

Qy  146 SLYGQLAGLKELGLLDCVSYITGASGSTWALANLYEDPEWSQKDLAGPTELLKTQVTKNK  205
        ||||:||||:|||||||:|:|:|:|||:||:|:||:||:||||| |||| ||: :|:|:|
Db  355 SLYGSLAGLQELGLLDAVTYLSGVSGSWCISTLYRDPSWSQKALQGPIKYASERVCSSK   414

Qy  206 LGVLAPSQLQRYRQELAERARLGYPSCFTNLWALINEALLHDEPHDHKLSDQREALSHGQ  265
        :| |:|:| :|| :  |: : : :|   : ||| ||:||||||||| ||||||||:||||
Db  415 IGMLSPKQFBYYSREKRAWESRGHSMSFTDLWGLIIEYFLNQEENPAKLSDQQETVSGQGQ  474

Qy  266 NPLPIYCALNTKGQSLITFEFGEWCEFSPYEVGFPKYGAFIPSELFGSEFFMGQLMKRLP  325
        || |||:::|   :   | :|:|||||:|||||||||| :|||||||||||||:|:  :|
Db  475 NPYPIYASINVH-KNISGDYFAEWCEFTPYEVGFPKYGVVPTELFGSEFFMGRLLHFWP   533

Qy  326 ESRICFLEGIWSNLYAANLQDSLYWASEPSQFWDRWVRNQANLDKEQVPLLKIEEPPSTA  385
        | ||| | | |:  :| :|  :    :  |:||||   :  : |:   |::||| :
Db  534 EPRICYLQGMWGSAFAASLYRIFLKLGGLSLSFLDWHRGSVSV-TDDWPKLRKQDPTRLP  592

Qy  386 GRI------AEFFTDLLTWRPLAQATHNPLRGLHFHKDYFQHPHF---STWKATTL--   432
          :      |   |:|::     :  |:| |||   :||| :      ||:|
Db  593 TRLFTPMSSRFSQAVLDIFTSRITCAQTFNFTRGLCMYKDYTARKDFVVSEDAWHSHNYGY  652

Qy  433 -DGLPNQLTPSEPHLCLLDVGYLINTSCLPLLQPTRDVDLILSLDYNLHGAFQQLQLLGR  491
          | |||||| | : || ||| |||  ||| ||| | |||||| |||||| ||| | | :
Db  653 PDACPNQLTPMKDFLSLVDGGFAINSPFPLVLQPQRAVDLIVSFDYSLEGPFEVLQVTEK  712

Qy  492 FCQEQGIPFPPISPSPEEQLQPRECHTFSDPTCPGAPAVLHF-----------SSGV-RR  539
        :| :||||||  : | :: ||||:| ||:  :  :  |:|||             |:
Db  713 YCRDRGIPFPRIEVDPKDSEDPRECYLFTEAEDPCSSPIVLHFPLVNRTFRTHLAPGVERQ  772

Qy  540 TPEEAAAGEVNLSSSDSPYHYTKVTYSQEDVDKLLHLTHYNVCNNQEQLLEALRQAVQRR  599
        | || |:|:.:|:.||:.|:|||:|||: |:  |  :||||:|||:|: | ||: |::||
Db  773 TAEEKAFGDFIINGPDTAYGMMDFTYEPKEFDRLVTLSRYNVLNNKETIRHALQLALDRR  832

Qy  600 RQ  601
        ||
Db  833 RQ  834
```

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RESULT 7
Q8BX44
ID   Q8BX44        PRELIMINARY;    PRT;   356 AA.
AC   Q8BX44;
DT   01-MAR-2003 (TrEMBLrel. 23, Created)
DT   01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   Hypothetical lysophospholipase catalytic domain containing
DE   protein.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
```

OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=Cerebellum;
RX   MEDLINE=22354683; PubMed=12466851;
RA   The FANTOM Consortium;
RA   the RIKEN Genome Exploration Research Group Phase I & II Team;
RT   "Analysis of the mouse transcriptome based on functional annotation of
RT   60,770 full-length cDNAs.";
RL   Nature 420:563-573 (2002).
DR   EMBL; AK049063; BAC33531.1; -.
DR   GO; GO:0004620; F:phospholipase activity; IEA.
DR   GO; GO:0009395; P:phospholipid catabolism; IEA.
DR   InterPro; IPR002642; PLAc.
DR   Pfam; PF01735; PLA2_B; 1.
DR   SMART; SM00022; PLAc; 1.
KW   Hypothetical protein.
SQ   SEQUENCE   356 AA; 40682 MW; 5968D5518E290FEB CRC64;

Query Match   21.9%; Score 708; DB 11; Length 356;
Best Local Similarity   49.2%; Pred. No. 8.6e-53;
Matches 145; Conservative   43; Mismatches   81; Indels   26; Gaps   4;

Qy   72 SCLS------LPSSWDYRLR-------ELAVRLGFGPCAEEQAFLSRRKQVVAAALRQA 117
             :||| |:| ||: ||:| :||:
Db   65 NCLSDGQVTTLPVGENYELHMKSSPCSDTLDVRLGFSLCQEEVEFVQKRRMVVAKTLSQM 124

Qy   118 LQLDGDLQEDEIPVVAIMATGGGIRAMTSLYGQLAGLKELGLLDCVSYITGASGSTWALA 177
             ||| | |:::||||||| | :| ||| | |:|:::||: |||||::| :
Db   125 LQLEGLHEDEVPIIAIMATGGGTRSMVSLYGHLLGLQKLNFLDASTYITGLSGATWTMA 184

Qy   178 NLYEDPEWSQKDLAGPTELLKTQVTKNKLGVLAPSQLQRYRQELAERARLGYPSCFTNLW 237
             | |||| || |: : | :| |:||| || | | |:::| |: || | ::
Db   185 TLYSDPEWSSKNLETVVFEARRHVVKDKMPALFPDQLYKWREDLQKHSQEGYKTFTDFW 244

Qy   238 ALINEALLHDEPHDKLSDQREALSHGQNPLPIYCALNTKGQSLITTFEFGEWCEFSPYEV 297
             || |:| | | | ||: ||||||||||||: | | |||||||||||||||||||||
Db   245 GKLIEYSLGDKKNECKLSDQRAALCKGQNPLPIYLTINVK-DDVSNQDFREWFEFSPYEV 303

Qy   298 GFPKYGAFIPSELFGSEFFMGQLMKRLPESRICFLEGIWSNLYAANLQDSLYWAS 352
             | |:|||||||||||||||||| :|: ||| : :
Db   304 GMQKYGAFIPSELFGSEFFMGRLMKRIPEPEMCYMLG------------DSLRYSA 347

RESULT 8
Q80VQ8
ID   Q80VQ8;   PRELIMINARY;   PRT;   372 AA.
AC   Q80VQ8;
DT   01-JUN-2003 (TrEMBLrel. 24, Created)
DT   01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Similar to phospholipase A2 (Fragment).
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=NMRI; TISSUE=Breast tumor;
RA   Strausberg R.;
RL   Submitted (FEB-2003) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC046400; AAH46400.1; -.
DR   GO; GO:0004620; F:phospholipase activity; IEA.
DR   GO; GO:0009395; P:phospholipid catabolism; IEA.
DR   InterPro; IPR002642; PLAc.
DR   Pfam; PF01735; PLA2_B; 1.
FT   NON_TER   1   1
SQ   SEQUENCE   372 AA; 42638 MW; 17BD15B5B9207ABBC CRC64;

Query Match   21.2%; Score 685; DB 11; Length 372;
Best Local Similarity   39.5%; Pred. No. 9.1e-51;
Matches 145; Conservative   68; Mismatches 126; Indels   28; Gaps   7;

Qy   261 LSHGQNPLPIYCALNTKGQSLITTFEFGEWCEFSPYEVGPKYGAFIPSELFGSEFFMGQL 320
             :| |||| | || |:: | :| ||||||| | |:|||||:|||||||||||||
Db   1 VSCGQNPYPIYASINVH-KNISGDYFAEWCEFTPYEVGPFKYGVYVPTELFGSEFFMGRL 59

Qy   321 MKRLPESRICFLEGIWSNLYAANLQDSLYWASEPSQFWDRWRVNQANLDKEQVPLLKIEE 380
             ||| | :| | | | || |: :|:|:| | | |: :| | :| : |:
Db   60 LHFWPEPRICYLQGMWGSAFAASLYEIFLKLGGLSLSFLDWHRGSVSV-TDDWPKLRKQD 118

Qy   381 PPSTAGRI------ABFFTDLLTWRPLAQATHNFLRGLHFHKDYFQHPHF----STWKA 429
             || | ||
Db   119 PTRLPTRLFTPMSSFSQAVLDIFTSRITCAQTFNFTRGLCMYKDYTARKDFVVSEDAWHS 178

Qy   430 TTL---DGLPNOLTPSEPHLCLLDVGVLINTSCLPLLQPTRDVDLIISLLDYNLHGAFQQL 486
             ||: ||||| || || | || | ||: ||| | | ||||: :|:|| || |||
Db   179 HNYGYPDACPNQLTPMKDFLSLVDGGFAINSPFPLVLQPQRAVDLIVSFDYSLEGPFEVL 238

Qy   487 QLLGRFCQEQGIPFPFPISPSPEEQLQPRECHTFSDPTCPGAPAVLHF---------SS 535
             | :: ::||:|||::
Db   239 QVTEKYCRDRGIPFPRIEVDPKDSEDPRECYLFTEAEDPCSPIVLHFPLVNRTFRTHLAP 298

Qy   536 GV-RRTPEEAAAGEVNLSSSDSPYHYTKVTYSQEDVDKLLHLTHYNVCNNQEQLLEALRQ 594
             |: ||| | | |::| |:| :| :: :|:| || :: :|:| |::| | |:|
Db   299 GVERQTAEEKAFGDFIINGPDTAYGMMDFTYEPKEFDRLVTLSRYNVLNNKETIRHALQL 358

Qy   595 AVQRRRQ 601
             |:|:||
Db   359 ALDRRRQ 365

RESULT 9
Q9TT38
ID   Q9TT38;   PRELIMINARY;   PRT;   748 AA.
AC   Q9TT38;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Phosphatidyl choline 2-acylhydrolase cPLA2.
OS   Oryctolagus cuniculus (Rabbit).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX   NCBI_TaxID=9986;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=New Zealand White; TISSUE=Heart;
RA   Al-Khalili O.K., Eaton D.C.;
RT   "Molecular cloning of cDNA coding for phospholipase A2.";
RL   Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases.
CC   -!- SIMILARITY: CONTAINS 1 C2 DOMAIN.
DR   EMBL; AF204923; AAF15299.1; -.
     HSSP; P47712; 1BCI.
DR   GO; GO:0016787; F:hydrolase activity; IEA.
DR   GO; GO:0004620; F:phospholipase activity; IEA.
DR   GO; GO:0004289; F:subtilase activity; IEA.
DR   GO; GO:0009395; P:phospholipid catabolism; IEA.
DR   GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR   InterPro; IPR000008; C2.
DR   InterPro; IPR008973; C2_CalB.
DR   InterPro; IPR000209; Peptidase_S8.
DR   InterPro; IPR002642; PLAc.
DR   Pfam; PF00168; C2; 1.
DR   Pfam; PF01735; PLA2_B; 1.
DR   SMART; SM00239; C2; 1.
DR   SMART; SM00022; PLAc; 1.
DR   PROSITE; PS50004; C2_DOMAIN_2; 1.
DR   PROSITE; PS00136; SUBTILASE_ASP; 1.
KW   Hydrolase.
SQ   SEQUENCE   748 AA; 85235 MW; 7661A3EFC41FF668 CRC64;

Query Match   19.8%; Score 639.5; DB 6; Length 748;
Best Local Similarity   28.1%; Pred. No. 2.4e-46;
Matches 181; Conservative 118; Mismatches 237; Indels 107; Gaps   22;

Qy   44 ESLSVAQAGVQWRDLGSLQPPPLGFKRFS------CLSLPSSWDYRLRELAVRLGFGPCA 97

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RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA   Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA   Jones S.J., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [3]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Spleen;
RA   Klein S., Strausberg R.;
RL   Submitted (AUG-2003) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC056041; AAH56041.1; -.
KW   Hypothetical protein.
SQ   SEQUENCE   749 AA;  85282 MW;  CE769904144C4DE2 CRC64;

Query Match             19.2%;
Best Local Similarity   27.6%;                    Length 749;
Matches  177;  Conservative 113;  Mismatches 219;  Indels 132;  Gaps 22;
Score 622;  DB 13;  Pred. No. 7.9e-45;

Qy    59 GSLQPPLGFKRFS------CLSLPSSWDYRLRELAVRLGFGPCAEEQAFLSRRKQVVAA 112
         :  ||.|.|:||:
Db   115 GEKKQVPFTFNKVTEMLLEFSLEVCSSTD------LRFSMALCDQEKLFRQKRKNKVIN 167

Qy   113 ALRQAL--QLDGDLQED-EIPVAIMATGGIRAMTSLYGOLAGLKELGLLDCVSYITG 168
Db   168 GLRKLLGPEKTQDLNSTSRDVPVIAVLGSGGFRAMIGFSGVMKALYESGVLDCATYVAG 227

Qy   169 ASGSTWALANLYEDPEWSQKDLAGPTEL---LKTQVTKNKLGVLAPSQLQRYRQELAERA 225
Db   228 LSGSTWYMSTLYSHPDFPTK---GPKEINKELMHNVSYNPLLLLTPQKVKRYVEALWKKK 284

Qy   226 RLGYPSCFTNLWA-LINEALLHDEPHDHKLSDQREALSHGQNPLPIYCALNTKGQSLTTF 284
Db   285 SSGQPVTFTDIFAMLIGETLIKDR-MNRKLSHMQEKINDGQCPLPFTCLHVK-PDVSEL 342

Qy   285 EFGEWCEFSPYEVGFPKYGAFIPSELFGSEFFMGQLMKRLPESRICFLEGIWSNLYAANL 344
Db   343 MFADWVEFSPYEIGMAKYGTFMPPGLFGSKFPMGTVIKKYEENPLHFFMGVWGSAFSILI 402

Qy   345 QDSLYWASEPSQFWDRWVRNQANLDKEQVPLLK---------IEEPPSTAGRIA 389
Db   403 NRVLGVSN---------NSKGSTMEEEIENLKPKHILGNDSSDDEMQEPKGTENAKA 452

Qy   390 E---FFTDLLTW--RPL--------AQATHNFLRGLHFHKDYFQHPHFSTWK 428
Db   453 EEEYLRNNQASWVQRMLMAILGDSAIFNTREGRAGKVHNFMLGLNLNTSYPYSP------ 506

Qy   429 ATTLDGLPNQLTPSEPHL----------CLLDVGYLINTSCLPLLQ 464
Db   507 ---LSGLCTQQSMEEDELDAAVADPDEFEQIYEPLDVKSKKIHIVDSGLTFNLPYPLILR 563

Qy   465 PTRDVDLIISLDYNLHGA---------FQQLQLLGRFCQEOQGIPFPPISPSPEEQLQPRECHTF 519
Db   564 PQRGVDLIISFDFSARPSDSSPPFKELLLAEKWARMNKLPFPKIDPHVFDREGLKECYIF 623

Qy   520 S-----DPTCPGAPAVLHF----------SSGV-RRTPEEAAAGEVNL-SSSDSPYHY 560
Db   624 KPKNTSVEKDC---PTVIHFVLANLQFRNFKAPGVPRETTEEKESADFDIFDDDETPFST 680

Qy   561 TKVTYSQEDVDKLLHLTHYNVCNNQEBLLEALRQAVQRRRQ 601
Db   681 FNFQYPNVAFKQLHDLMEFNTLNNNINVIKQAMVESIEYRRQ 721
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Db   100 ETLGTATFPVSSMKVGEKKEVPFIFNQVTEMILEMSLEVCSSPD------LRFSMALCD 152
Qy    98 EEQAFLSRRKQVVAAALRQAL---QLDGDLQEDEIPVAIMATGGIRAMTSLYGQLAGL 154
Db   153 QEKAFRQQRKENIKENMRKLLGPKKSBGLYSTRDVPVVAILGSGGFRAMVGFSGVMKAL 212
Qy   155 KELGLLDCVSYITGASGSTWALANLYEDPEWSQKDLAGPTEL---LKTQVTKNKLGVLAP 211
Db   213 YESGILDCATYIAGLSGSTWYMSTLYSHPDFPEK---GPQEINEELMKNVSHNPLLLLTP 269
Qy   212 SQLQRYRQELAERARLGYPSCFTNLWA-LINEALLHDEPHDHKLSDQREALSHGQNPLPI 270
Db   270 QKVKRYVESLWKKKSSGQPVTFTDIFGMLIGETLIHNRMHT-TLSSLKEKVSSAQCPLPL 328
Qy   271 YCALNTKGQSLTTFEFGEWCEFSPYEVGFPKYGAFIPSELFGSEFFMGQLMKRLPESRIC 330
Db   329 FTCLHVK-PDVSELMFADWVEFSPYEIGMAKYGTFMAPDLFGSKFFMGTVKKYEENPLH 387
Qy   331 FLEGIWSNLYAANLQDSLYWASEPSQFWDRWVRNQAANLDKEQVPLL---------376
Db   388 FLMGVWGSAFSILFNRVLGVSGS-------HNKGSTMEEELENITAKGHIVSNDSDSD 438
Qy   377 -KIEEPPSTAGRIA--EFFTD-LLTW--RPL----------AQATHNFLRGLHF 414
Db   439 DESQEPKGTEGEDAEREYQNDHQASWVHRMLMALVSDSALFNTREGRAGKVHNFMLGLNL 498
Qy   415 HKDY-------FQHPHFSTWKATTLDGLPNQ-----ITPSEPHLCLLDVGYLINTSCL 460
Db   499 NTSYPLSPLRDFTQESFDDDELDAAVADPDEFERIYEPLDVKSKKIHVVDSGLTFNLPYP 558
Qy   461 PLLQPTRDVDLIISLDYNLHGA----FQQLQLLGRFCQEQGIPFPPISPSPEEQLQPRE 515
Db   559 LILRPQRGVDLIISFDFSARPSDTSPPFKELLLAEKWAKMNKLPFPKIDPYVFDREGLKE 618
Qy   516 CHTFSDPTCP----GAPAVLHF----------SSGV-RRTPEEAAAGEVNL-SSSDSPY 558
Db   619 CYVFK-PKNPDVEKDCPIIIHFVLANINFRKYKSPGVPRETKEKEIADFDIFDDPESPF 677
Qy   559 HYTKVTYSQEDVDKLLHLTHYNVCNNQEQLLEALRQAVQRRRQ 601
Db   678 STFNFQYPNQAFKRLHDLMYFNTLNNIDVIKDAMVESIEYRRQ 720
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RESULT 10
Q7T0T9
ID   Q7T0T9   PRELIMINARY;   PRT;   749 AA.
AC   Q7T0T9;
DT   01-OCT-2003 (TrEMBLrel. 25, Created)
DT   01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Hypothetical protein.
OS   Xenopus laevis (African clawed frog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
OC   Xenopodinae; Xenopus.
OX   NCBI_TaxID=8355;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Spleen;
RX   MEDLINE=22341112; PubMed=12454917;
RA   Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
RA   Richardson P.;
RT   "Genetic and genomic tools for Xenopus research: The NIH Xenopus
RT   initiative.";
RL   Dev. Dyn. 225:384-391(2002).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Spleen;
RX   MEDLINE=22388257; PubMed=12477932;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
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RESULT 11

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Q9DBX5
ID   Q9DBX5          PRELIMINARY;      PRT;    740 AA.
AC   Q9DBX5;
DT   01-JUN-2001 (TrEMBLrel. 17, Created)
DT   01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Phospholipase A2, group IV.
GN   PLA2G4A OR PLA2G4.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=Lung;
RX   MEDLINE=21085660; PubMed=11217851;
RA   Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA   Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA   Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA   Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA   Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA   Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA   Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA   Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA   Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA   Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA   Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA   Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA   Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA   Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA   Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA   Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA   Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA   Hayashizaki Y.;
RT   "Functional annotation of a full-length mouse cDNA collection.";
RL   Nature 409:685-690(2001).
CC   -!- SIMILARITY: CONTAINS 1 C2 DOMAIN.
DR   EMBL; AK004701; BAB23486.1; -.
DR   HSSP; P47712; 1BCI.
DR   MGD; MGI:1195256; Pla2g4a.
DR   GO; GO:0004620; F:phospholipase activity; IEA.
DR   GO; GO:0004289; F:subtilase activity; IEA.
DR   GO; GO:0009395; P:phospholipid catabolism; IEA.
DR   GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR   InterPro; IPR000008; C2.
DR   InterPro; IPR008973; C2_CalB.
DR   InterPro; IPR000209; Peptidase_S8.
DR   InterPro; IPR002642; PLAC.
DR   Pfam; PF00168; C2; 1.
DR   Pfam; PF01735; PLA2_B; 1.
DR   SMART; SM00239; C2; 1.
DR   SMART; SM00022; PLAC; 1.
DR   PROSITE; PS50004; C2_DOMAIN_2; 1.
DR   PROSITE; PS00136; SUBTILASE_ASP; 1.
SQ   SEQUENCE  740 AA;  84268 MW;  E2A1296AAF52937E CRC64;
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Query Match   18.5%; Score 599.5; DB 11; Length 740;
Best Local Similarity 26.9%; Pred. No. 7e-43;
Matches 172; Conservative 126; Mismatches 242; Indels 99; Gaps 22;

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Qy      44  ESLSVAQGVQWRDLGSLQPPPLGFKRFSCLSLPSSWDYRLRELA---VRLGFGPCAEE 99
                :|| :|     |   |: :|| |     | :      :|  :|
Db      92  ETLGTATPPVSSMKVGEKKEVPIFNQVTEMILEMS----LEVCSCPDLRFSMALCDQE 146

Qy     100  QAFLSRRKQVVAAALRQAL--QLDGDLIQEDEIPVVAIMATGGGIRAMTSLYGQLAGLKE 156
                |: ||||:||||:||    |:::|||:|||:|::||||:||:|| |||  :| :: ::
Db     147  KTFRQQRKENIKENMKKLLGPKKSEGLYSTRDVPVVAILGSGSGFRAMVGFSGVMKALYB 206

Qy     157  LGLLDCVSYITGASGSTWALANLYEDPEWSQKDLAGPTEL---LKTQVTKNKLGVLLAPSQ 213
                |::|||  | |||||    |: ::|   ||:  |  :||    |||||||||||||||
Db     157  GLLDCVSYITGASGSTWALANLYB---DPEWSQKDLAGPTELLKTQVTKNKLGVLAPSQL 214
```

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Db     207  SGILDCATYIAGLSGSTWYMSTLYSHPDFPEK---GPEEINEELMKNVSHNPLLLLTPQK 263
                |||||  |||| ||||| || || |:  |          ::||||||| | |  :| |:
Qy     214  LQRYRQELAERARLGYPSCFTNLWA-LINEALLHDEPHDHKLSDQREALSHGQNPLPIYC 272
                 ::|| :|   ||||  ||  ||: |  :| |||||:|:||||: |:||||:|| :|::
Db     264  VKRYVESLWKKKSSGQPVTFTDIFGMLIGETLIQNR-MSMTLSSLKEKVNAARCPLPLFT 322

Qy     273  ALNTKGQSLTTFEFGEWCEFSPYEVGPPKYGAFIPSELFGSEFFMGQLMKRLPESRICFL 332
                |:  || |   | :||  ||: |: |: | |  |   |  |  | |::::  ||   ||
Db     323  CLHVK-PDVSELMFADMVEFSPYEIGMAKYGTFMAPLFGSKFFMGTVVKKYEENPLHFL 381

Qy     333  EGIWSNLYA--------ANLQDSL-------YWASEPSQFWDRWVRNQANLDK 370
                ||   |||          |:||:            |  | | | :  :| ||:
Db     382  MGVWGSAFSILFNRVLGVSGSGSQNKGSTMEEELENTTAKHIVSNDSSDDEAQGPKGTEN 441

Qy     371  EQVPLLKIEBPPSTAGRIAEFFTDLLTWRPL-------AQATHNFLRGLHFFHKDYFQHP- 422
                |: ||:|||  | |: ||:|   |:|     |            |::| :|::|| |:
Db     442  EEAE--KEYQSDNQASWVHRMLMALVSDSALFNTREGRAGKVHNFMLGLNLNTSYPLSPL 499

Qy     423  -HFSTWKATTLDGLPNQLTPS--------EP----HLCLLDVGYLINTSCLPLLQ 464
                   |   :|:|  | |          :          |  | || |:| | || |
Db     500  RDFS----SQDSFDDELDAVADPDFEFERIYEPLDVKSKKIHVVDSGLTFNLPYPHLR 554

Qy     465  PTRDVDLILSLDYNLHGA------FQQLQLLGRFCQEQGIPFPPISPSPEEQLQPRBCHTF 519
                |  ::|:::  |::|  |          :|  ::   :  ||  |  :|  | |:::
Db     555  PQRGVDLIISFDFSARPSDTSPPFKELLLAEKWAKMNKLPFPKIDPYVFDREGLKECYVF 614

Qy     520  SDPTCP----GAPAVLHF--------SSGV-RRTPEEAAAGEVNL-SSSDSPYHYTK 562
                |||         |:     |           |||    |  : |   || | ||:||
Db     615  K-PKNPDVEKDCPTIHFVLANINFRKYKAPGVLRETKEEKEIADPFDFDDPESPFSTFN 673

Qy     563  VTYSQEDVDKLLHLTHYNVCNNQEQLLEALRQAVQRRQ 601
                  | :|  ||  | :   :::   | :| : |: |||:
Db     674  FQYPNQAFKRIHDLMYFNTLNNIDVIKDAIVESIEYRRQ 712
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RESULT 12

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Q9UP65
ID   Q9UP65          PRELIMINARY;      PRT;    541 AA.
AC   Q9UP65;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   Cytosolic phospholipase A2 gamma.
GN   CPLA2 GAMMA.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=99185108; PubMed=10085124;
RA   Pickard R.T., Strifler B.A., Kramer R.M., Sharp J.D.;
RT   "Molecular cloning of two new human paralogs of 85-kDa cytosolic
RT   phospholipase A2.";
RL   J. Biol. Chem. 274:8823-8831(1999).
DR   EMBL; AF065214; AAC78835.1; -.
DR   PIR; T13162; T13162.
DR   GO; GO:0004620; F:phospholipase activity; IEA.
DR   GO; GO:0009395; P:phospholipid catabolism; IEA.
DR   InterPro; IPR002642; PLAC.
DR   Pfam; PF01735; PLA2_B; 1.
DR   SMART; SM00022; PLAC; 1.
SQ   SEQUENCE  541 AA;  60948 MW;  63E6AEE7F7550741 CRC64;
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Query Match   15.4%; Score 498.5; DB 4; Length 541;
Best Local Similarity 27.8%; Pred. No. 2.5e-34;
Matches 158; Conservative 86; Mismatches 190; Indels 135; Gaps 23;

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Qy      98  EEQAFLSRRKQVVAAALRQALQLQDGDLQEDEIPVVAIMATGGGIRAMTSLYGQLAGLKEL 157
                ||:| ||||:||| |:|:| :||:  : :|||:|::||:||:|| |||  :| :|
Db      15  EEKAAVERRLHVLKALKKL----RIEADEAPVVAVLGSGGGLRAHIACLGVLLSEMKEQ 69

Qy     158  GLLDCVSYITGASGSTWALANLYB---DPEWSQKDLAGPTELLKTQVTKNKLGVLAPSQL 214
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Db         ||||| |:| :| ||||||                   ||  |:  :||
       70  GLLDAVTYLAGVSGSTWAISSLYTNDGDMEALEAD------LKHRFTRQEW------DL 116

Qy    215  QRYRQELAERARLGYPSCFTNLWA-LINEALLHDEPHDHKLSDQREALSHGQNPLPIYCA 273
           |||:|:  ||  :                :  :  :::
Db    117  AKSLQKTIQAARSENYS-LTDFWAYMVISKQTRELPESH-LSNMKKPVEEGTLPYPIFAA 174

Qy    274  ---LNTKGQSLITPFPGEWCEFSPYEVGFPKYGAFIPSELFGSEFFMGQLMKRLPESRI 329
           :|||  ||| ||||  ::| :| | :|
Db    175  IDNDLQPSWQEARAPE--TWFEFTPHHAGFSALGAFVSITHFGSKFKKGRLVRTHPERDL 232

Qy    330  CFLEGIWSN----------------------------------LYA--ANLQDSLY 349
           || |:|:
Db    233  TFLRGLWGSSALGNTEVIREYIFDQLRNLTLKGLWRRAVANAKSIGHLIFARLLRLQESSQ 292

Qy    350  W--------ASEPSQFW-----DRWVRNQANLDKEQVPLLKIEPPSTAGRIAEFF----- 392
           :|  :|              :|:|
Db    293  GEHPPPEDEGGEPEHTWLTEMLENWTR--TSLEKQEQP---HEDPERKGSLSNLMDFVK 346

Qy    393  -TDLLTWRPLAQATHNFLRGLHFHKDYFQHPHFSTWKATTLDGLPNQLTPSEPHLCLLDV 451
           |||      :   ||||
Db    347  KTGICASKWEWGTTHNFL---------------YKH----------GGIRDKIMSSRKHLHLVDA 386

Qy    452  GYLINTSCLPLLQPTRDVDLILSLDYNLHGAFQQLQLLGRFCQEQGIPFPPISPSPEEQL 511
           |||||                                       :  |:|
Db    387  GLAINTPFPLVLPPTREVHLILSFDFSAGDPFETIRATTDYCRRHKIPFPQVE---EAEL 443

Qy    512  Q-----PRECHTFSDPTCPGAPAVLHFSSGVRRTP----EEAAAGEVNLSSSDSPYHYTKV 563
           |        |:|:|:
Db    444  DLWSKAPASCYILKGET---GPVMHF------------PLFNIDACGGDIEAWSDTYDTFKLAD 493

Qy    564  TYSQEDVDKLLHLTHYNVCNNQEQLLEAL 592
           ||: :|:|       ||::::|
Db    494  TYTLDVVVLLLALAKKNVRENKKKILREL 522
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```
RESULT 13
O75457
ID   O75457        PRELIMINARY;    PRT;   541 AA.
AC   O75457;
DT   01-NOV-1998 (TrEMBLrel. 08, Created)
DT   01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   Cytosolic phospholipase A2-gamma.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Skeletal muscle;
RX   MEDLINE=9371032; PubMed=9705332;
RA   Underwood K.W., Song C., Kriz R.W., Chang X.J., Knopf J.L., Lin L.L.;
RT   "A novel calcium-independent phospholipase A2, cPLA2-gamma, that is
RT   prenylated and contains homology to cPLA2.";
RL   J. Biol. Chem. 273:21926-21932(1998).
DR   EMBL; AF058921; AAC32823.1; -.
DR   Genew; HGNC:9037; PLA2G4C.
DR   GO; GO:0016020; C:membrane; TAS.
DR   GO; GO:0004628; F:calcium-independent cytosolic phospholipase. . .; TAS.
DR   InterPro; IPR002642; PLAC.
DR   Pfam; PF01735; PLA2_B; 1.
DR   SMART; SM00022; PLAc; 1.
SQ   SEQUENCE   541 AA;  60920 MW;  BBB972A611FB5237 CRC64;

Query Match             15.2%;    Score 490.5;  DB 4;  Pred. No. 1.3e-33;
Best Local Similarity   27.6%;    Mismatches 191;  Indels 135;  Gaps 23;
Matches  157;  Conservative  86;

Qy    98  EEQAFLSRRKQVVAAALRQALQLDGDIQEDEIPVVAIMATGGGIRAMTSLYGQLAGLKEL 157
          ||  |:    :|||||| || :: |      |:||:  |||||:|
Db    15  EEKAAVERRRLHVLKALKKL----RIEADEAPVVAVLGSGGGLRAHIACLGVLSEMKEQ 69
```

```
Qy    158  GLLDCVSYITGASGSTWALANLYE---DPEWSQKDLAGPTELLKTQVTKNKLGVLAPSQL 214
           ||||  : | |||| ||||:|||  :::                 ||: :|
Db     70  GLLDAVTYLAGVSGSTWAISSLYTNDGDMEALEAD------LKHRFTRQEW------DL 116

Qy    215  QRYRQELAERARLGYPSCFTNLWA-LINEALLHDEPHDHKLSDQREALSHGQNPLPIYCA 273
           |||:|:  ||  :                :  :  :::
Db    117  AKSLQKTIQAARSENYS-LTDFWAYMVISKQTRELPESH-LSNMKKPVEEGTLPYPIFAA 174

Qy    274  ---LNTKGQSLITPFPGEWCEFSPYEVGFPKYGAFIPSELFGSEFFMGQLMKRLPESRI 329
           :|||  ||| ||||  ::| :| | :|
Db    175  IDNDLQPSWQEARAPE--TWFEFTPHHAGFSALGAFVSITHFGSKFKKGRLVRTHPERDL 232

Qy    330  CFLEGIWSN----------------------------------LYA--ANLQDSLY 349
           || |:|:
Db    233  TFLRGLWGSSALGNTEVIREYIFDQLRNLTLKGLWRRAVANAKSIGHLIFARLLRLQESSQ 292

Qy    350  W--------ASEPSQFW-----DRWVRNQANLDKEQVPLLKIEPPSTAGRIAEFF----- 392
           :|  :|              :|:|
Db    293  GEHPPPEDEGGEPEHTWLTEMLENWTR--TSLEKQEQP---HEDPERKGSLSNLMDFVK 346

Qy    393  -TDLLTWRPLAQATHNFLRGLHFHKDYFQHPHFSTWKATTLDGLPNQLTPSEPHLCLLDV 451
           |||      :   ||||
Db    347  KTGICASKWEWGTTHNFL---------------YKH----------GGIRDKIMSSRKHLHLVDA 386

Qy    452  GYLINTSCLPLLQPTRDVDLILSLDYNLHGAFQQLQLLGRFCQEQGIPFPPISPSPEEQL 511
           |||||                                       :  |:|
Db    387  GLAINTPFPLVLPPTREVHLILSFDFSAGDPFETIRATTDYCRRHKIPFPQVE---EAEL 443

Qy    512  Q-----PRECHTFSDPTCPGAPAVLHFSSGVRRTP----EEAAAGEVNLSSSDSPYHYTKV 563
           |        |:|:|:
Db    444  DLWSKAPASCYILKGET---GPVIHF------------PLFNIDACGGDIEAWSDTYDTFKLAD 493

Qy    564  TYSQEDVDKLLHLTHYNVCNNQEQLLEAL 592
           ||: :|:|       ||::::|
Db    494  TYTLDVVVLLLALAKKNVRENKKKILREL 522
```

```
RESULT 14
Q8N176
ID   Q8N176        PRELIMINARY;    PRT;   216 AA.
AC   Q8N176;
DT   01-OCT-2002 (TrEMBLrel. 22, Created)
DT   01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT   01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE   Similar to phospholipase A2, group IVB (Cytosolic).
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Brain;
RA   Strausberg R.;
RL   Submitted (JUL-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC034571; AAH34571.1; -.
SQ   SEQUENCE   216 AA;  24371 MW;  6198D0A387F1071B CRC64;

Query Match             12.3%;    Score 397.5;  DB 4;  Length 216;
Best Local Similarity   39.5%;    Pred. No. 3.6e-26;
Matches   92;  Conservative  37;  Mismatches  75;  Indels  29;  Gaps   8;

Qy    317  MGQLMKRLPESRICFLEGIWSNLYAANLQDSLYWASEPSQFWDRWVRNQA-NLDKEQVPL 375
           |    |:| ||  ||||| ||||  |:::| |:  |     ||:|||||:  ::|:|:|
Db      1  MGRLMRRIPEPRICFLEAIWSNIFSLNLLDAWYDLTSSGESWKQHIDKTRSLEKE--PL 58

Qy    376  L-----KIEE--PPSTAGRIAEFFTDLLTWRPLAQATHNFLRGLHFHKDYFQHPHFST 426
           :     |:||   |:|:|  |:|:|  |   |:|:|       ||||||||| |::|
Db     59  TTSGTSSRLEASWLQPGTA--LAQAFKGFLTGRPLHQRSPNFLQGLQLHQDYCSHKDFST 116

Qy    427  WKATTLDGLPNQLTPSEPHLCLLDVGYLINTSLYGQLAGLKEL 486
           |  |  || :   || |||:|  ||   :   :|: |
Db    117  WADYQLDSMPSQLTPKEPRLCLVDAAYFINTSSPSMFRPGRRLDLILSFDYSLSAPFE-- 174
```

```
Qy   487 QLLGRFCQEQGIPFPPI-SPSPEEQLQPRECHTFSDPTCPGAPAVLHFSSGVR 538
             ::|: .:||:|       ::|.|           |||
Db   175 -------------VPWSPQGNPSAQPGQAPEASSRATEP-LPHTARVPKGRGRGVR 215

RESULT 15
Q7TN01
ID   Q7TN01        PRELIMINARY;      PRT;    530 AA.
AC   Q7TN01;
DT   01-OCT-2003 (TrEMBLrel. 25, Created)
DT   01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Hypothetical protein (Fragment).
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6;
RX   MEDLINE=22388257; PubMed=12477932;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA   Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA   Jones S.J., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6;
RA   Strausberg R.;
RL   Submitted (JUL-2003) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC054740; AAH54740.1; -.
KW   Hypothetical protein.
FT   NON_TER    1    1
SQ   SEQUENCE  530 AA;  60927 MW;  2029EA78CDBC4265 CRC64;

Query Match      11.5%;   Score 371.5;   DB 11;   Length 530;
Best Local Similarity  24.8%;   Pred. No. 2.6e-23;
Matches 135;  Conservative 73;  Mismatches 177;  Indels 159;  Gaps 20;

Qy   155 KELGLLDCVSYITGASGSTWALANLYEDPEWSQKDLAGPTELLKTQVTKNKLGVLAPSQL 214
             ||||||.|   |||.:::||||| |:|          ::|      |||: :: :|
Db     1 KELGLLDAVTYLAGVSGSTWALSSLIYT---KNGNMEGIEEELKHRYEKNEWDF------ 50

Qy   215 QRYRQELAERA----RLGYPSCFTNLWALINEALLHDEPHDHKLSDQREALSHGQNPLP 269
             |.:|:    .    |:|            ||::|:        :.|  .::
Db    51 ---HESLEKAIQASKRENY--SLTDFWAYLIVSRQIRELQDSNLSSLKKQVEEGVLPYP 104

Qy   270 IYCALN---------TKGQSLTTPEFGEWCEFSPYEVGFPKYGAFIPSELFGSEFFMGQL 320
             |:|:|.         |||::    || | |     |: :|:|           ||||:|
Db   105 IFAAIDEDLLADWRERKTQN------SWFEFTPHHAGYPALGAYVPITEFGSRFENGKL 157

Qy   321 MKRLPESRICFLEGIWSNLYAANLQDSLYWASEPSQFWDRMWVRNQ-ANLDKEQVPLLKIE 379
             :.|           |::|  :         |: .::|        :   :.|::||.|:.
Db   158 VKSEPERDLTFLRGLWGSAF-ADIKE-----------IKNYILNYFRNPFGKLKFI 201

Qy   380 EPPSTAGR----------IAEFFTD------------------------------L 395
             |||                : ||||
```

```
Db   202 EGPVTYSEAPRMNVDAMLLDLVMAYFTDMNDPSIKDKLCALQQALGTETDEFGIEMAEII 261
             ||
Qy   396 LTWRPL-AQATHNFL-------------------------------RGLHFHKDYFQHPH--FSTWK 428
             |: .|
Db   262 QNWNETSAEKKEQFLDHLLDRFKKTQEDTTTYSLMNWNTGLVWDRCVFVNETRKCVSKWQ 321
             :: |:
Qy   429 ATTL------DGLPNQLTPSEPHLCLLDVGYLINTSCLPLLQPTRDVDLLILSLDYNLHG 481
             .|              |||| :|::      ||:| |:|
Db   322 WGTVNFLYKHGKIADETMCSRELLHLVDAGFAINTPYPLVLPPVRETHLILSFDFSAGD 381
             :|::: |:  |.| |||||  :|||||  |  |||  |       ||||| :| .|.
Qy   482 AFQQLQLLGRFCQEQGIPFPPISPSPEEQLQ----PRECHTFSDPTCPGAPAVLHF--- 533
             |.||| |||       :||:. |:|:        |::  |::  || |||||:|
Db   382 PLETIRATADYCQRHEIPFPEVS---EDQLKEWAKAPASCYVLRGET---GPVVMHFTLF 435
             ||:: |:|  |:|:|||| :   .  :::|   |:|:   :|: .    |||::||||.
Qy   534 ---SSGVRRTPEEAAAGEVNLSSSDSPYHYTKVTYSQEDVDKLLHLTHYNVCNNQEQLLE 590
             :|.   : :    ||::|::|:|:||   |::  :.:||:|:|| : ||| ::|:||
Db   436 NKDNCGDDIETWRKKYGTVKLSDS----------YTPDLVRDLLRVSKENVKKNKINILS 485
             ||.|   .|  |::: |:|:|:|          :|::|: :||: |::|::|:|:|||:|

Qy   591 ALRQ 594
             :|:|
Db   486 EMRK 489
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Search completed: October 5, 2004, 19:24:07
Job time : 125.193 secs

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                GenCore version 5.1.6
          Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on:   October  7, 2004, 12:49:19 ; Search time 1674.58 Seconds
                                       (without alignments)
                            10556.917 Million cell updates/sec

Title:          US-09-830-321A-4
Perfect score:  592
Sequence:       1 tctgctccactgctctgtg.........cccagcctccccccggaaccc 592

Scoring table:  IDENTITY_NUC
                Gapop 10.0 , Gapext 1.0

Searched:       27513289 seqs, 1493109276 residues

Total number of hits satisfying chosen parameters:   55026578

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :  EST:*
       1:  em_estba:*
       2:  em_esthum:*
       3:  em_estin:*
       4:  em_estmu:*
       5:  em_estov:*
       6:  em_estpl:*
       7:  em_estro:*
       8:  em_htc:*
       9:  gb_est1:*
      10:  gb_est2:*
      11:  gb_htc:*
      12:  gb_est3:*
      13:  gb_est4:*
      14:  gb_est5:*
      15:  em_estfun:*
      16:  em_estom:*
      17:  em_gss_hum:*
      18:  em_gss_inv:*
      19:  em_gss_pln:*
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      21:  em_gss_fun:*
      22:  em_gss_man:*
      23:  em_gss_mus:*
      24:  em_gss_rod:*
      25:  em_gss_vrl:*
      26:  em_gss_phg:*
      27:  em_gss_vrl:*
      28:  gb_gss1:*
      29:  gb_gss2:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Str	Score	% Match	Query Length	DB	ID	Description
1		587.2	99.2	726	14	CD691591	CD691591 EST8114 h
2		527.6	89.1	680	12	BI836812	BI836812 603084703
3		436.4	73.7	438	29	AY417051	AY417051 Homo sapi
4		436.4	73.7	438	29	AY417052	AY417052 Pan trogl
5	c	427.2	72.2	463	12	BM153087	BM153087 TCBAP1Q13
6		323	54.6	461	14	CB481980	CB481980 jns85_C09
7		308.6	52.1	424	14	CD687559	CD687559 EST4080 h
8		296.6	50.1	623	13	BY752231	BY752231 BY752231
9		296	50.0	1582	11	AK018005	AK018005 Mus muscu
10		289.8	49.0	438	29	AY417053	AY417053 Mus muscu
11		268.8	45.4	460	9	AI430241	AI430241 vv49h02.y
12		268.8	45.4	501	9	AA762051	AA762051 vv49h02.r
13		265.8	44.9	601	13	BQ418599	BQ418599 ik55a07.y
14		265.8	44.9	998	13	BY704474	BY704474 BY704474
15		265.8	44.9	1206	11	AK004232	AK004232 Mus muscu
16		259.8	43.9	484	12	BM106914	BM106914 510989 MA
17		259.6	43.9	472	10	BE138146	BE138146 ug49a11.y
18		252.8	42.7	629	14	CB437446	CB437446 684916 MA
19		249.4	42.1	603	14	CB451900	CB451900 706716 MA
20		247.4	41.8	432	10	BB850720	BB850720 BB850720
21		240.6	40.6	388	10	BF150826	BF150826 uy88e10.y
22		234.2	39.6	367	10	BB869347	BB869347 BB869347
23		225	38.0	352	13	BY221065	BY221065 BY221065
24		219.4	37.1	359	13	BY214853	BY214853 BY214853
25		213.6	36.1	339	13	BY215822	BY215822 BY215822
26		210	35.5	558	12	BM363855	BM363855 BS3200330
27		208	35.1	334	13	BY216497	BY216497 BY216497
28		201.4	34.0	360	13	BY211786	BY211786 BY211786
29		194	32.8	356	10	BB868695	BB868695 BB868695
30		192.6	32.5	340	13	BY216553	BY216553 BY216553
31	c	187	31.6	442	13	AI769633	AI769633 wj25a06.x
32		179.4	30.3	392	10	AW659630	AW659630 97101 MAR
33		140.4	23.7	233	10	AW418175	AW418175 55737 MAR
34	c	135.6	22.9	643	14	CB453372	CB453372 708348 MA
35		131.8	22.3	224	13	BY008213	BY008213 BY008213
36	c	124	20.9	554	29	CE203341	CE203341 tigr-gss-
37		121.2	20.5	416	29	AY417601	AY417601 Pan trogl
38		119.6	20.2	417	29	AY417600	AY417600 Homo sapi
39		119.6	20.2	688	14	CK003597	CK003597 AGENCOURT
40		117.4	19.8	521	10	AW660275	AW660275 98221 MAR
41		117.4	19.8	558	10	AW658438	AW658438 94468 MAR
42		117.4	19.8	567	10	AW658432	AW658432 94462 MAR
43		117.4	19.8	579	12	BI540965	BI540965 454461 MA
44		115.8	19.6	570	12	BI975432	BI975432 483814 MA
45		114.8	19.4	544	10	BE015249	BE015249 127486 MA

ALIGNMENTS

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RESULT 1
CD691591
LOCUS       CD691591                726 bp    mRNA    linear   EST 25-JUN-2003
DEFINITION  EST8114 human nasopharynx Homo sapiens cDNA, mRNA sequence.
ACCESSION   CD691591
VERSION     CD691591.1  GI:32213459
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 726)
  AUTHORS   Liu,X.-Q., Zhou,Y., Zhang,L.-J., Xu,H., Chen,H.-K., Pan,Z.-G. and
            Zeng,Y.-X.
  TITLE     Transcriptional Gene Expression Profile of Human Nasopharynx
  JOURNAL   Unpublished (2003)
  COMMENT   Contact: YiXin Zeng
            Cancer Center
            Sun Yat-sen University
            651 DongFeng Road East, GuangZhou 510060, China
            Tel: 86-1380-9770-743
            Fax: 86-20-8775-4506
            Email: yxzeng@gzsums.edu.cn.
FEATURES             Location/Qualifiers
     source          1..726
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
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/db_xref="taxon:9606"
/tissue_type="normal nasopharynx"
/clone_lib="human nasopharynx"
/note="ESTs generated from a normal nasopharynx cDNA
library from southern Chinese"

ORIGIN

Query Match   99.2%;   Score 587.2; DB 14; Length 726;
Best Local Similarity 99.5%; Pred. No. 1.8e-133;
Matches 589; Conservative   0; Mismatches   3; Indels   0; Gaps   0;

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Qy     1 TCTGCCTCCACTGCTCTGTGCTGGGATCATGGAACTTGCACTGCTGTGTGGGCTGGTGGT 60
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Db    45 TCTGCCTCCACTGCTCTGTGCTGGGATCATGGAACTTGCACTGCTGTGTGGGCTGGTGGT 104

Qy    61 GATGGCTGGTGTGATTCCAATCCAGGGGCGGGATCCTGAACCTGAACAAGAGATGGTCAAGCA 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   105 GATGGCTGGTGTGATTCCAATCCAGGGGCGGGATCCTGAACCTGAACAAGAGATGGTCAAGCA 164

Qy   121 AGTGACTGGGAAAATGCCATCTCCTACTGCCCTACGGCTGTCACTGCGGACTAGG 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   165 AGTGACTGGGAAAATGCCATCTCCTACTGCCCTACGGCTGTCACTGCGGACTAGG 224

Qy   181 TGGCAGAGGCCAACCCAAAGATGCCACGGACTGGTGCTGCCAGACCCATGACTGCTGCTA 240
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   225 TGGCAGAGGCCAACCCAAAGATGCCACGGACTGGTGCTGCCAGACCCATGACTGCTGCTA 284

Qy   241 TGACCACCTGAAGACCCAGGGGTGCGGCATCTACAAGGACTATTACAGATACAACTTTTC 300
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   285 TGACCACCTGAAGACCCAGGGGTGCGGCATCTACAAGGACTATTACAGATACAACTTTTC 344

Qy   301 CCAGGGGAACATCCACTGCTCTGACAAGGGAAGCTGGTGTGAGCGAGCAGCTGGTGTGCCTG 360
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   345 CCAGGGGAACATCCACTGCTCTGACAAGGGAAGCTGGTGTGAGCGAGCAGCTGGTGTGCCTG 404

Qy   361 TGACAAGGAGGTGGCCTTCTGCCTGAAGCGCAACCTGGGTGCTAGAGCGCCACCCTC 420
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   405 TGACAAGGAGGTGGCCTTCTGCCTGAAGCGCAACCTGGGTGCTAGAGCGCCACCCTC 464

Qy   421 TTTCTACTGGCGGCCCCACTGCCCGGGGCAGACCCCCTGGGTGCTAGAGAAGCCCACCCCTC 480
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   465 TTTCTACTGGCGGCCCCACTGCCCGGGGCAGACCCCCTGGGTGCTAGAGAAGCCCACCCCTC 524

Qy   481 TACCCTGTTCCTCAGCATGGAGCTCTGGCATCCCCACCTCAGTATCTAACCTGAACCAGC 540
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   525 TACCCTGTTCCTCAGCATGGAGCTCTGGCATCCCCACCTCAGTATCTAACCTGAACCAGC 584

Qy   541 CTGGCTTTTCAAAACACTCCGGGGGGAGGTAGTCCCCAGCCTCCCCCGGAACCC 592
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   585 CTGGCTTTTCAAAACACTCCGGGGGGAGGTAGTCCCCAGCCTCCCCCGGAACCC 636
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RESULT 2
BI836812
LOCUS   BI836812   680 bp   mRNA   linear   EST 04-OCT-2001
DEFINITION 603084703F1 NIH_MGC_120 Homo sapiens cDNA clone IMAGE:5223912 5',
            mRNA sequence.
ACCESSION   BI836812
VERSION   BI836812.1 GI:15948362
KEYWORDS   EST.
SOURCE   Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 680)
AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
TITLE   National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL   Unpublished (1999)
COMMENT   Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Life Technologies, Inc.
            cDNA Library Preparation: Life Technologies, Inc.
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM11563 row: e column: 01
High quality sequence start: 4
High quality sequence stop: 680.

FEATURES   Location/Qualifiers
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                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:5223912"
                     /lab_host="DH10B"
                     /clone_lib="NIH_MGC_120"
                     /note="Organ: pooled pancreas and spleen; Vector:
                     pCMV-SPORT6; Site_1: NotI; Site_2: EcoRV (destroyed); RNA
                     source anonymous pool of spleen and pancreas from 28 yo
                     male. Library is oligo-dT primed and directionally cloned
                     (EcoRV site is destroyed upon cloning). Average insert
                     size 1.5 kb, insert size range 1-2.5 kb. Library is
                     normalized and enriched for full-length clones and was
                     constructed by C. Gruber (Invitrogen). Research Genetics
                     tracking code 025. Note: this is a NIH_MGC Library."

ORIGIN

Query Match   89.1%;   Score 527.6; DB 12; Length 680;
Best Local Similarity 98.6%; Pred. No. 7.7e-119;
Matches 574; Conservative   0; Mismatches   4; Indels   4; Gaps   4;

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Qy    12 TGCTCTGTGCTGGGATCATGGAACTTGCACTGCTGTGTGGGCTGGTGGTGATGGCTGGTG 71
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1 TGCTCTGTGCTGGGATCATGGAACTTGCACTGCTGTGTGGGCTGGTGGTGATGGCTGGTG 60

Qy    72 TGATTCCAATCCAGGGGCGGGATCCTGAACCTGAACAAGAGATGGTCAAGCAAGTGACTGGGA 131
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    61 TGATTCCAATCCA-GGCGGGATCCTGAACCTGAACAAGAGATGGTCAAGCAAGTGACTGGGA 119

Qy   132 AAATGCCATCTCCTACTGCCCTACGGCTGTCACTGCGGACTAGGTGGCAGAGGCC 191
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   120 AAATGCCATCTCCTACTGCCCTACGGCTGTCACTGCGGACTAGGTGGCAGAGGCC 179

Qy   192 AACCCAAAGATGCCACGGACTGGTGCTGCCAGACCCATGACTGCTGCTATGACCACCTGA 251
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   180 AACCCAAAGATGCCACGGACTGGTGCTGCCAGACCCATGACTGCTGCTATGACCACCTGA 239

Qy   252 AGACCCAGGGGTGCGGCATCTACAAGGACTATTACAGATACAACTTTTCCCAGGGGAACA 311
           |||||||| |||||||||||||||||||||||||||||||||||||||||||||||||||
Db   240 AGACCCA-GGGTGCGGCATCTACAAGGACTATTACAGATACAACTTTTCCCAGGGGAACA 298

Qy   312 TCCACTGCTCTGACAAGGGAAGCTGGTGTGAGCGAGCAGCTGGTGTGCCTGTGACAAGGAGG 371
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   299 TCCACTGCTCTGACAAGGGAAGCTGGTGTGAGCGAGCAGCTGGTGTGCCTGTGACAAGGAGG 358

Qy   372 TGGCCTTCTGCCTGAAGCGCAACCTGGGTGCTAGAGCGCCACCACCTTCTACTGGC 431
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   359 TGGCCTTCTGCCTGAAGCGCAACCTGGGTGCTAGAGCGCCACCACCTTCTACTGGC 418

Qy   432 GGCCCCACTGCCCGGGGG-CAGACCCCTGGGTGCTAGAGAAGCCCCACCACCCTCGTTC 490
           ||||||||||||||||||  ||||||| ||||||||||||||||||||||||||||||
Db   419 GGCCCCACTGCCCGGGGGGCCAGACCCCTGGGTGCTAGAGAAGCCCCACCACCCTCGTTC 478

Qy   491 CTCAGCATGGAGCTCTGGCATCCCCACCTCAGTATCTAACCTGAACCAGCCTGGCTTTTC 550
           |||||||||||||||||||  ||||||||||||||||||||||||||||||||||||||
Db   479 CTCAGCATGGAGCTCTGGCAT-CCCACCTCAGTATCTAACCTGAACCAGCCTGGCTTTTC 537

Qy   551 AAACACTCCGGGGGGAGGTAGTCCCCAGCCTCCCCCGGAACCC 592
           |||||||||||||||||||||||||||||||||||||||||||
Db   538 AAACACTCCGGGGGGAGGTAGTCCCCAGCCTCCCCCGGAACC 579
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RESULT 3
AY417051

LOCUS   AY417051   438 bp   DNA   linear   GSS 17-DEC-2003
DEFINITION Homo sapiens PLA2G2D gene, VIRTUAL TRANSCRIPT, partial sequence,
            genomic survey sequence.
ACCESSION   AY417051
VERSION   AY417051.1 GI:39773011
KEYWORDS   GSS.
SOURCE   Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 438)
AUTHORS   Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
            Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
            Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
            Adams,M.D. and Cargill,M.
TITLE   Inferring nonneutral evolution from human-chimp-mouse orthologous
            gene trios
JOURNAL   Science 302 (5652), 1960-1963 (2003)
PUBMED   14671302
REFERENCE   2 (bases 1 to 438)
AUTHORS   Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
            Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
            Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
            Adams,M.D. and Cargill,M.
TITLE   Direct Submission
JOURNAL   Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
            Rockville, MD 20850, USA
COMMENT   This sequence was made by sequencing genomic exons and ordering
            them based on alignment.
FEATURES   Location/Qualifiers
     source   1..438
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
     gene   <1..>438
                     /gene="PLA2G2D"
                     /locus_tag="HCM6095"
ORIGIN

Query Match   73.7%; Score 436.4; DB 29; Length 438;
Best Local Similarity   99.8%; Pred. No. 1.6e-96;
Matches   437; Conservative   0; Mismatches   0; Indels   1; Gaps   0;

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Qy  29 ATGGAACTTGCACTGCTGTGTGGGCTGGTGGTGTTGATTCCAATCCAGGGC 88
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Db   1 ATGGAACTTGCACTGCTGTGTGGGCTGGTGGTGTTGATTCCAATCCAGGGC 60

Qy  89 GGGATCCTGAACCTGAACAAGATGGTCAAGCAAGTGACTAGGTGGCCACG 148
       |||||||||||||||||||||||||||||||||||||||||||||||||
Db  61 GGGATCCTGAACCTGAACAAGATGGTCAAGCAAGTGACTAGGTGGCCACG 120

Qy 149 TACTGGCCCTACGGCGTCACTCGCGACTAGGTGGCCACG 208
       |||||||||||||||||||||||||||||||||||||||
Db 121 TACTGGCCCTACGGCGTCACTCGCGACTAGGTGGCCACG 180

Qy 209 GACTGGTGTCGCCGAGACCCATGCTATGACGACTGCTGCCAGACCCAGGGGTGCGGC 268
       ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 181 GACTGGTGTCGCCGAGACCCATGCTATGACGACTGCTGCCAGACCCAGGGGTGCGGC 240

Qy 269 ATCTACAAGGACTATTACAGATACAACTTTCCCAGGGGAACATCCACTGCTCTGACAAG 328
       |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 241 ATCTACAAGGACTATTACAGATACAACTTTCCCAGGGGAACATCCACTGCTCTGACAAG 300

Qy 329 GGAAGCTGGTGTGAGCAGCAGCTGCCGTTTCTACTGGCCGCCCCACTGCCGGGGG 388
       ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 301 GGAAGCTGGTGTGAGCAGCAGCTGCCGTTTCTACTGGCCGCCCCACTGCCGGGGG 360

Qy 389 CGCAACCTGGACACCTACCAGGAGCGACTGCGCTTTCTACTGCGCCGGGGG 448
       ||||||||||||||||||||||||||||||||||||||||||||||||||
Db 361 CGCAACCTGGACACCTACCAGGAGCGACTGCGCTTTCTACTGCGCCGGGGG 420

Qy 449 CAGACCCCTGGGTGCTAG 466
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Db 421 CAGACCCCTGGGTGCTAG 438
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RESULT 4
AY417052

LOCUS   AY417052   438 bp   DNA   linear   GSS 17-DEC-2003
DEFINITION Pan troglodytes PLA2G2D gene, VIRTUAL TRANSCRIPT, partial sequence,
            genomic survey sequence.
ACCESSION   AY417052
VERSION   AY417052.1 GI:39773012
KEYWORDS   GSS.
SOURCE   Pan troglodytes (chimpanzee)
ORGANISM   Pan troglodytes
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
REFERENCE   1 (bases 1 to 438)
AUTHORS   Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
            Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
            Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
            Adams,M.D. and Cargill,M.
TITLE   Inferring nonneutral evolution from human-chimp-mouse orthologous
            gene trios
JOURNAL   Science 302 (5652), 1960-1963 (2003)
PUBMED   14671302
REFERENCE   2 (bases 1 to 438)
AUTHORS   Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
            Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
            Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
            Adams,M.D. and Cargill,M.
TITLE   Direct Submission
JOURNAL   Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
            Rockville, MD 20850, USA
COMMENT   This sequence was made by sequencing genomic exons and ordering
            them based on alignment.
FEATURES   Location/Qualifiers
     source   1..438
                     /organism="Pan troglodytes"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9598"
     gene   <1..>438
                     /gene="PLA2G2D"
                     /locus_tag="HCM6095"
ORIGIN

Query Match   73.7%; Score 436.4; DB 29; Length 438;
Best Local Similarity   99.8%; Pred. No. 1.6e-96;
Matches   437; Conservative   0; Mismatches   0; Indels   1; Gaps   0;

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Qy  29 ATGGAACTTGCACTGCTGTGTGGGCTGGTGGTGTGATTCCAATCCAGGGC 88
       |||||||||||||||||||||||||||||||||| |||||||||||||||
Db   1 ATGGAACTTGCACTGCTGTGTGGGCTGGTGGTGTGATTCCAATCCAGGGC 88

Qy  89 GGGATCCTGAACCTGAACAAGATGGTCAAGCAAGTGACTGGTGCGGAAAATGCCCATCCTCTCC 148
       |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  61 GGGATCCTGAACCTGAACAAGATGGTCAAGCAAGTGACTGGTGCGGAAAATGCCCATCCTCTTC 120

Qy 149 TACTGGCCCTACGGCGTCACTGCGACCAGGTGGCCACG 208
       ||||||||||||||||||||| ||||||||||||||||
Db 121 TACTGGCCCTACGGCGTCACTGCGACCAGGTGGCCACG 180

Qy 209 GACTGGTGTCGCCAGACCATGACGCTCTATGACCAGGGGTGCGGC 268
       |||||||||||||||||||||||||||||||||||||||||||||
Db 181 GACTGGTGTCGCCAGACCATGACGCTCTATGACCAGGGGTGCGGC 240

Qy 269 ATCTACAAGGACTATTACAGATACAACTTTTCCCAGGGGAACATCCACTGCTCTGACAAG 328
       ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 241 ATCTACAAGGACTATTACAGATACAACTTTTCCCAGGGGAACATCCACTGCTCTGACAAG 300

Qy 329 GGAAGCTGGTGTGAGCAGCAGCTGTGTCCTGACACAAGGAGGTGGCCTTCTGCCTGAAG 388
       |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 301 GGAAGCTGGTGTGAGCAGCAGCTGTGTCCTGACACAAGGAGGTGGCCTTCTGCCTGAAG 360

Qy 389 CGCAACCTGGACACCTACCAGGAGCGACTGCGCTTTCTACTGGCGGGGCCCCACTGCCGGGGG 448
       ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 389 CGCAACCTGGACACCTACCAGGAGCGACTGCGCTTTCTACTGGCGGGGCCCCACTGCCGGGGG 448
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Db 361 CGCAACCTGGACACCTACCAGAAGCGACTGCGTTTCTACTGCGCCCCACTGCCGGGGG 420
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Qy 449 CAGACCCCTGGGTGCTAG 466
        ||||||||||||||||||
Db 421 CAGACCCCTGGGTGCTAG 438

RESULT 5
BM153087
LOCUS   BM153087   463 bp   mRNA   linear   EST 30-NOV-2001
DEFINITION TCBAP1Q13560 Pediatric pre-B cell acute lymphoblastic leukemia
            Baylor-HGSC project=TCBA Homo sapiens cDNA clone TCBAP1356, mRNA
            sequence.
ACCESSION   BM153087
VERSION   BM153087.1 GI:17177919
KEYWORDS   EST.
SOURCE   Homo sapiens (human)
  ORGANISM Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 463)
  AUTHORS   Wei,Y., Tsang,Y.T.M., Mei,G., Ku,J.M., Ali-Osman,F.R. Jr.,
            Gunaratne,P.H., Muzny,D., Bouck,J., Gibbs,R.A. and Margolin,J.F.
  TITLE   Pediatric leukemia cDNA Sequencing Project (2001)
  JOURNAL   Unpublished (2001)
COMMENT   Contact: Dr. Judith F. Margolin
            Texas Children's Cancer Center and Human Genome Sequencing Center
            at Baylor College of Medicine
            1102 Bates, MC3-3320 Houston, TX 77030, USA
            Tel: 832-824-4536
            Fax: 832-825-4038
            Email: clones@xcccc.org
            Seq primer: M13 primer.
FEATURES   Location/Qualifiers
     source 1..463
            /organism="Homo sapiens"
            /mol_type="mRNA"
            /db_xref="taxon:9606"
            /clone="TCBAP1356"
            /sex="male"
            /tissue_type="leukopheresis"
            /cell_type="pre-B cell"
            /dev_stage="pediatric 2 years"
            /lab_host="DH10B"
            /clone_lib="Pediatric pre-B cell acute lymphoblastic
            leukemia Baylor-HGSC project=TCBA"
            /note="Vector: lambda pSB; Site_1: BamHI; Site_2: EcoRI;
            First strand cDNA was primed with an anchored
            XhoI-oligo(dT) primer [5'GGAGGACTCGAGCGGCCGCAGGAGGAG(T)VN
            3'; V=A,C,G; N=A,C,G,T] and then dG tailed. Second strand
            was primed with a BamHI-dC primer
            [5'AGGAGAGCTCGGATCCGCGGCCGCCAATAATAATAAT(C) 3'].
            Double-stranded cDNA was then digested with BamHI and XhoI
            and directionally cloned into the BamHI and SalI sites of
            lambda pSB vector. Library went through one round of
            normalization. Library was constructed by Wei Yu at RIKEN
            of Japan (Carninci P, Westover A, Nishiyama Y, Ohsumi T,
            Itoh M, Nagaoka S, Sasakin, Okazaki Y, Muramatsu M,
            Schneider C, Hayashizaki Y, High efficiency selection of
            full-length cDNA by improved biotinylated cap trapper.,
            DNA Res 4: 1, 61-6, Feb 28, 1997)"
ORIGIN

Query Match   72.2%; Score 427.2; DB 12; Length 463;
Best Local Similarity   99.3%; Pred. No. 2.9e-94;
Matches 429; Conservative   0; Mismatches   3; Indels   0; Gaps   0;

Qy   1 TCTGCCTCCACTGCTCTGTGCTGGGATCATGGAACTTGCACTGCTGTGTGGGCTGGTGGT 60
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Db 32 TCTGCCTCCACTGCTCTGTGCTGGGATCATGGAACTTGCACTGCTGTGTGGGCTGGTGGT 91

Qy 61 GATGGCTGGTGTGATTCAATCCAGGGCGGATCCTCAGGGCGGGATCCTGAACCAGAAGATGGTCAAGCA 120

Db 92 GATGGTTTTTGTGATTCAATCCAGGGCGGGATCCTCAGGGCGGGATCCTGAACCTGTCACTGCGGACTAGG 151
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Qy 121 AGTGACTGGGAAAATGCCATCCTCCTCCTCTACTGGCCCTACTGGCCGTGTCACTGCGGACTAGG 180
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 152 AGTGACTGGGAAAATGCCCATCCTCCTCCTCTACTGGCCCTACTGGCCGTGTCACTGCGGACTAGG 211

Qy 181 TGGCAGAGGCCAACCCAAAGATGCCACGGACTGGTGCTGCCAGACCCATGACTGCTGCTA 240
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 212 TGGCAGAGGCCAACCCAAAGATGCCACGGACTGGTGCTGCCAGACCCATGACTGCTGCTA 271

Qy 241 TGACCACCTGAAGACCCAGGGTGCGGCATCTACAAGGACTATTACAGATACAACTTTC 300
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 272 TGACCACCTGAAGACCCAGGGTGCGGCATCTACAAGGACTATTACAGATACAACTTTC 331

Qy 301 CCAGGGGACACATCCACTGCTCTGACAAGGGAAGTGGTGTGAGCAGCAGCTGTGTGCCTG 360
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 332 CCAGGGGACACATCCACTGCTCTGACAAGGGAAGCTGGTGTGAGCAGCAGCTGTGTGCCTG 391

Qy 361 TGACAAGGAGGTGGCCTTCTGCCTGAAGGCAACCTGGACAACCTCACCAGAAGCGACTGCG 420
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 392 TGACAAGGAGGTGGCCTTCTGCCTGAAGGCAACCTGGACAACCTCACCAGAAGCGACTGCG 451

Qy 421 TTTCTACTGCGCG 432
        |||||||||||||
Db 452 TTTCTACTGCGCG 463

RESULT 6
CB481980/c
LOCUS   CB481980   461 bp   mRNA   linear   EST 26-MAR-2003
DEFINITION jns85_C09.f jns Sus scrofa cDNA 5', mRNA sequence.
ACCESSION   CB481980
VERSION   CB481980.1 GI:29288366
KEYWORDS   EST.
SOURCE   Sus scrofa (pig)
  ORGANISM Sus scrofa
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
REFERENCE   1 (bases 1 to 461)
  AUTHORS   Neilan,J.G., Kutish,G.F., Lu,Z., Zsak,A. and Rock,D.L.
  TITLE   Sequence analysis of African swine fever virus infected and
            non-infected porcine macrophage cDNA libraries
  JOURNAL   Unpublished (2003)
COMMENT   Contact: Neilan JG
            Plum Island Animal Disease Center
            US Department of Agriculture, Agricultural Research Service
            PO Box 848, Greenport, NY 11944-848, USA
            Tel: 631 323 3133
            Fax: 631 323 3044
            Email: jneilan@piadc.ars.usda.gov
            Single pass sequencing. Bases called with phred v0.020425.c and
            trimmed with the aid of the trim_alt option. Vector identified by
            cross_match v0.990329 and lucy v1.17p.
            Seq primer: M13 Forward.
FEATURES   Location/Qualifiers
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            /mol_type="mRNA"
            /db_xref="taxon:9823"
            /tissue_type="lymphoid"
            /cell_type="macrophage"
            /lab_host="DH10B"
            /clone_lib="jns"
            /note="Vector: pSPORT1; Site 1: NotI; Site 2: SalI;
            Library made from pools of polyA selected RNA. Macrophages
            were derived from peripheral blood mononuclear cells
            cultured for 48 hrs on plastic in the presence of 30% L929
            supernatant."
ORIGIN

Query Match   54.6%; Score 323; DB 14; Length 461;
Best Local Similarity   84.8%; Pred. No. 1.2e-68;

Matches 362; Conservative 0; Mismatches 65; Indels 0; Gaps 0;

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Db    427 CTGCCTCCACTGCTCTGTGCTGGGACCATGGAACTTCCCCTGCTGTGTGCTTCTTGTGGCA 368

Qy     62 ATGGCTGGTGTGATTCCAATCCAGGGCGGATCCTGAACCTGAACAAGATGGTCAAGCAA 121
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Db    367 TTTGTGTGGTGATTCCAGCCCAGGGTGGGATCCTGAACCTGAACAAGATGATCAAAACAA 308

Qy    122 GTGACTGGGAAAAATGCCCATCCTCCTCCTACTGGCCCTACGGCTGTCACTGCGGACTAGGT 181
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Db    307 GTGACCGGGAAGGTGCCCCTTCTTCTTCCTATTGGCCCTACGGCTGTCACTGTGGAATCGGT 248

Qy    182 GGCAGAGGCCAACCCAAAGATGCCACGGACTGGTGCTGCCAGACCCATCGCTGTGCTAT 241
          ||||||||||||||||| |||||||||||||||||||||| ||||
Db    247 GGCAGAGGCTGAACCCAAAGATGCCACGGACTGGTGCTGCCAGACCCATGACTGTGCTAC 188

Qy    242 GACCACCTGAAGACCCAGGGTGCGGCATCTACAAGGACTATTACAGATACAACTTTTCC 301
          ||||||||||||||| ||||| ||||||||||||||||||||
Db    187 AGTCACCTGAAGGGGCCATGCTGCGCCGCGCCCACCCACCTACAGATACACCTTTTCC 128

Qy    302 CAGGGGAACATCCACTGCTCTGACAAGGGAAGCTGGTGTGAGCAGCAGCAGCA-GCTGTGT 361
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Db    127 CAGGGGACCGTCCAGTGCTCTGACAAGGGGAGCTGGTGTCGAGCGAGAGCTGTGCCCTGT 68

Qy    362 GACAAGGAGGTGGCCTTCTGGCCTTCTGACAAGCGCAACCTGGACACCTACCAGAAGCCGACTGCGT 421
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Db     67 GACAAGGGGGTGGGCTGGTTTCTGCATGAAGCCGGAACCTGGAACCTGGACCACTGGGT 8
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Qy    422 TTCTACT 428
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Db      7 TACTACT 1
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RESULT 7

CD687559

Query Match 52.1%; Score 308.6; DB 14; Length 424;
Best Local Similarity 96.3%; Pred. No. 3.9e-65;
Matches 369; Conservative 0; Mismatches 0; Indels 9; Gaps 5;

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Qy      1 TCTGCCTCCACTGCTCTGTGGGATCATGAAACTTGCACTGCTGTGTGGGCTGGTGGGTGGT 60
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Db     42 TCTGCCTCCACTGCTCTGTGGGATCATGAAACTTGCACTGCTGTGTGGGCTGGTGGGTGGT 101

Qy     61 GATGGCTGGTGTGATTCCAATCCAGGGCGGGGATCCTGAACCTGAACAAGATGGTCAAGCA 120
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Db    102 GATGGCTGGTGGTGTGATGCCAGCCAGGGGCGGGATCCTGAACCTGAACAAGATGGTCAAGCA 161

Qy    121 AGTGACTGGGAAAAATGCCCATCCTCCTCCTACTGGCCCTACGGCTGTCACTGCGGACTAGG 180
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Db    162 AGTGACTGGGAAAAATGCCCATCCTCCTCCTACTGGCCCTACGGCTGTCACTGCGGACTAGG 221

Qy    181 TGGCAGAGGCC-AACCCAAAGATGCCACGGACTGGTGCTGCCAGACCCATCGCTGTGCT 239
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Qy    240 ATGACCACCTGAAGACCCAGGGGTGCGG-CATTACAAGGA-CTATTACAGATA-CAACT 296
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Db    282 ATGACCACCTGAAGGGGCCAGGGGTGCGGTGATCTACAAGGAGATATTACAGATAGCAACT 341

Qy    297 TTTCCCAGGGGAACATCCACTGCTCTGACAAGGGAAGCTGGTGTGAGCAGCA-GCTGTGT 355
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Db    342 TTTCCCAGGGGAACATCCACTGCTCTGACAAGGGGAGCTGTGTGTGACCAGCATGCTGTGT 401

Qy    356 GCCTGTGCACAAGGAGGTGGCCTT 378
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Db    402 GCCTGTGACAAGGAGGTGGCCTT 424
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RESULT 8

BY752231

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Db    247 GCCCACCTGAAGATCGATGGATGCAAGAGCCTGACAGACAACTACAAATACAGCATCTCC 306

Qy    302 CAGGGGACATCCACTGCTCTGACAAGGGAAGCTGGTGTGACAGCAGTGTGTGCCTGT 361
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Db    307 CAGGGCACTATCCAGTGTCTGACAACGGGAGCTGGTGTGAAAGGCAACTGTGTGCTTGT 366

Qy    362 GACAAGGAGGTGGCCTTCTGCCTGAAGCGCAACCTGACACCTACCAGAAGCGACTGCGT 421
          ||||||||||| |||||||||||||| ||||| ||||||||||||||||||||||||||
Db    367 GACAAGGAGGTGGCCTTGTTGCTTGAAGCANAACCTGGATAGCTACAATAAGCGCTGCGT 426

Qy    422 TTCTACTGGCGCGCCCCACTGCCGGGGGCCAGACCCTGGGTGCTAGAAGCCCACCCCTCT 481
          ||||||||||||||| ||||||||| ||||||||||| |||||| ||||||||||||| |
Db    427 TACTACTGGCGCGCCCCGTTGCAAAGGCCAAGACTCCAGCATGCTAAGGGAGTCCACTCTGT 486

RESULT 9
AK018005
LOCUS          AK018005          1582 bp    mRNA     linear     HTC   20-SEP-2003
DEFINITION     Mus musculus adult male thymus cDNA, RIKEN full-length enriched
               library, clone:5830452G11 product:phospholipase A2, group IID, full
               insert sequence.
ACCESSION      AK018005
VERSION        AK018005.1  GI:12857529
KEYWORDS       HTC; CAP trapper.
SOURCE         Mus musculus (house mouse)
  ORGANISM     Mus musculus
               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
               Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE      1
  AUTHORS      Carninci,P. and Hayashizaki,Y.
  TITLE        High-efficiency full-length cDNA cloning
  JOURNAL      Meth. Enzymol. 303, 19-44 (1999)
  MEDLINE      99279253
   PUBMED      10349636
REFERENCE      2
  AUTHORS      Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K.,
               Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
  TITLE        Normalization and subtraction of cap-trapper-selected cDNAs to
               prepare full-length cDNA libraries for rapid discovery of new genes
  JOURNAL      Genome Res. 10 (10), 1617-1630 (2000)
  MEDLINE      20499374
   PUBMED      11042159
REFERENCE      3
  AUTHORS      Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P.,
               Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M.,
               Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A.,
               Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K.,
               Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M.,
               Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J.,
               Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.
  TITLE        RIKEN integrated sequence analysis (RISA) system--384-format
               sequencing pipeline with 384 multicapillary sequencer
  JOURNAL      Genome Res. 10 (11), 1757-1771 (2000)
  MEDLINE      20530913
   PUBMED      11076861
REFERENCE      4
  AUTHORS      The RIKEN Genome Exploration Research Group Phase II Team and the
               FANTOM Consortium.
  TITLE        Functional annotation of a full-length mouse cDNA collection
  JOURNAL      Nature 409, 685-690 (2001)
REFERENCE      5
  AUTHORS      The FANTOM Consortium and the RIKEN Genome Exploration Research
               Group Phase I & II Team.
  TITLE        Analysis of the mouse transcriptome based on functional annotation
               of 60,770 full-length cDNAs
  JOURNAL      Nature 420, 563-573 (2002)
REFERENCE      6  (bases 1 to 1582)
  AUTHORS      Adachi,J., Aizawa,K., Akahira,S., Akimura,T., Arai,A., Aono,H.,
               Arakawa,T., Bono,H., Carninci,P., Fukuda,S., Fukunishi,Y.,
               Furuno,M., Hanagaki,T., Hara,A., Hayatsu,N., Hiramoto,K.,
               Hiraoka,T., Hori,F., Imotani,K., Ishii,Y., Itoh,M., Izawa,M.,
               Kasukawa,T., Kato,H., Kawai,J., Kojima,Y., Konno,H., Kouda,M.,
               Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Nishi,K.,
```

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PUBMED      12466851
COMMENT     Contact: Yoshihide Hayashizaki
            Laboratory for Genome Exploration Research Group, RIKEN Genomic
            Sciences Center(GSC), Yokohama Institute
            The Institute of Physical and Chemical Research (RIKEN)
            1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
            Tel: 81-45-503-9222
            Fax: 81-45-503-9216
            Email: genome-res@gsc.riken.go.jp,
            URL:http://genome.gsc.riken.go.jp/
            Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Carninci,P.,
            Fukuda,S., Hashizume,W., Hayashida,K., Hirozane,T., Hori,F.,
            Imotani,K., Ishii,Y., Itoh,M., Kawagawa,I., Kawai,J., Kojima,Y.,
            Kondo,S., Konno,H., Koya,S., Miyazaki,A., Murata,M., Nakamura,M.,
            Nomura,K., Numazaki,R., Ohno,M., Ohsato,N., Saito,R., Sakazume,N.,
            Sano,H., Sasaki,D., Sato,K., Shibata,K., Shiraki,T., Tagami,M.,
            Takeda,Y., Waki,K., Watahiki,A., Muramatsu,M. and Hayashizaki,Y.
            Direct Submission
            Computational Analysis of Full-Length Mouse cDNAs Compared with
            Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)
            Normalization and subtraction of cap-trapper-selected cDNAs to
            prepare full-length cDNA libraries for rapid discovery of new
            genes. Genome Res. 10 (10), 1617-1630 (2000)
            RIKEN integrated sequence analysis (RISA) system--384-format
            sequencing pipeline with 384 multicapillary sequencer. Genome Res.
            10 (11), 1757-1771 (2000)
            Computer-based methods for the mouse full-length cDNA
            encyclopedia: real-time sequence clustering for construction of a
            nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
            Encyclopedia Project of Genome Exploration Research Group in Riken
            Genomic Sciences Center and Genome Science Laboratory in RIKEN.
            Division of Experimental Animal Research in Riken contributed to
            prepare mouse tissues.
            Tissues were provided by Dr. John Todd (Dept. of Medical Genetics
            Wellcome Trust Centre for Molecular Mechanisms in Disease Wellcome
            Trust/MRC building Addenbrookes Hospital Cambridge) whose
            assistance we gratefully acknowledge.
            Please visit our web site (http://genome.gsc.riken.go.jp) for
            further details.
FEATURES             Location/Qualifiers
     source          1..623
                     /organism="Mus musculus"
                     /mol_type="mRNA"
                     /strain="NOD"
                     /db_xref="taxon:10090"
                     /clone="F830213F07"
                     /tissue_type="activated spleen"
                     /clone_lib="RIKEN full-length enriched, activated spleen"
ORIGIN

Query Match       50.1%;     Score 296.6; DB 13;    Length 623;
Best Local Similarity   77.5%;     Pred. No. 4.3e-62;
Matches  372;    Conservative   0;    Mismatches 105;    Indels   3;    Gaps   1;

Qy      2 CTGCCTCCACTGCTCTGTGCTGGGATCATGGAACTTGCACTGCTGTGTGGGCTGGTGGTG 61
          |||||||||| |||||||||||||||| |||||||||||||| ||||||||||||||
Db     10 CTGCCTGCCTTGCCTCTGGGCTTGGGAACTATCGAGACTTCGCCCCTGCTGTGTGGGCTGCTGC-- 67

Qy     62 ATGGCTGGTGTGATTCCAATCCAGGCGCGGGATCCTGAACCTGAACAAGATGGTCAAGCAA 121
          ||||||||||||||    |||||||||||||||||||||||||||||||||||||||||||
Db     68 -TGGCCGGTATAACTGCAACCCAGGGAGGGCTCCTGAACCTGAACAAGATGGTCACCACAC 126

Qy    122 GTGACTGGGAAAATGCCAATCCTCCTACTGGCCCTACGGCTGTCACTGCGGACTAGGT 181
          ||| ||||| ||||||| |||||||||||||||||| ||||||||||| |||||||||||
Db    127 ATGACGGGAAGAAAGCCTTTCTTCAGCTACTGCCCTACGGCTGTCACTGTGGACTTGGT 186

Qy    182 GGCAGAGGCCAACCCAAAGATGCCACGGACTGGTGCTGCCAGACCCATGACTGCTGCTAT 241
          ||| |||| |||||||||| ||| ||| |||||||| ||||||||||||| |||||| ||
Db    187 GGCAAAGGGCAACCCAAAGATGCCACAGACTGTGCTGCTCAGAAGCATGATTGTTGCTAT 246

Qy    242 GACCACCTGAAGACCCGAAGACCCGAGGGTGCGCATCTACAACGGACTATTACAGATACAACTTTTCC 301
          |||||||||| |||  ||| |  |||  ||| ||  |||     || |  ||| ||| ||  |||||
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Db   187 GGCAAAGGGCAACCCAAAGATGCCACAGACTGTGTCGTGTCGCTCAGAGACATGATTGTTGCTAT 246
         ||||   |||      ||||||||||||||||||||||||  ||| |||||||||||  |||||
Qy   242 GACCACCTGAAGACCCAGGGGCTGCGGCATCTACAAGGACTATTACAGATACAACTTTCC 301
         ||||||||||||||| |||||||||||||||| |||||||||||||||||||||||||||||
Db   247 GCCCACCTGAAGATGATGGATGCAAGAGCCTGACAGCAACTACAATACAGCATCTCC 306

Qy   302 CAGGGAACATCCACTGCTCTGACAAGGGAAGCTGGTGTGAGCAGCAGCTGTGTCGTGT 361
         ||||  |||||||||||||||||||||||||||| ||||||||||||||||||||||||
Db   307 CAGGGCACTATCCAGTGCTCTGACAACGGGAGCTGGTGTGAAAGGCAACTGTGTGCTTGT 366

Qy   362 GACAAGGAGGTGGCCTTCTGCTGAGCCGCAACCTGACACCTACCAGAAGCGACTGCGT 421
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   367 GACAAGGAGGTGGCCTTGTGCTTGAAGCAAAACCTGATAGCTACAATAAGGCCTGCGT 426

Qy   422 TTCTACTGGCGCCCACTGCCGCGGGGCAGACCCCTGGGTGCTAGAAGCCCACCCTCT 481
         ||||||||||||||||||||||||||||||||||| |||||||||||||||||||
Db   427 TACTACTGGCGCGCCCCGTTGCAAAGGCAAGACTCCAGCATCCTAAGGGAGTCCACTCTGT 486
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RESULT 10
AY417053
LOCUS   AY417053   438 bp   DNA   linear   GSS 17-DEC-2003
DEFINITION Mus musculus PLA2G2D gene, VIRTUAL TRANSCRIPT, partial sequence.
            genomic survey sequence.
ACCESSION   AY417053
VERSION   AY417053.1   GI:3977301
KEYWORDS   GSS.
SOURCE   Mus musculus (house mouse)
ORGANISM   Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1 (bases 1 to 438)
AUTHORS   Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
            Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
            Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
            Adams,M.D. and Cargill,M.
TITLE   Inferring nonneutral evolution from human-chimp-mouse orthologous
            gene trios
JOURNAL   Science 302 (5652), 1960-1963 (2003)
PUBMED   14671302
REFERENCE   2 (bases 1 to 438)
AUTHORS   Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
            Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
            Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
            Adams,M.D. and Cargill,M.
TITLE   Direct Submission
JOURNAL   Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
            Rockville, MD 20850, USA
COMMENT   This sequence was made by sequencing genomic exons and ordering
            them based on alignment.
FEATURES   Location/Qualifiers
     source   1..438
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:10090"
     gene   <1..>438
                     /gene="PLA2G2D"
                     /locus_tag="HCM6095"

ORIGIN

Query Match   49.0%;   Score 289.8; DB 29; Length 438;
Best Local Similarity 78.9%;   Pred. No. 1.7e-60;
Matches 345; Conservative 0; Mismatches 92; Indels 0; Gaps 0;

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Qy    29 ATGGAACTTGACTGCTGTGTGGGCTGGTGTGGTGATGGCTGGTGTGATTCCAATCCAGGGC 88
         ||  || |||||||||| |||||||  ||||||||||| |||||||||||||| |||||||
Db     1 ATGAGACTCGCCCCTGCTGTGTGTGGGCTGGTGTGGGTATAACTGCAACCAGGGA 60

Qy    89 GGGATCCTGAACCTGACAAGATGTCAAGCAAGTGACTGGGAAAAATGCCATCCTCTCC 148
         ||||| ||||||||||||  |||||| |||||||||||||||| || ||||||||| |||
Db    61 GGGCTCCTGGAACCTGACAACAAGATGGTCACACATGACGGGGAGAAGAAGCCTTTCCAGC 120
```

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                                                      rounds of normalization, and was constructed by Bento
                                                      Soares and M.Fatima Bonaldo."

ORIGIN

                  Query Match          45.4%;  Score 268.8;  DB 9;  Length 460;
                  Best Local Similarity  77.7%;  Pred. No. 2.5e-55;
                  Matches  324;  Conservative  0;  Mismatches  93;  Indels  0;  Gaps  0;

Qy    65  GCTGGTGTGATTCCAATCCAGGGGGGATCCTGAACCTGAACCAAGAGATGGTCAAGCAAGTG  124
          | ||||| || ||||||||||||||||| ||||| ||||| |||||||||||||||||||||
Db     1  GCCCGTATAACTGCAACCCAGGGAGGGCTTCCTGAACCTGAACCAAGAGATGGTCACACACATG  60

Qy   125  ACTGGGAAAATGCCCATCTCTCCTACTGGCCCCTACGGCTGTCACTGGCGACTAGGTGGC  184
          | ||||||| |||||| |||||||| |||||| ||||||| ||||||||||||||||||||
Db    61  ACGGGGAGAAAGCCTTCTTCAGTCATGCCCCTACGGCTGTCACTGTGGACTTGGTGGC  120

Qy   185  AGAGGCCAACCCAAAGATGCCACGACTGGTGCGCCATCTACAAGGACTATTTACAGATACAACTTTTCCCAG  304
          |||||| |||||| ||||||||| ||||||| |||||||||||||||||||||||||||||||||||||
Db   121  AAAGGGCAACCCAAAGATGCCACAGACTGGTGCTGTCAGAAGCATGATTGTTGTCATAGCC  180

Qy   245  CACCTGAAGACCCAGGGGTGCGGCATCTACAAGGAAGCTGGTGTGAGCAGCGCAGCTGTGTGCCGTTC  304
          |||||||| | ||||| ||| |||||||||||| |||||||||||| |||||||||||||||||||||||
Db   181  CACCTGAAGATCGATGGATGCAAGAGCCTGACAGACAACTACAATACAGCCATCTCCCAG  240

Qy   305  GGGAACATCCACTGCTTCTGACAACAGGGAAGCTGGTGTGAGCAGCGCAGCTGTGTGCCGTTC  364
          ||||| ||||||||||||||| |||| |||||| |||||||||||| |||||||||||||||||
Db   241  GGCACTATCCAGTGCTTCTGACAACAGGGAGCTGGTGTGAGCAACTGTGTGCTTGTGAC  300

Qy   365  AAGGAGGTGGCCTTCTGCCTGGAAGCGCAACCTGACACCTACCAGAAGCGACTGGCGTTC  424
          |||||||||||| ||||||||| ||| ||||||||||||||||||||||| |||||||||
Db   301  AAGGAGGTGGCCTTGTCGTTGAAGCAAAACCTGNATAGCTACAATAAGCGCCTGCGTTAC  360

Qy   425  TACTGCGGCCCACTGCCCGGGGCAGACCCCCTGGGTGCTGTAGAAGCCCACACCCTCT  481
          |||||||||||| ||||||||||||||||||| |||||||||||| ||||||||||||
Db   361  TACTGCGGCCCCGTTGCAAGGCAAGACTCCAGCAGTGTCCAGACTCTAAGGGAGTCCACTCTGT  417
```

RESULT 12

AA762051

LOCUS   AA762051   501 bp   mRNA   linear   EST   27-JAN-1998
DEFINITION   vv49h02.r1 Soares_thymus_2NbMT Mus musculus cDNA clone
             IMAGE:1225779 5' similar to SW:PA2M_CAVPO P47711 PHOSPHOLIPASE A2,
             MEMBRANE ASSOCIATED PRECURSOR ;, mRNA sequence.
ACCESSION   AA762051
VERSION   AA762051.1   GI:2811798
KEYWORDS   EST.
SOURCE   Mus musculus (house mouse)
  ORGANISM   Mus musculus
             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
             Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1 (bases 1 to 501)
  AUTHORS   Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
             Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
             Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
             Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
             Waterston,R.
  TITLE   The WashU-HHMI Mouse EST Project
  JOURNAL   Unpublished (1996)
COMMENT   Contact: Marra M/Mouse EST Project
             WashU-HHMI Mouse EST Project
             Washington University School of MedicineP
             4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
             Tel: 314 286 1800
             Fax: 314 286 1810
             Email: mouseest@watson.wustl.edu
             This clone is available royalty-free through LLNL ; contact the
             IMAGE Consortium (info@image.llnl.gov) for further information.
             MGI:651371
             Seq primer: -28m13 rev2 ET from Amersham
             High quality sequence stop: 492.
FEATURES   Location/Qualifiers
     source   1..501
                     /organism="Mus musculus"

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Qy   149  TACTGGCCCTACGGCTGTCACTGCGGACTAGGTGGCAGAGGCCAACCCAAAGATGCCACG  208
          |||||||||||| ||||||||||||||| ||||| |||| || ||||||||||||||||||
Db   121  TACTGGCCCTACGGCTGTCACTGTGGACTTGGTGGCAAAGGGCAACCCAAAGATGCCACA  180

Qy   209  GACTGGTGCTGCCAGACCCATGACTGCTGTCTGCCATGACCCACCTGAAGACCCAGGGTGCGGC  268
          |||||| ||| |||| |||| |||||||||| ||||||| |||| |||||||||||||||||||
Db   181  GACTGGTGCTGCAGAAGCATGATTGTGTCATGATTGCTGTCTGCCACCTGAAGATCGATGGATGCAAG  240

Qy   269  ATCTACAAGGACTATTACAGATACAACTTTTCCCAGGGGGAACATCCACTGCTTCTGACAAG  328
          |||||||||||||||| ||||||||||| |||| |||||||| |||||||||||||| |||||
Db   241  AGCCTGACAGACAACTACAATACAGCCATCTCCAGGGCACTATCCAGTGCTTCTGACAAC  300

Qy   329  GGAAGCTGGTGTGAGCAGCAGCTGTGTGCCTTCTGCCTGGAGGTGGCCTTCTGCCTGAAG  388
          ||||| |||||||||||| ||||||||||| ||||| ||||||||||||||| ||||||||
Db   301  GGGAGCTGGTGTGAGCAACTGTGTGCTTGTGCTTGTGACAAGGAGGTGGCCTTGTCGTTGAAG  360

Qy   389  CGCAACCTGACACCTACCAGAAGCGACTGGCGTTTCTACTGCGGCCCCACTGCCCGGGGG  448
          |||||||| |||| |  ||||||| ||||||| ||||||| ||||||| |||||||||| |
Db   361  CAAAACCTGGATAGCTACAATAAGCGCCTGCGGTACTACTGCGGCCCCGTTGCAAGGC  420

Qy   449  CAGACCCCTGGGTGCTA  465
          || |||||||||||||||
Db   421  AAGACTCCAGCAGTGCTA  437
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RESULT 11

AI430241

LOCUS   AI430241   460 bp   mRNA   linear   EST   09-MAR-1999
DEFINITION   vv49h02.y1 Soares_thymus_2NbMT Mus musculus cDNA clone
             IMAGE:1225779 5' similar to SW:PA2M_CAVPO P47711 PHOSPHOLIPASE A2,
             MEMBRANE ASSOCIATED PRECURSOR ;, mRNA sequence.
ACCESSION   AI430241
VERSION   AI430241.1   GI:4276077
KEYWORDS   EST.
SOURCE   Mus musculus (house mouse)
  ORGANISM   Mus musculus
             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
             Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1 (bases 1 to 460)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE   National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
             Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT   Contact: Robert Strausberg, Ph.D.
             Email: cgapbs-r@mail.nih.gov
             This clone is available royalty-free through LLNL ; contact the
             IMAGE Consortium (info@image.llnl.gov) for further information.
             MGI:651371
             This read is a RESEQUENCE of a previously sequenced mouse clone
             This read has been verified (found to hit its original self in the
             correct orientation)
             Seq primer: -40RP from Gibco
             High quality sequence stop: 459.
FEATURES   Location/Qualifiers
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                     /organism="Mus musculus"
                     /mol_type="mRNA"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="IMAGE:1225779"
                     /sex="male"
                     /tissue_type="thymus"
                     /dev_stage="4 weeks"
                     /lab_host="DH10B"
                     /clone_lib="Soares_thymus_2NbMT"
                     /note="Vector: pT7T3D-Pac (Pharmacia) with a modified
                     polylinker; Site_1: Not I ; Site_2: Eco RI; 1st strand cDNA
                     was primed with a Not I - oligo(dT) primer [5'
                     TGTTACCAATCGAAGTGGGACGCGGCCGCGTTTTTTTTTTTTTTTTTTTTT
                     3']; double-stranded cDNA was ligated to Eco RI adaptors
                     (Pharmacia), digested with Not I and cloned into the Not I
                     and Eco RI sites of the modified pT7T3 vector. RNA
                     provided by Dr. Bertrand Jordan. Library went through two
```

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/mol_type="mRNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="IMAGE:1225779"
/sex="male"
/tissue_type="Thymus"
/dev_stage="4 weeks"
/lab_host="DH10B"
/clone_lib="Soares thymus 2NbMT"
/note="Vector: pT7T3D-Pac (Pharmacia) with a modified
polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA
was primed with a Not I - oligo(dt) primer [5'
TGTTACCAATCTGAAGTGGGAGCGGCGCGCGTTTTTTTTTTTTTTTTTTTTTTT
3']; double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Not I and cloned into the Not I
and Eco RI sites of the modified pT7T3 vector. RNA
provided by Dr. Bertrand Jordan. Library went through two
rounds of normalization, and was constructed by Bento
Soares and M.Fatima Bonaldo."
```

ORIGIN

Query Match   45.4%;   Score 268.8; DB 9; Length 501;
Best Local Similarity   77.7%;   Pred. No. 2.6e-55;
Matches 324; Conservative   0; Mismatches 93; Indels   0; Gaps   0;

```
Qy      65 GCTGTGATTCAATCCAGGGCGGGATCCTGAACCTGAACAAGATGGTCAAGCAAGTG 124
            ||||| ||||||||||  ||||||||||||||||||||||||||||||||||||||
Db       1 GCGNTATAACTGCAACCCAGGGAGGGCTCCTGAACCTGAACAAGATGGTCACACACATG 60

Qy     125 ACTGGGAAAATGCCCATCCTCTCCTACTGGCCCTACTGGCGTCACTGCGGACTAGGTGGC 184
            || ||||| || |||||||||||||||||||||||||||||||||||||||||||||||
Db      61 ACCGGGGAAGAAAGCCTTCTTCAGCTACTGGCCCTACTGGCGTCACTGGGACTTGGTGGC 120

Qy     185 AGAGGCCAACCCAAAGATGCCACGGACTGGTCGTGCCAGACCCATGACTGCTGCTATGAC 244
            | ||||||||||||||||||||||||| || |||||||||||||||||||||||||||||
Db     121 AAAGGGCAACCCAAAGATGCCACAGACTGGTGCTGTCAGAAGCATGATTGTTGCTATGCC 180

Qy     245 CACCTGAGACCCAGGGGTGCGCGCATCTACAAGGACTATTACAGATACAACTTTTCCCAG 304
            |||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||
Db     181 CACCTGAAGATGCATGATGCAAGAGCCACAGAGCTGGTGCTGTCTGAGCAGCAGCATCTCCCAG 240

Qy     305 GGGAACATCCACTGCTTCTGCCTGAACAAGGGAAGCTGGTGTGAGCAGCAGCTGTGCCTGTGAC 364
            |||| ||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     241 GGCACTATCCAGTGCTTCTGCCTGAACAACGGAGACTGGTGTGAGACAAGGCCAACTGTGTGCTTGTGAC 300

Qy     365 AAGGAGGTGGCCTTCTGCCTGAAGCGCAACCTACCAGAAGCGACTGCGTTTC 424
            |||||||||||||||||| |||||||||| ||||||||||||||||||||||||
Db     301 AAGGAGGTGGCCTTGTGCTTGAAGCAAAACCTGATAGCTACAATAAGCGGCCTCCCTTAC 360

Qy     425 TACTGGCGGCCCCACTGCCGCGGGGCCGAGACCCCTGGGTGCTAGAAGCCCACACCCTCT 481
            ||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||
Db     361 TACTGGCGGCCCCGTTGCAAAGGCAAGACTCCAGCATGCTCAAGGGAGTCCACTCTGT 417
```

RESULT 13

BQ418599
LOCUS   BQ418599   601 bp   mRNA   linear   EST 23-MAY-2002
DEFINITION ik55a07.y1 Kaestner ngn3 wt Mus musculus cDNA 5' similar to
            TR:Q9WVF6 Q9WVF6 GROUP IID SECRETED PHOSPHOLIPASE A2 ; , mRNA
            sequence.
ACCESSION   BQ418599
VERSION   BQ418599.1 GI:21123800
KEYWORDS   EST.
SOURCE   Mus musculus (house mouse)
ORGANISM   Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1 (bases 1 to 601)
AUTHORS   Melton,D., Brown,J., Kenty,G., Permutt,A., Lee,C., Kaestner,K.,
            Lemishka,I., Scearce,M., Brestelli,J., Gradwohl,G., Clifton,S.,
            Hillier,L., Marra,M., Pape,D., Wylie,T., Martin,J., Blistain,A.,
            Schmitt,A., Theising,B., Ritter,E., Ronko,I., Bennett,J.,
            Cardenas,M., Gibbons,M., McCann,R., Cole,R., Tsagareishvili,R.,

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Williams,T., Jackson,Y. and Bowers,Y.
Endocrine Pancreas Consortium
Unpublished (2000)
Other ESTs: ik55a07.x1
Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue
Endocrine Pancreas Consortium
Harvard University, Howard Hughes Medical Institute
Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge,
MA 02138
Tel: 617-495-1812
Fax: 617-495-8557
Email: dmelton@biohp.harvard.edu

COMMENT   Pancreas was obtained from Gerard Gradwohl (PNAS 97 P1607-1611,
            2000) Library was constructed by Catherine Lee DNA sequencing by:
            Washington University Genome Sequencing Center For information on
            obtaining a clone please contact: Dr. Marie Scearce
            (mscearce@mail.med.upenn.edu)
            Seq primer: -40RP from Gibco
            High quality sequence stop: 456.

FEATURES   Location/Qualifiers
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                     /organism="Mus musculus"
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                     /dev_stage="p.c. 14.5"
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                     /clone_lib="Kaestner ngn3 wt"
                     /note="Organ: Pancreas; Vector: pSPORT1 (GIBCO); Site_1:
                     Not I; Site 2: Sal I; The library was prepared by
                     Catherine S_ Lee and has not been published. The pancreas
                     was obtained from Gerard Gradwohl (PNAS 97 P1607-1611,
                     2000). The cDNA's were prepared with an oligo containing a
                     NoI site, and SalI linkers were added to the ends. The
                     inserts were cut with NotI before being cloned into the
                     NotI-SalI sites in the vectors. This is one of two
                     libraries, ngn3 wt and ngn3 -/-. The wt library is in
                     pSPORT1, T7 promoter is 5'."

ORIGIN

Query Match   44.9%;   Score 265.8; DB 13; Length 601;
Best Local Similarity   77.7%;   Pred. No. 1.6e-54;
Matches 321; Conservative   0; Mismatches 92; Indels   0; Gaps   0;

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Qy      69 GTGTGATTCAATCCAGGGCGGGATCCTGAACCTGAACAAGATGGTCAAGCAAGTGACTG 128
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Qy     189 GCCAACCCAAAGATGCCACGGACTGGTGCTGTCGCAGACCCATGACTGCTGCTATGACCACC 248
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Db     408 AGGTGGCCTTGTGCTTGAAGCAAAACCTGATAGCTACAATAAGCGGCCTCCCTTACTACT 467

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DEFINITION BY704474 RIKEN full-length enriched, 18-day embryo whole body Mus
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ACCESSION   BY704474
VERSION   BY704474.1 GI:27115602
KEYWORDS   EST.
SOURCE   Mus musculus (house mouse)
  ORGANISM Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1 (bases 1 to 998)
  AUTHORS   Okazaki,Y., Furuno,M., Kasukawa,T., Adachi,J., Bono,H., Kondo,S.,
            Nikaido,I., Osato,N., Saito,R., Suzuki,H., Yamanaka,I.,
            Kiyosawa,H., Yagi,K., Tomaru,Y., Hasegawa,Y., Nogami,A.,
            Schonbach,C., Gojobori,T., Baldarelli,R., Hill,D.P., Bult,C.,
            Hume,D.A., Quackenbush,J., Schriml,L.M., Kanapin,A., Matsuda,H.,
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            Chothia,C., Corbani,L.E., Cousins,S., Dalla,E., Dragani,T.A.,
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            Kawaji,H., Kawasawa,Y., Kedzierski,R.M., King,B.L., Konagaya,A.,
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            Ravasi,T., Reed,J.C., Reed,D.J., Reid,J., Ring,B.Z., Ringwald,M.,
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            Wells,C., Wilming,L.G., Wynshaw-Boris,A., Yanagisawa,M., Yang,I.,
            Yang,L., Yuan,Z., Zavolan,M., Zhu,Y., Zimmer,A., Carninci,P.,
            Hayatsu,N., Hirozane-Kishikawa,T., Konno,H., Nakamura,M.,
            Sakazume,N., Sato,K., Shiraki,T., Waki,K., Kawai,J., Aizawa,K.,
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            Itoh,M., Kagawa,I., Miyazaki,A., Sakai,K., Sasaki,D., Shibata,K.,
            Shinagawa,A., Yasunishi,A., Yoshino,M., Waterston,R., Lander,E.S.,
            Rogers,J., Birney,E. and Hayashizaki,Y.
  TITLE   Analysis of the mouse transcriptome based on functional annotation
            of 60,770 full-length cDNAs
  JOURNAL   Nature 420, 563-573 (2002)
  MEDLINE   22354683
   PUBMED   12466851
COMMENT   Contact: Yoshihide Hayashizaki
            Laboratory for Genome Exploration Research Group, RIKEN Genomic
            Sciences Center(GSC), Yokohama Institute
            The Institute of Physical and Chemical Research (RIKEN)
            1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
            Tel: 81-45-503-9222
            Fax: 81-45-503-9216
            Email: genome-res@gsc.riken.go.jp,
            URL:http://genome.gsc.riken.go.jp/,
            cDNA library was prepared and sequenced in Mouse Genome
            Encyclopedia Project of Genome Exploration Research Group in RIKEN.
            Genomic Sciences Center and Genome Science Laboratory in RIKEN.
            Division of Experimental Animal Research in Riken contributed to
            prepare mouse tissues.
            Please visit our web site (http://genome.gsc.riken.go.jp) for
            further details.
FEATURES   Location/Qualifiers
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                     /clone_lib="RIKEN full-length enriched, 18-day embryo
                     whole body"
ORIGIN

Query Match   44.9%; Score 265.8; DB 13; Length 998;
Best Local Similarity   79.3%; Pred. No. 2.1e-54;
Matches   315; Conservative   0; Mismatches   82; Indels   0; Gaps   0;

Qy   69 GTGTGATTCCAATCCAGGGCGGATCCTGAACCTGAACAAGATGGTCAAGCAAGTGACTG 128
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Qy   369 AGGTGGCCTTCGCCTGAAGCGCAACTGGACACCTACCAGAAGCGACTGCGTTTTCTACT 428
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Qy   429 GGCGGCCCACTGCCGCGGGGCAGACCCCTGGGTGCTA 465
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Db   438 GGGCGGCCCCGTGTGCAAAGGCAGCAAGACTCCAGCATGCTA 474

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DEFINITION Mus musculus 18-day embryo whole body cDNA, RIKEN full-length
            enriched library, clone:1110051K23 product:phospholipase A2, group
            IID full insert sequence.
ACCESSION   AK004232
VERSION   AK004232.1 GI:12835341
KEYWORDS   HTC; CAP trapper.
SOURCE   Mus musculus (house mouse)
  ORGANISM Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1
  AUTHORS   Carninci,P. and Hayashizaki,Y.
  TITLE   High-efficiency full-length cDNA cloning
  JOURNAL   Meth. Enzymol. 303, 19-44 (1999)
  MEDLINE   99279253
   PUBMED   10349636
REFERENCE   2

```
AUTHORS   Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K.,
          Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
TITLE     Normalization and subtraction of cap-trapper-selected cDNAs to
          prepare full-length cDNA libraries for rapid discovery of new genes
JOURNAL   Genome Res. 10 (10), 1617-1630 (2000)
MEDLINE   20499374
PUBMED    11042159
REFERENCE 3
AUTHORS   Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P.,
          Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M.,
          Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A.,
          Yamamoto,R., Matsumoto,K., Sakaguchi,S., Ikegami,T., Kashiwagi,K.,
          Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M.,
          Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J.,
          Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.
TITLE     RIKEN integrated sequence analysis (RISA) system--384-format
          sequencing pipeline with 384 multicapillary sequencer
JOURNAL   Genome Res. 10 (11), 1757-1771 (2000)
MEDLINE   20530913
PUBMED    11076861
REFERENCE 4
AUTHORS   The RIKEN Genome Exploration Research Group Phase II Team and the
          FANTOM Consortium.
TITLE     Functional annotation of a full-length mouse cDNA collection
JOURNAL   Nature 409, 685-690 (2001)
REFERENCE 5
AUTHORS   The FANTOM Consortium and the RIKEN Genome Exploration Research
          Group Phase I & II Team.
TITLE     Analysis of the mouse transcriptome based on functional annotation
          of 60,770 full-length cDNAs
JOURNAL   Nature 420, 563-573 (2002)
REFERENCE 6  (bases 1 to 1206)
AUTHORS   Adachi,J., Aizawa,K., Akahira,S., Akimura,T., Arai,A., Aono,H.,
          Arakawa,T., Bono,H., Carninci,P., Fukuda,S., Fukunishi,Y.,
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          Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Nishi,K.,
          Nomura,K., Nunazaki,T., Ohno,M., Okazaki,Y., Okido,T., Owa,C.,
          Saito,H., Saito,R., Sakai,C., Sakai,K., Sano,H., Sasaki,D.,
          Shibata,K., Shibata,Y., Shinagawa,A., Shiraki,T., Sogabe,Y.,
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          Tejima,Y., Toya,T., Yanamura,T., Yasunishi,A., Yoshida,K.,
          Yoshino,M., Muramatsu,M. and Hayashizaki,Y.
TITLE     Direct Submission
JOURNAL   Submitted (10-JUL-2000) Yoshihide Hayashizaki, The Institute of
          Physical and Chemical Research (RIKEN), Laboratory for Genome
          Exploration Research Group, RIKEN Genomic Sciences Center (GSC),
          RIKEN Yokohama Institute, 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,
          Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp,
          URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222,
          Fax:81-45-503-9216)
COMMENT   Please visit our web site (http://genome.gsc.riken.go.jp/) for
          further details.
          cDNA library was prepared and sequenced in Mouse Genome
          Encyclopedia Project of Genome Exploration Research Group in Riken
          Genomic Sciences Center and Genome Science Laboratory in RIKEN.
          Division of Experimental Animal Research in Riken contributed to
          prepare mouse tissues. First strand cDNA was primed with a primer
          [5' GAGAGAGAGAGCGGCCGCAACTCGAGTTTTTTTTTTTTTTTVN 3'], cDNA was
          prepared by using trehalose thermo-activated reverse transcriptase
          and subsequently enriched for full-length by cap-trapper. Second
          strand cDNA was prepared with the primer adapter of sequence[5'
          GAGAGAGAGAAGATCCAAGAGCTCAATTAATTTAATTAAACCCCCCCCCC 3']. cDNA was
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ORIGIN

Query Match             44.9%;  Score 265.8;  DB 11;  Length 1206;
Best Local Similarity   79.3%;  Pred. No. 2.3e-54;
Matches   315;  Conservative    0;  Mismatches   82;  Indels    0;  Gaps    0;

Qy     69 GTGTGAATTCAATCCAGGGCGGGATCCTGAACCTGAACAAGATGGTCAAGCAAGTGACTG 128
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Db     78 GTATAACTGCAACCCAGGGACGGGCTCCTGAACCTGAACAAGATGGTCACACACATGACGG 137

Qy    129 GGAAAATGCCCATCCTCTCTACTGGCCCTACGGCTGTCACTGCCGGACTAGGTGGCAGAG 188
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Db    138 GGAGAAAGCCTTCTTCAGCTACTGGCCCTACGGCTGTCACTGTTGGCTTGTGGCAAAG 197

Qy    189 GCCAACCCAAAGATGCCACGGACTGGTGCTGCCAGACCCATGACTGCTGCTATGACCACC 248
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OM nucleic - nucleic search, using sw model

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GenCore version 5.1.6

Run on: October 7, 2004, 11:15:59 ; Search time 2398.28 Seconds
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10698.960 Million cell updates/sec

Title: US-09-830-321A-4
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Gapop 10.0 , Gapext 1.0
Searched: 3470272 seqs, 2167516995 residues
Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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SUMMARIES

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	2	590.4	99.7	1938	9	AF188625	AF188625 Homo sapi
	3	579.4	97.9	2747	9	BC025706	BC025706 Homo sapi
	4	296	50.0	1233	6	E37214	E37214 Mouse secre
	5	296	50.0	1233	10	AF112983	AF112983 Mus muscu
	6	296	50.0	1975	10	AF169407	AF169407 Mus muscu
	7	296	50.0	2166	10	AF169408	AF169408 Mus muscu
	8	284.2	48.0	496	6	AX464400	AX464400 Sequence
	9	284.2	48.0	496	6	AX697309	AX697309 Sequence
	10	284.2	47.8	496	10	AY358606	AY358606 Homo sapi
	11	282.8	47.8	904	10	AF124374	AF124374 Mus muscu
c	12	272	45.9	98743	9	AL158172	AL158172 Human DNA
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	14	133.8	22.6	760	10	CPIIPHA2	X82631 C.porcellus
	15	119.6	20.2	1016	6	AR274880	AR274880 Sequence
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	26	112.4	19.0	479	6	I23845	I23845 Sequence 9
	27	110.8	18.7	854	6	I09230	I09230 Sequence 34
	28	110.8	18.7	854	6	AR380662	AR380662 Sequence
	29	110.8	18.7	854	6	AX337559	AX337559 Sequence
	30	110.8	18.7	854	6	AX587679	AX587679 Sequence
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c	35	110.8	18.7	1268	6	AX015532	AX015532 Sequence
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c	38	109.8	18.5	222086	2	AC106106	AC106106 Rattus no
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	43	105	17.7	906	10	AF166099	AF166099 Mus muscu
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ALIGNMENTS

RESULT 1
AF112982
LOCUS   AF112982   878 bp   mRNA   linear   PRI 30-AUG-1999
DEFINITION   Homo sapiens group IID secretory phospholipase A2 (PLA2) mRNA,
complete cds.
ACCESSION   AF112982
VERSION   AF112982.1   GI:5771419
KEYWORDS   .
SOURCE   Homo sapiens (human)
ORGANISM   Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 878)
AUTHORS   Ishizaki,J., Suzuki,N., Higashino,K., Yokota,Y., Ono,T.,
Kawamoto,K., Fujii,N., Arita,H. and Hanasaki,K.

Pred. No. is the number of results predicted by chance to have a

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TITLE       Cloning and characterization of novel mouse and human secretory
            phospholipase A(2)s
JOURNAL     J. Biol. Chem. 274 (35), 24973-24979 (1999)
MEDLINE     99386983
PUBMED      10455175
REFERENCE   2  (bases 1 to 878)
AUTHORS     Ishizaki,J., Suzuki,N., Higashino,K. and Hanasaki,K.
TITLE       Direct Submission
JOURNAL     Submitted (11-DEC-1998) Shionogi Research Laboratories,
            Fukushima-ku, Sagisu 5-12-4, Osaka 553-0002, Japan
FEATURES             Location/Qualifiers
     source          1..878
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                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
     gene            1..878
                     /gene="PLA2"
     CDS             29..466
                     /gene="PLA2"
                     /note="group IID sPLA2"
                     /codon_start=1
                     /product="group IID secretory phospholipase A2"
                     /protein_id="AAD51390.1"
                     /db_xref="GI:5771420"
                     /translation="MELALLCGLVVMAGVIPIQGGIILNLNKMVKQVTGKMPILSYWPY
                     GHCGLGGRGQPKDATDWCCYDHLKTQGCGIYKDYYRYNFSQGNIHCSDKGS
                     WCEEQQLCACDKEVAFCLKRNLDTYQKRLRFYWRPHCRGQTPGC"
     variation       266
                     /gene="PLA2"
                     /note="results in glycine to serine substitution"
                     /replace="a"

ORIGIN

Query Match         100.0%;    Score 592;   DB 9;   Length 878;
Best Local Similarity 100.0%;    Pred. No. 2.3e-139;
Matches 592;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1  TCTGCCTCCACTGCTCTGTGCTGGATCATGGAACTTGCACTGCTGTGTGGCTGGTGGT   60
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Db      1  TCTGCCTCCACTGCTCTGTGCTGGATCATGGAACTTGCACTGCTGTGTGGCTGGTGGT   60

Qy     61  GATGGCTGGTGTGATTCAATCCAGGGCGGGATCCTGAACCTGAACAAGATGGTCAAGCA  120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61  GATGGCTGGTGTGATTCAATCCAGGGCGGGATCCTGAACCTGAACAAGATGGTCAAGCA  120

Qy    121  AGTGACTGGGAAAATGCCCATCCTCTTCTACTGGCCGTCACTGCGGACTAGG         180
           |||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121  AGTGACTGGGAAAATGCCCATCCTCTTCTACTGGCCGTCACTGCGGACTAGG         180

Qy    181  TGGCAGAGGCCAACCCAAAGATGCCACGGACTGGTGCTGCCAGACCCATGACTGCTGCTA  240
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Db    181  TGGCAGAGGCCAACCCAAAGATGCCACGGACTGGTGCTGCCAGACCCATGACTGCTGCTA  240

Qy    241  TGACCACCTGAAGACCCAGGGCTGCGGCATCTACAAGGACTATTACAGATACAACTTTTC  300
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241  TGACCACCTGAAGACCCAGGGCTGCGGCATCTACAAGGACTATTACAGATACAACTTTTC  300

Qy    301  CCAGGGGAACATCCACTGCTCTGACAAGGGAAGCTGGTGTGAGCAGCAGCTGTGTCCTG  360
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301  CCAGGGGAACATCCACTGCTCTGACAAGGGAAGCTGGTGTGAGCAGCAGCTGTGTCCTG  360

Qy    361  TGACAAGGAGGTGGCCTTTGCCTGAAGCGCAACCTGGACACACTTACCAGAAGCGACTGCG  420
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Db    361  TGACAAGGAGGTGGCCTTTGCCTGAAGCGCAACCTGGACACACTTACCAGAAGCGACTGCG  420

Qy    421  TTTCTACTGGCGGCCCCACTGCCGCGGGGGGCAGACCCCTGGGTGCTAGAAGCCCACACCCTC  480
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421  TTTCTACTGGCGGCCCCACTGCCGCGGGGGGCAGACCCCTGGGTGCTAGAAGCCCACACCCTC  480

Qy    481  TACCCTGTTCCTCAGCATGGAGCTCTTGGACTCTTGGCATGCCCAGTATCTAACCTGAACCAGC  540
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Db    481  TACCCTGTTCCTCAGCATGGAGCTCTTGGACTCTTGGCATGCCCAGTATCTAACCTGAACCAGC  540
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Qy    541  CTGGCTTTTCAAACACTCCGGGGGGAGGTAGTCCAGCCTCCCCGGAACCC  592
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Db    541  CTGGCTTTTCAAACACTCCGGGGGGAGGTAGTCCAGCCTCCCCGGAACCC  592
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RESULT 2
AF188625
LOCUS       AF188625              1938 bp   mRNA    linear   PRI 28-AUG-2000
DEFINITION  Homo sapiens phospholipase A2 (SPLASH) mRNA, complete cds.
ACCESSION   AF188625
VERSION     AF188625.1   GI:6453792
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1938)
  AUTHORS   Shakhov,A.N., Rubtsov,A.V., Lyakhov,I.G., Tumanov,A.V. and
            Nedospasov,S.A.
  TITLE     SPLASH (PLA2IID), a novel member of phospholipase A2 family, is
            associated with lymphotoxin deficiency
  JOURNAL   Genes Immun. 1 (3), 191-199 (2000)
  MEDLINE   21040292
  PUBMED    11196711
REFERENCE   2  (bases 1 to 1938)
  AUTHORS   Shakhov,A.N., Rubtsov,A.V., Lyakhov,I.G., Tumanov,A.V. and
            Nedospasov,S.A.
  TITLE     Direct Submission
  JOURNAL   Submitted (20-SEP-1999) Laboratory of Molecular Immunoregulation,
            IRSP, SAIC, NCI-FCRDC, P.O. Box B, Frederick, MD 21702, USA
FEATURES             Location/Qualifiers
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                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /chromosome="1"
                     /map="1q35"
     gene            1..1938
                     /gene="SPLASH"
     CDS             37..474
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                     /db_xref="GI:6453793"
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ORIGIN

Query Match         99.7%;    Score 590.4;   DB 9;   Length 1938;
Best Local Similarity 99.8%;    Pred. No. 5.7e-139;
Matches 591;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      1  TCTGCCTCCACTGCTCTGTGCTGGATCATGGAACTTGCACTGCTGTGTGGCTGGTGGT   60
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Db      9  TCTGCCTCCACTGCTCTGTGCTGGATCATGGAACTTGCACTGCTGTGTGGCTGGTGGT   68

Qy     61  GATGGCTGGTGTGATTCAATCCAGGGCGGGATCCTGAACCTGAACAAGATGGTCAAGCA  120
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Db     69  GATGGCTGGTGTGATTCAATCCAGGGCGGGATCCTGAACCTGAACAAGATGGTCAAGCA  128

Qy    121  AGTGACTGGGAAAATGCCCATCCTCTTCTACTGGCCGTCACTGCGGACTAGG         180
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Db    129  AGTGACTGGGAAAATGCCCATCCTCTTCTACTGGCCGTCACTGCGGACTAGG         188

Qy    181  TGGCAGAGGCCAACCCAAAGATGCCACGGACTGGTGCTGCCAGACCCATGACTGCTGCTA  240
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Db    189  TGGCAGAGGCCAACCCAAAGATGCCACGGACTGGTGCTGCCAGACCCATGACTGCTGCTA  248

Qy    241  TGACCACCTGAAGACCCAGGGTGCGGCATCTACAAGGACTATTACAGATACAACTTTTC  300
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Db   249 TGACCACCTGAAGACCCAGGGTGCAGCATCTACAGGACTATTACAGATACAACTTTC 308
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Qy   301 CCAGGGGAACATCCACTGCTCTGACAAGGGAAGAGTCGGTGTGAGCAGCTGTGTGCCTG 360
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Db   309 CCAGGGGAACATCCACTGCTCTGACAAGGGAAGAGTCGGTGTGAGCAGCTGTGTGCCTG 368

Qy   361 TGACAAGGAGGTGGCCTTCTGCCTGAAGCGCCAACCTGGACACCTACCAGAGAGCGACTGCG 420
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Db   369 TGACAAGGAGGTGGCCTTCTGCCTGAAGCGCCAACCTGGACACCTACCAGAGAGCGACTGCG 428

Qy   421 TTTCTACTGGCGGCGCCCACTGCCCGGGGCAGACCCCTGGTGCTAGAAGCCCACACCCTC 480
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Qy   481 TACCCTGTTCCTCAGCATGAGCTCGGCATCCCACCTGAGTATCTAACCTGAACCAGC 540
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Db   489 TACCCTGTTCCTCAGCATGAGCTCGGCATCCCACCTGAGTATCTAACCTGAACCAGC 548

Qy   541 CTGGCTTTTCAAACACTCCGGGGGAGTAGTCCCCGGAACCTCCCCCGGAACCC 592
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RESULT 3
BC025706
LOCUS   BC025706   2747 bp   mRNA   linear   PRI 06-OCT-2003
DEFINITION Homo sapiens phospholipase A2, group IID, mRNA (cDNA clone
            MGC:34386 IMAGE:5223912), complete cds.
ACCESSION   BC025706
VERSION   BC025706.1   GI:19344000
KEYWORDS   MGC.
SOURCE   Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 2747)
AUTHORS   Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G.,
            Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D.,
            Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K.,
            Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F.,
            Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L.,
            Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L.,
            Scheetz,T.E., Brownstein,M.J., Usdin,T.B., Toshiyuki,S.,
            Carninci,P., Prange,C., Raha,S.S., Loquellano,N.A., Peters,G.J.,
            Abramson,R.D., Mullahy,S.J., Bosak,S.A., McEwan,P.J.,
            McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S.,
            Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W.,
            Villalon,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A.,
            Fahey,J., Helton,E., Ketteman,M., Madan,A., Rodrigues,S.,
            Sanchez,A., Whiting,M., Madan,A., Young,A.C., Shevchenko,Y.,
            Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D.,
            Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M.,
            Butterfield,Y.S., Krzywinski,M.I., Skalska,U., Smailus,D.E.,
            Schnerch,A., Schein,J.E., Jones,S.J. and Marra,M.A.
TITLE   Generation and initial analysis of more than 15,000 full-length
            human and mouse cDNA sequences
JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
MEDLINE   22388257
PUBMED   12477932
REFERENCE   2 (bases 1 to 2747)
AUTHORS   Strausberg,R.
TITLE   Direct Submission
JOURNAL   Submitted (06-MAR-2002) National Institutes of Health, Mammalian
            Gene Collection (MGC), Cancer Genomics Office, National Cancer
            Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
            USA
REMARK   NIH-MGC Project URL: http://mgc.nci.nih.gov
COMMENT   Contact: MGC help desk
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Life Technologies, Inc.
            cDNA Library Preparation: Life Technologies, Inc.
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: National Institutes of Health Intramural

            Sequencing Center (NISC),
            Gaithersburg, Maryland;
            Web site: http://www.nisc.nih.gov/
            Contact: nisc_mgc@nhgri.nih.gov
            Akhter,N., Ayele,K., Beckstrom-Sternberg,S.M., Benjamin,B.,
            Blakesley,R.W., Bouffard,G.G., Breen,K., Brinkley,C., Brooks,S.,
            Dietrich,N.L., Granite,S., Guan,X., Gupta,J., Haghighi,P.,
            Hansen,N., Ho,S.-L., Karlins,E., Kwong,P., Laric,P., Legaspi,R.,
            Maduro,Q.L., Masiello,C., Maskeri,B., Mastrian,S.D.,McCloskey,J.C.,
            McDowell,J., Pearson,R., Stantripop,S., Thomas,P.J., Touchman,J.W.,
            Tsurgeon,C., Vogt,J.L., Walker,M.A., Wetherby,K.D., Wiggins,L.,
            Young,A., Zhang,L.-H. and Green,E.D.

            Clone distribution: MGC clone distribution information can be found
            through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
            Series: IRAK Plate: 49 Row: m Column: 9
            This clone was selected for full length sequencing because it
            passed the following selection criteria: matched mRNA gi: 21314652.
FEATURES   Location/Qualifiers
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                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
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                     /tissue_type="Pancreas, Spleen, adult pooled"
                     /clone_lib="NIH_MGC_120"
                     /lab_host="DH10B"
                     /note="Vector: pCMV-SPORT6"
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                     /gene="PLA2G2D"
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                     /protein_id="AAH25706.1"
                     /db_xref="GI:19344001"
                     /db_xref="LocusID:26279"
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                     WCEQQLCACDKEVAFCLKRNLDTYQKRLRFYWRPHCRGQTPGC"
     misc_feature   78..386
                     /note="phoslip; Region: Phospholipase A2. Phospholipase A2
                     releases fatty acids from the second carbon group of
                     glycerol. Perhaps the best known members are secreted
                     snake venoms, but also found in secreted pancreatic and
                     membrane-associated forms. Structure is all-alpha, with
                     two core disulfide-linked helices and a calcium-binding
                     loop. This alignment represents the major family of PLA2s.
                     A second minor family, defined by the honeybee venom PLA2
                     PDB:1POC and related sequences from Gila monsters
                     (Heloderma), is not recognized. This minor family
                     conserves the core helix pair but is substantially
                     different elsewhere"
                     /db_xref="CDD:pfam00068"
ORIGIN
Query Match   97.9%; Score 579.4; DB 9; Length 2747;
Best Local Similarity   99.8%; Pred. No. 3.5e-136;
Matches 580; Conservative   0; Mismatches 1; Indels   0; Gaps   0;

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Db     1 TGCTCTGTGCTGGGATCATGGAACTTGCACTCGTGTGGGCTGGTGTGTGGTGATGGCTGGTG 60

Qy    72 TGATTCCAATCCAGGGCGGGATCCTGAACCTGAACAAGATGGTCAAGCAAGTGACTGGGA 131
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Qy   132 AAATGCCCATCCTCCTCACTCGCCCTACGGCCGTCACTCGCGGACTAGGTGGCAGAGCC 191
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Db   121 AAATGCCCATCCTCCTCACTCGCCCTACGGCCGTCACTCGCGGACTAGGTGGCAGAGCC 180
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Db      9 CTTGCCTGCCTTGCTCTGGGCTGAACTATGAGACTCGCCCTGCTGTGTGGGCTGCTGC--  66

Qy     62 ATGGCTGTGTGATTCCAATCCAGGGGCCGGATCCTGAACCTGAACAAGAGATGGTCAAGCAA 121
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Db     67 -TGGCCGGTATAACTGCAACCCAGGAGGGCTCCTGAACCTGAACAAGAGATGGTCACACAC 125

Qy    122 GTGACTGGGAAAATGCCCATCCTCTCTACTGGGCTGTCACTGGCTGCGAGCTAGGT 181
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Db    126 ATGAGGGGAGAAAGCCCTTCTTCAGCTACTGGGCTCGTCACTGGGACTTGGT 185

Qy    182 GGCAGAGGCCAACCCAAAGATGCCACGGACTGTGTGCCTGGACGACCCCATGACTGTCGTCTAT 241
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Qy    242 GACCACCTGAAGACCCAGGGTGCGGCATCTACAAGGACTATTACAGATACAACTTTCC 301
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Qy    302 CAGGGGAACATCCACTGCTCTGACAAGGAAGCTGGTGTGACGCAGCTGTGTGCCTGT 361
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Qy    362 GACAAGGAGTGGTGCCTTGCCTTGCTGCTCCACTGGCAACCAGGCTGGCTTTTCA 421
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Db    366 GACAAGGAGTGGTGGCCTTGTGCTTGCTGAAGCAAAACTGGATAGCTACAAATAAGCGCCTGCGT 425

Qy    422 TTCTACTGGGCCCCACTGCCCGGGGCGCAGACCCCTGGGTGCGTAGAGCCCACACCCTCT 481
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Db    426 TACTACTGGGCGGCCCGTTGCAAAGGCAAGGCTGGAGGCAGCTAAGGGAGTCCACTCTGT 485
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Qy    192 AACCCAAAGATGCCACGGACTGGTGCTGCGCCAGACCCATGACTGCTGCTATGACCACCTGA 251
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Qy    252 AGACCCAGGGTGCGGCATCTACAAGGACTATTACAGATACAACAACTTTCCCAGGGGAACA 311
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Db    241 AGACCCAGGGTGCGGCATCTACAAGGACTATTACAGATACAACAACTTTCCCAGGGGAACA 300

Qy    312 TCCACTGCTCTGACAAGGAGAGCTGGTGTGAGCAGCAGCTGTGTGCCTGTGACAAGGAGG 371
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RESULT 5
AF112983
LOCUS   AF112983   1233 bp   mRNA   linear   ROD 30-AUG-1999
DEFINITION Mus musculus group IID secretory phospholipase A2 (Pla2) mRNA,
            complete cds.
ACCESSION   AF112983
VERSION   AF112983.1 GI:5771421
KEYWORDS   .
SOURCE   Mus musculus (house mouse)
  ORGANISM Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1 (bases 1 to 1233)
  AUTHORS   Ishizaki,J., Suzuki,N., Higashino,K., Yokota,Y., Ono,T.,
            Kawamoto,K., Fujii,N., Arita,H. and Hanasaki,K.
  TITLE   Cloning and characterization of novel mouse and human secretory
            phospholipase A(2)s
  JOURNAL   J. Biol. Chem. 274 (35), 24973-24979 (1999)
  MEDLINE   99386983
   PUBMED   10455175
REFERENCE   2 (bases 1 to 1233)
  AUTHORS   Ishizaki,J., Suzuki,N., Higashino,K. and Hanasaki,K.
  TITLE   Direct Submission
  JOURNAL   Submitted (11-DEC-1998) Shionogi Research Laboratories,
            Fukushima-ku, Sagisu 5-12-4, Osaka 553-0002, Japan
FEATURES   Location/Qualifiers
     source   1..1233
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                     /mol_type="mRNA"
                     /strain="BALB/C"
                     /db_xref="taxon:10090"
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     CDS   36..470
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                     /translation="MRLALLCGLLLAGITATQGGLLNLNKMVTHMTGKKAFPSYWPYG
                     CHCGLGGKGQPKDATDWCCQKHDCYAHLKIDGKSLTDNYYSISQCTIQCSDNGSW

RESULT 4
E37214
LOCUS   E37214   1233 bp   DNA   linear   PAT 31-JAN-2002
DEFINITION Mouse secretory phospholipase A2.
ACCESSION   E37214
VERSION   E37214.1 GI:11826624
KEYWORDS   JP 2000166544-A/13.
SOURCE   Mus musculus (house mouse)
  ORGANISM Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1 (bases 1 to 1233)
  AUTHORS   Ishizaki,J., Suzuki,N. and Hanasaki,K.
  TITLE   Mouse secretory phospholipase A2
  JOURNAL   Patent: JP 2000166544-A 13 20-JUN-2000;
            SHIONOGI & CO LTD
COMMENT   OS   Mus musculus (mouse)
            PN   JP 2000166544-A/13
            PD   20-JUN-2000
            PF   09-DEC-1998 JP 1998349602
            PR
            PI   JUN ISHIZAKI,NORIKO SUZUKI,KOJI HANASAKI
            PC   C12N9/16,C12N5/10,C12N5/09,C12Q1/44,G01N33/15//(C12N9/16, PC
                 C12R1:91),
            PC   (C12N5/10,C12R1:91),(C12N5/09,C12R1:91),(C12N5/00,C12N15/00,
            PC   (C12N5/00,C12R1:91),(C12N15/00,C12R1:91)
            CC
            FH   Key   Location/Qualifiers
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            FT   mat_peptide   (93)..(467).
FEATURES   Location/Qualifiers
     source   1..1233
                     /organism="Mus musculus"
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Query Match   50.0%; Score 296; DB 6; Length 1233;
Best Local Similarity 77.5%; Pred. No. 2.7e-64;
Matches 372; Conservative   0; Mismatches 105; Indels   3; Gaps   1;

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Qy      2 CTGCCTCCACTGCGTCGTGCTGGGATCATGGAACTTGCCACTGCTGCTGTGTGGGCTGGTGGTG 61
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ORIGIN

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Query Match          50.0%;   Score 296;  DB 10;   Length 1233;
Best Local Similarity 77.5%;   Pred. No. 2.7e-64;
Matches  372; Conservative   0; Mismatches 105;  Indels   3;  Gaps   1;

Qy    2 CTGCCTCCACTGCTCGTCGTGGGATCATGGAACTTGCACTGCTGTGTGGGCTGGTGGTG  61
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Db    9 CTGCCTGCCTTGCTCTGGGCTGGAACTATGAGACTTGCACTGCTGTGTGGGCTGCTGC-- 66

Qy   62 ATGGCTGGTGTGATTCCAATCCAGGGCGGGATCCTGAACAGAGATGGTCAAGCAA  121
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Db   67 -TGGCCGGTATAACTGCAACCCAGGGAGGGCTCCTGAACCTGAACCAAGATGGTCACACAC 125

Qy  122 GTGACTGGGAAAATGCCATCCTCCTACTGGCCTACGGCGTGTCACTGCGGACTAGGT  181
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Db  126 ATGACGGGGAAGAAAGCCTTCTTCAGCTACTGGCCCTACGGCGTGTCACTGTGGGACTTGGT 185

Qy  182 GGCAGAGGCCAACCCAAAGATGCCACGGACTGGTGCTGCCAGACCCATGACTGCTGCTAT  241
          |||||||||||||||||||||||||||||||| ||| || ||||||||||||||||||||
Db  186 GGCAAAGGGCCAACCCAAAGATGCCACAGACTGGTGCTGTGTCAGAAGCATGATTGTTGCTAT 245

Qy  242 GACCACCTGAAGACCAGGGGTGCGGCATCTACAGGACTATTACAGATACAACTTTTCC  301
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Db  246 GCCCACCTGAAGATCGATGGATGCAAGAGCCTGACAGACAACTACAAATACAGCATCTCC 305

Qy  302 CAGGGGAACATCCACTGCTCTGACAAGGGAAGCTGGTGTGAGCAGCAGCTGTGTGCCTGT  361
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Db  306 CAGGGCACTATCCAGTGCTCTGACAACGGGAGCTGGTGTGAAAGGCAACTGTGTGCTTGT 365

Qy  362 GACAAGGAGGTGGCCTTGCTTCTGCCTTCGCCAACCTACCAGGAAGCGACTGCGT  421
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Db  366 GACAAGGAGGTGGCCTTGGCCTTGTGCTTGAAGCAAACCTGGATAGCTACAATAAGCGCCTGCGT 425

Qy  422 TTCTACTGGCGGCCCCACTGCCCGGGGCGAGAACCCTGGGTGCTAGAAGCCACACCCTCT  481
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RESULT 6
AF169407
LOCUS   AF169407   1975 bp   mRNA   linear   ROD 13-MAR-2000
DEFINITION Mus musculus phospholipase A2 (Splash) mRNA, complete cds; nuclear
           gene for mitochondrial product.
ACCESSION AF169407
VERSION   AF169407.1   GI:7230429
KEYWORDS   .
SOURCE   Mus musculus (house mouse)
  ORGANISM Mus musculus
           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
           Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 1975)
  AUTHORS Shakhov,A.N., Rubtsov,A.V., Lyakhov,I.G., Tumanov,A.V. and
           Nedospasov,S.A.
  TITLE   SPLASH (PLA2IID), a novel member of phospholipase A2 family, is
           associated with lymphotoxin deficiency
  JOURNAL Genes Immun. 1 (3), 191-199 (2000)
  MEDLINE 21040292
   PUBMED 11196711
REFERENCE 2 (bases 1 to 1975)
  AUTHORS Shakhov,A.N., Rubtsov,A., Lyakhov,I.G. and Nedospasov,S.A.
  TITLE   Direct Submission
  JOURNAL Submitted (16-JUL-1999) Laboratory of Molecular Immunoregulation,
           IRSP, SAIC, NCI-FCRDC, Sultan Str. 560, Frederick, MD 21702, USA
FEATURES   Location/Qualifiers
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                     /strain="129 x C57/B6"
                     /db_xref="taxon:10090"
                     /chromosome="4"
                     /map="between D4Mit158 and D4Mit283"

gene   1..1975
                /gene="Splash"
CDS   80..514
                /gene="Splash"
                /note="SPLASH"
                /codon_start=1
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repeat_region   1811..1975
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ORIGIN

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Query Match          50.0%;   Score 296;  DB 10;   Length 1975;
Best Local Similarity 77.5%;   Pred. No. 2.6e-64;
Matches  372; Conservative   0; Mismatches 105;  Indels   3;  Gaps    1;

Qy    2 CTGCCTCCACTGCTCGTCGTGGGATCATGGAACTTGCACTGCTGTGTGGGCTGGTGGTG  61
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Db   53 CTGCCTGCCTTGCTCTGGGCTGGAACTATGAGACTTGCACTGCTGTGTGGGCTGCTGC-- 110

Qy   62 ATGGCTGGTGTGATTCCAATCCAGGGCGGGATCCTGAACAGAGATGGTCAAGCAA  121
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Db  111 -TGGCCGGTATAACTGCAACCCAGGGAGGGCTCCTGAACCTGAACCAAGATGGTCACAC 169

Qy  122 GTGACTGGGAAAATGCCATCCTCCTACTGGCCTACGGCGTGTCACTGCGGACTAGGT  181
          ||||||||||||||||||||||||||  ||||||||||| ||||||||||||| ||||
Db  170 ATGACGGGGAAGAAAGCCCTTCTTCAGCTACTGGCCCTACGGCGTGTCACTGTGGGACTTGGT 229

Qy  182 GGCAGAGGCCAACCCAAAGATGCCACGGACTGGTGCTGCCAGACCCATGACTGCTGCTAT  241
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Db  230 GGCAAAGGGCCAACCCAAAGATGCCACAGACTGGTGCTGTGTCAGAAGCATGATTGTTGCTAT 289

Qy  242 GACCACCTGAAGACCAGGGGTGCGGCATCTACAGGACTATTACAGATACAACTTTCC  301
          |||||| |||||| | ||||||||| ||| |||||||| ||||||||||||| |||||
Db  290 GCCCACCTGAAGATCGATGGATGCAAGAGCCTGACAGACAACTACAAATACAGCATCTCC 349

Qy  302 CAGGGGAACATCCACTGCTCTGACAAGGGAAGCTGGTGTGAGCAGCAGCTGTGTGCCTGT  361
          ||||||  |||| ||||||||||| ||||||||||||||||||||||||| |||||||||
Db  350 CAGGGCACTATCCAGTGCTCTGACAACGGGAGCTGGTGTGAAAGGCAACTGTGTGCTTGT 409

Qy  362 GACAAGGAGGTGGCCTTGCTTCTGCCTTCGCCAACCTACCAGGAAGCGACTGCGT  421
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Db  410 GACAAGGAGGTGGCCTTGGCCTTGTGCTTGAAGCAAACCTGGATAGCTACAATAAGCGCCTGCGT 469

Qy  422 TTCTACTGGCGGCCCCACTGCCCGGGGCGAGAACCCTGGGTGCTAGAAGCCACACCCTCT  481
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Db  470 TACTACTGGCGGCCCCCGTTGCAAAGGCAAGAGACTCAGCATGCGTTCAAGGGAGTCCACTCTGT 529
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RESULT 7
AF169408
LOCUS   AF169408   2166 bp   mRNA   linear   ROD 13-MAR-2000
DEFINITION Mus musculus non-secreted phospholipase A2 (Splash) mRNA, complete
           cds; nuclear gene for mitochondrial product.
ACCESSION AF169408
VERSION   AF169408.1   GI:7230431
KEYWORDS   .
SOURCE   Mus musculus (house mouse)
  ORGANISM Mus musculus
           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
           Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 2166)
  AUTHORS Shakhov,A.N., Rubtsov,A.V., Lyakhov,I.G., Tumanov,A.V. and
           Nedospasov,S.A.
  TITLE   SPLASH (PLA2IID), a novel member of phospholipase A2 family, is
           associated with lymphotoxin deficiency
  JOURNAL Genes Immun. 1 (3), 191-199 (2000)
  MEDLINE 21040292
   PUBMED 11196711

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REFERENCE    2  (bases 1 to 2166)
AUTHORS      Shakhov,A.N., Rubtsov,A., Lyakhov,I.G. and Nedopasov,S.A.
TITLE        Direct Submission
JOURNAL      Submitted (16-JUL-1999) Laboratory of Molecular Immunoregulation,
             IRSP, SAIC, NCI-FCRDC, Sultan Str. 560, Frederick, MD 21702, USA
FEATURES             Location/Qualifiers
source          1..2166
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                /map="between D4Mit158 and D4Mit283"
gene            1..2166
                /gene="Splash"
CDS             158..514
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                /codon_start=1
                /product="non-secreted phospholipase A2"
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                /db_xref="GI:7230432"
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ORIGIN
Query Match         50.0%;  Score 296; DB 10; Length 2166;
Best Local Similarity  77.5%;  Pred. No. 2.6e-64;
Matches  372;  Conservative  0;  Mismatches  105;  Indels  3;  Gaps  1;

Qy      2 CTGCCTCCACTGCTCTGTGCTGGATCATGGAACTTGCACTGCTGTGTGGGCTGGTGGTG  61
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Db     53 CTGCCTGCTGCCTTGCTCTGGGCTGGAACTATGAGACTCGCCCCTGCTGTGTGTGGGCTGGTGGTCTCGC--  110

Qy     62 ATGGCTGGTGTGTATAACTGCAACCCAGGGCGGGATCCTGAACCTGAACCTGAACAAGATGGTCAAGCAA  121
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Db    111 -TGGCCGGTATAACTGCAACCCAGGGAGGGCTCCTGAACCTGAACCTGAACAAGATGGTCACACAC  169

Qy    122 GTGACTGGGAAAAATGCCCATCCTCTTCCTACTGGCCCTACGGCGTGTCACTGCGGACTAGGT  181
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Db    170 ATGACGGGGAAGAAAGCCTTCTTCTTCAGCAGTACTGGCCCTACGGCGTGTCACTGCGGACTTGGT  229

Qy    182 GGCAGAGGCCAACCCAAGATGCCACCGGACTGGTGCTGCCAGACCCATGACTGCTGCTAT  241
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Db    230 GGCAAAGGGCCAACCCAAAGATGCCACCAGGGTGCTGTCTGTCAGAAGCATGATTGTTGCTAT  289

Qy    242 GACCACCTGCAAGACCCAGGGGTGCGGCATCTACAAGGACTATTACAGATACAACTTTTCC  301
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    290 GCCCACCTGAAGATCGATGGATGCAAGAGCCTGACAGACAACTACAAAATACAGATACTCC  349

Qy    302 CAGGGGAACATCCACTGCTCTCGACAAGGGAAGCTCGGTGTGAGCAGCAGCTGTGCCTGT  361
          |||||||||||| ||||||||||||||||||||||||||||||||||| ||||
Db    350 CAGGGCCACTATCCAGTGCTCTCGACAAGGGGAGCTCGGTGTGAAAGGCAACTGTGTGCTTGT  409

Qy    362 GACAAGGAGTGGCTTCTGCCTGAAGCGACCTACCAGGAGCGACTGCGT  421
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Db    410 GACAAGGAGTGGCGCCTTGTGCTTGAAGCAAAACCTGGATAGCTACAATAAGGCCTGCGT  469

Qy    422 TTCTACTGGCGGCCCACCCGCGGGGCGAGACCCCCTGGGTGCTAGAAGCCCACCCCTCT  481
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Db    470 TACTACTGGCGGCCCCCGTTGCAAGGCAAGACTCCAGCATGCTAAGGGAGTCCACTCTGT  529

RESULT 8
AX464400
LOCUS        AX464400      496 bp    DNA      linear   PAT 16-JUL-2002
DEFINITION   AX464400 Sequence 533 from Patent WO0140466.
ACCESSION    AX464400
VERSION      AX464400.1    GI:21899216
KEYWORDS     .
SOURCE       Homo sapiens (human)
ORGANISM     Homo sapiens
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             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
             Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
REFERENCE    1
AUTHORS      Baker,K.P., Beresini,M., Deforge,L., Desnoyers,L., Filvaroff,E.,
             Gao,W.Q., Gerritsen,M.E., Goddard,A., Godowski,P.J., Gurney,A.L.,
             Sherwood,S., Smith,V., Stewart,T.A., Tumas,D., Watanabe,C.K.,
             Wood,W.L. and Zhang,Z.
TITLE        Secreted and transmembrane polypeptides and nucleic acids encoding
             same
JOURNAL      Patent: WO 0140466-A 533 07-JUN-2001;
             Genentech Inc. (US)
FEATURES             Location/Qualifiers
source          1..496
                /organism="Homo sapiens"
                /mol_type="unassigned DNA"
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Query Match         48.0%;  Score 284.2; DB 6;  Length 496;
Best Local Similarity  97.3%;  Pred. No. 2.7e-61;
Matches  289;  Conservative  0;  Mismatches  8;  Indels  0;  Gaps  0;

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Db      1 TCTGCCTCCACTGCTCTGTGCTGGATCATGGAACTTGCACTGCTGTGTGGGCTGGTGGT  60

Qy     61 GATGGCTGGTGTGATTCCAATCCAGGGCGGGATCCTGAACCTGAACAAGATGGTCAAGCA  120
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Db     61 GATGGCTGGTGTGATTCCAATCCAGGGCGGGATCCTGAACCTGAACAAGATGGTCAAGCA  120

Qy    121 AGTGACTGGGAAAATGCCCATCCTCCTACTGGCCCTACGGCGTGTCACTGCGGACTAGG  180
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Db    121 AGTGACTGGGAAAATGCCCATCCTCCTACTGGCCCTACGGCGTGTCACTGCGGACTAGG  180

Qy    181 TGGCAGAGGCCAACCCAAAGATGCCAGACCTGGGTGCTGCCAGACCCATGACTGCTGCTA  240
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Qy    241 TGACCACCTGAAGACCCAGGGGTGCGGCATCTACAAGGACTATTACAGATACAACTT  297
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Db    241 TGACCACCTGAAGACCCAGGGGTGCGGCATCTACAAGGACAACAACAAAGCAGCAT  297

RESULT 9
AX697309
LOCUS        AX697309      496 bp    DNA      linear   PAT 02-APR-2003
DEFINITION   AX697309 Sequence 377 from Patent WO0078961.
ACCESSION    AX697309
VERSION      AX697309.1    GI:29498451
KEYWORDS     .
SOURCE       synthetic construct
ORGANISM     synthetic construct
             artificial sequences.
REFERENCE    1
AUTHORS      Ferrara,N., Stewart,T.A., Williams,P.M., Baker,K.P., Desnoyers,L.,
             Eaton,D.L., Gao,W.Q., Pan,J., Botstein,D., Fong,S., Goddard,A.,
             Godowski,P.J., Gurney,A.L., Smith,V., Tumas,D., Wood,W.I.,
             Grimaldi,C.J., Hillan,K.J., Paoni,N.F., Roy,M.A. and Watanabe,C.K.
TITLE        Secreted and transmembrane polypeptides and nucleic acids encoding
             the same
JOURNAL      Patent: WO 0078961-A 377 28-DEC-2000;
             Genentech Inc. (US)
FEATURES             Location/Qualifiers
source          1..496
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ORIGIN

Query Match         48.0%;  Score 284.2; DB 6;  Length 496;
Best Local Similarity  97.3%;  Pred. No. 2.7e-61;
Matches  289;  Conservative  0;  Mismatches  8;  Indels  0;  Gaps  0;
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Qy     1 TCTGCCTCCACTGCTCTGTGCTGGGATCATGGAACTTGCACTGCTGTGTGGGCTGGTGGT 60
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Qy    61 GATGGCTGGTGTGATTCCAATCCAGGGCGGGATCCTGAACCTGAACAAGATGGTCAAGCA 120
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Db    61 GATGGCTGGTGTGATTCCAATCCAGGGCGGGATCCTGAACCTGAACAAGATGGTCAAGCA 120

Qy   121 AGTGACTGGGAAAATGCCCATCCTTCCTACTGCCTCTACGGCGTCACTGCGGACTAGG 180
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Db   121 AGTGACTGGGAAAATGCCCATCCTTCCTACTGCCTCTACGGCGTCACTGCGGACTAGG 180

Qy   181 TGGCAGAGGCCAACCCAAAGATGCCACGGACTGGTGCTGCCAGACCCATGACTGCTGCTA 240
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Qy   241 TGACCACCTGAAGACCCAGGGGTGCGGCATCTACAAGGACTATTACAGATACAACTT 297
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Db   241 TGACCACCTGAAGACCCAGGGGTGCGGCATCTACAAGGACTATTACAGATACAACTT 297
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RESULT 10
LOCUS   AY358606   496 bp   mRNA   linear   PRI 03-OCT-2003
DEFINITION Homo sapiens clone DNA76538 PLA2G2D (UNQ768) mRNA, complete cds.
ACCESSION   AY358606
VERSION   AY358606.1 GI:37182333
KEYWORDS   FLI_CDNA.
SOURCE   Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 496)
AUTHORS   Clark,H.F., Gurney,A.L., Abaya,E., Baker,K., Baldwin,D., Brush,J.,
            Chen,J., Chow,B., Chui,C., Crowley,C., Currell,B., Deuel,B.,
            Dowd,P., Eaton,D., Foster,J., Grimaldi,C., Gu,Q., Hass,P.E.,
            Heldens,S., Huang,A., Kim,H.S., Klimowski,L., Jin,Y., Johnson,S.,
            Lee,J., Lewis,L., Liao,D., Mark,M., Robbie,E., Sanchez,C.,
            Schoenfeld,J., Seshagiri,S., Simmons,L., Singh,J., Smith,V.,
            Stinson,J., Vagts,A., Vandlen,R., Watanabe,C., Wieand,D., Woods,K.,
            Xie,M.H., Yansura,D., Yi,S., Yu,G., Yuan,J., Zhang,M., Zhang,Z.,
            Goddard,A., Wood,W.I. and Godowski,P.
TITLE   The Secreted Protein Discovery Initiative (SPDI), a Large-Scale
            Effort to Identify Novel Human Secreted and Transmembrane Proteins:
            A Bioinformatics Assessment
JOURNAL   Genome Res. 13 (10), 2265-2270 (2003)
PUBMED   12975309
REFERENCE   2 (bases 1 to 496)
AUTHORS   Clark,H.F.
TITLE   Direct Submission
JOURNAL   Submitted (01-AUG-2003) Department of Bioinformatics, Genentech,
            Inc., 1 DNA Way, South San Francisco, CA 94080, USA
FEATURES   Location/Qualifiers
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                     /db_xref="taxon:9606"
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                     /note="PRO1561"
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                     /protein_id="AAQ88969.1"
                     /db_xref="GI:37182334"
                     /translation="MELALLCGLVVMAGVIPIQGGILNLNKMVKQVTGKMPILSYWPY
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                     AVFNVILVENEDSE"
ORIGIN

Query Match   48.0%; Score 284.2; DB 9; Length 496;

Right column

Best Local Similarity 97.3%; Pred. No. 2.7e-61;
Matches 289; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

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Qy     1 TCTGCCTCCACTGCTCTGTGCTGGGATCATGGAACTTGCACTGCTGTGTGGGCTGGTGGT 60
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Db     1 TCTGCCTCCACTGCTCTGTGCTGGGATCATGGAACTTGCACTGCTGTGTGGGCTGGTGGT 60

Qy    61 GATGGCTGGTGTGATTCCAATCCAGGGCGGGATCCTGAACCTGAACAAGATGGTCAAGCA 120
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Db    61 GATGGCTGGTGTGATTCCAATCCAGGGCGGGATCCTGAACCTGAACAAGATGGTCAAGCA 120

Qy   121 AGTGACTGGGAAAATGCCCATCCTTCCTACTGCGTCACTGCGGACTAGG 180
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Db   121 AGTGACTGGGAAAATGCCCATCCTTCCTACTGCGTCACTGCGGACTAGG 180

Qy   181 TGGCAGAGGCCAACCCAAAGATGCCACGGACTGGTGCTGCCAGACCCATGACTGCTGCTA 240
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181 TGGCAGAGGCCAACCCAAAGATGCCACGGACTGGTGCTGCCAGACCCATGACTGCTGCTA 240

Qy   241 TGACCACCTGAAGACCCAGGGGTGCGGCATCTACAAGGACTACTACAGATACAACTT 297
         |||||||||||||||||||||||||||||||||||||| ||||||||||||||||
Db   241 TGACCACCTGAAGACCCAGGGGTGCGGCATCTACAAGGACAACAACAAAGCAGCAT 297
```

RESULT 11
LOCUS   AF124374   904 bp   mRNA   linear   ROD 06-JUL-1999
DEFINITION Mus musculus group IID secreted phospholipase A2 (Pla2a2) mRNA,
            complete cds.
ACCESSION   AF124374
VERSION   AF124374.1 GI:5359707
KEYWORDS   .
SOURCE   Mus musculus (house mouse)
ORGANISM   Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1 (bases 1 to 904)
AUTHORS   Valentin,E., Koduri,R.S., Scimeca,J.C., Carle,G., Gelb,M.H.,
            Lazdunski,M. and Lambeau,G.
TITLE   Cloning and recombinant expression of a novel mouse-secreted
            phospholipase A2
JOURNAL   J. Biol. Chem. 274 (27), 19152-19160 (1999)
MEDLINE   99315857
PUBMED   10383420
REFERENCE   2 (bases 1 to 904)
AUTHORS   Valentin,E., Koduri,R.S., Scimeca,J.C., Carle,G., Gelb,M.H.,
            Lazdunski,M. and Lambeau,G.
TITLE   Direct Submission
JOURNAL   Submitted (28-JAN-1999) CNRS, IPMC, Sophia Antipolis, 660 route des
            Lucioles, Valbonne 06560, France
FEATURES   Location/Qualifiers
     source   1..904
                     /organism="Mus musculus"
                     /mol_type="mRNA"
                     /db_xref="taxon:10090"
                     /chromosome="4"
     gene   1..904
                     /gene="Pla2a2"
     CDS   10..444
                     /gene="Pla2a2"
                     /EC_number="3.1.1.4"
                     /note="Ca2+-dependent secreted phospholipase A2"
                     /codon_start=1
                     /product="group IID secreted phospholipase A2"
                     /protein_id="AAD42773.1"
                     /db_xref="GI:5359708"
                     /translation="MRLALLCGLLLAGITATQGGLLNLNKMVTHMTGKAAFFSYWPYG
                     CHCGLGGKGQPKDATDWCCQKHDCCYAHLKIDGCKSLTDNYKYSISQGTIQCSDNGSW
                     CERQICACDKEVALCLKQNLDSYNKRLRYYWPRCKGKTPAC"
ORIGIN

Query Match   47.8%; Score 282.8; DB 10; Length 904;
Best Local Similarity 77.3%; Pred. No. 6e-61;

Matches 357; Conservative 0; Mismatches 102; Indels 3; Gaps 1;

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Qy     20  GCTGGGATCATGGAACTTGCACTGCTGTGTGGCGTGGGCTGGTGATGGCTGGTGTGATTCCA 79
               |||||| |||||||  |||  ||| |||| || ||||| |||| |||||| ||||||
Db      1  GCTGGAACTATGAGACTCGCCCTGCTGTGTGGGC---TGCTGCTGGCCGGTATAACTGCA 57

Qy     80  ATCCAGGGCGGGATCCTGAACCTGAACAAGATGGTCAAGCAAGTGACTGGGAAAATGCCC 139
               ||||||||||||  ||| ||||||||||||||||   |  |||||| |||||||||
Db     58  ACCCAGGGGAGGGCTCCTGAACCTGAACAAGAGTGTCACACACATGACGGGGAAGAAAGCC 117

Qy    140  ATCCTCCTACTGGCCCTACGGCGTGTCACTGCCGGACTAGTGGCGCAGAGGCCAACCCAAA 199
               ||| ||||||||||||  |||||||| |||| ||||||||||||||||||||||
Db    118  TTCTTCAGCTACTGGCCCTACGGCGTGTCACTGGCCTGGGACCTGGTGGCAAAGGCAACCCAAA 177

Qy    200  GATGCCACGGACTGGTGCTGCCAGACCCATGACTGCTGCTATGACCACCTGAAGACCCAG 259
               |||||||||| ||||||||||| |||||||| |||||||||||| |||||||||||
Db    178  GATGCCACAGACTGGTGCTGCTGTCAGAAGCATGATTGTTGCTATGCCCACCTGAAGAATCGAT 237

Qy    260  GGGTGCGCATCTACAAGGACTATTACAGATACAACTTTCCCAGGGGAACATCCACTGC 319
               ||||| |||||||  |||||| |||||||||||||| |||||||||||||||||||
Db    238  GGATGCAAGAGCCTGACAGACAGAACTACAAATACAACATCTCCCAGGGCACTATCCAGTGC 297

Qy    320  TCTGACAAAGGGAAGCTGTGTGAGCAGCAGCGTGTGCCCTGTGACAAGGAGGTGGCCTTC 379
               |||||||||| ||||  ||||| |  |||||| ||||||||||||||||||||||
Db    298  TCTGACAAAGGGGAGCTGGTGTGAAAGACAACTGTGTGCTTGTGTGTGACAAGGAGGTGGCCTTG 357

Qy    380  TGCCTGGAAGCGCAACCTGGACACCTACCAGAAGCGACTGCGTTTCTACTGGCCCCCAC 439
               ||||| |||  ||  ||||||| |||||||||| |||||||||||||||||||||||
Db    358  TGCTTGAAGCAAAAACCTGGATAGCTACAATAAGCGCCTGCACCTGCCTCTCTTACTACTGGCGCGCCCCGT 417

Qy    440  TGCCGGGGGCGAGACCCCTGGGTGCTGAGAAGCCCACACCCTCT 481
               ||||| || |||||  |||||||| |||||||||||||||||
Db    418  TGCAAAGGCAAGACTCCAGACTTCCAGCATGCTGAAGGAGTCCACTCTGT 459
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RESULT 12
AL158172/c

LOCUS   AL158172   98743 bp   DNA   linear   PRI 25-OCT-2000
DEFINITION Human DNA sequence from clone RP1-169023 on chromosome 1 Contains
            ESTs, STSs and GSSs. Contains the PLA2G5 gene for two isoforms of
            phospholipase A2 group V, a novel gene, the PLA2G2D gene for
            phospholipade 2 group IID and the 5' part of the gene for a novel
            phospholipase 2 group IIF similar to mouse phospholipase A2 group IIF
            (PLA2G2F), complete sequence.
ACCESSION   AL158172
VERSION   AL158172.5 GI:9801324
KEYWORDS   HTG; phospholipase; PLA2G2D; PLA2G2F; PLA2G5.
SOURCE   Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 98743)
AUTHORS   Wallis,J.
TITLE   Direct Submission
JOURNAL   Submitted (25-OCT-2000) Sanger Centre, Hinxton, Cambridgeshire,
            CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone
            requests: clonerequest@sanger.ac.uk
COMMENT   On Aug 14, 2000 this sequence version replaced gi:9714699.
            During sequence assembly data is compared from overlapping clones.
            Where differences are found these are annotated as variations
            together with a note of the overlapping clone name. Note that the
            variation annotation may not be found in the sequence submission
            corresponding to the overlapping clone, as we submit sequences with
            only a small overlap as described above.
            This sequence has been finished according to sequence map criteria
            as follows. An attempt is made to resolve all sequencing problems
            such as compressions and repeats, but not necessarily within known
            annotated human repeat sequence elements (e.g. Alu). Where the
            sequence is ambiguous, there is an annotation using the 'unsure'
            feature key.
            The following abbreviations are used to associate primary accession
            numbers given in the feature table with their source databases:
            Em:, EMBL; Sw:, SWISSPROT; Tr:, TREMBL; Wp:, WORMPEP; Information

            on the WORMPEP database can be found at
            http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence
            was generated from part of bacterial clone contigs of human
            chromosome 1, constructed by the Sanger Centre Chromosome 1 Mapping
            Group. Further information can be found at
            http://www.sanger.ac.uk/HGP/Chr1
            RP1-169023 is from the library RPCI-1 constructed at the Roswell
            Park Cancer Institute by the group of Pieter de Jong. For further
            details see http://bacpac.med.buffalo.edu/
            VECTOR: pCYPAC2
            IMPORTANT: This sequence is not the entire insert of clone
            RP1-169023 It may be shorter because we sequence overlapping
            sections only once, except for a 100 base overlap.
            The true left end of clone RP1-169023 is at 1 in this sequence. The
            true left end of clone RP3-340N1 is at 98644 in this sequence.
FEATURES   Location/Qualifiers
     source   1..98743
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
                     /chromosome="1"
                     /clone="RP1-169023"
                     /clone_lib="RPCI-1"
     misc_feature   107..371
                     /note="match: GSS: Em:B75013"
     misc_feature   complement(249..658)
                     /note="match: STS: Em:G50772"
                     match: GSS: Em:AQ201252"
     repeat_region   630..756
                     /note="MER83-internal repeat: matches 1668..1825 of
                     consensus"
     repeat_region   781..909
                     /note="MER65-internal repeat: matches 1665..1801 of
                     consensus"
     repeat_region   928..1655
                     /note="MER4-internal repeat: matches 1764..2472 of
                     consensus"
     repeat_region   1656..1896
                     /note="LTR8 repeat: matches 1..257 of consensus"
     repeat_region   1897..2592
                     /note="MER4-internal repeat: matches 2472..3484 of
                     consensus"
     repeat_region   2593..2950
                     /note="THE1B repeat: matches 1..364 of consensus"
     repeat_region   2951..3152
                     /note="MER4-internal repeat: matches 3484..3679 of
                     consensus"
     repeat_region   3157..5261
                     /note="MER4-internal repeat: matches 3840..6087 of
                     consensus"
     repeat_region   5262..5337
                     /note="AluY repeat: matches 228..303 of consensus"
     repeat_region   5338..5858
                     /note="MER4-internal repeat: matches 6087..6596 of
                     consensus"
     repeat_region   5866..6336
                     /note="MER4A2 repeat: matches 1..504 of consensus"
     repeat_region   6337..6694
                     /note="L1MC4 repeat: matches 6189..6548 of consensus"
     repeat_region   6897..7044
                     /note="L1MC2 repeat: matches 6050..6202 of consensus"
     repeat_region   7063..7122
                     /note="MLT1E repeat: matches 507..567 of consensus"
     repeat_region   7800..8099
                     /note="L1M4 repeat: matches 5497..5798 of consensus"
     misc_feature   complement(7990..8417)
                     /note="match: GSS: Em:AQ263839"
     misc_feature   complement(8044..8537)
                     /note="match: GSS: Em:AQ591805"
     repeat_region   8198..8361
                     /note="L2 repeat: matches 2537..2705 of consensus"
     repeat_region   8984..9131
                     /note="L2 repeat: matches 2414..2576 of consensus"

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repeat_region    9244..9359
                 /note="L1MC1 repeat: matches 6210. .6327 of consensus"
repeat_region    9376..9483
                 /note="L1PA13 repeat: matches -651. .-544 of consensus"
repeat_region    9520..10539
                 /note="L1M4 repeat: matches 2963. .3988 of consensus"
repeat_region    10553..10664
                 /note="L1M4 repeat: matches 2243. .2357 of consensus"
repeat_region    10665..10936
                 /note="AluSx repeat: matches 5. .276 of consensus"
repeat_region    10937..10951
                 /note="L1M4 repeat: matches 2230. .2244 of consensus"
repeat_region    10939..11702
                 /note="L1MEc repeat: matches 2206. .2980 of consensus"
repeat_region    12233..12282
                 /note="AluSx repeat: matches 251. .302 of consensus"
repeat_region    12293..12588
                 /note="AluJo repeat: matches 1. .306 of consensus"
gene             join(12774. .12834,16626. .16744,22015. .22080,44003. .44308)
                 /gene="dJ169023.2"
mRNA             join(<12774. .12834,16626. .16744,22015. .22080,44003. .44308)
                 /gene="dJ169023.2"
                 /product="dJ169023.2.1 (novel protein)"
                 /note="match: ESTs: Em:AA402475 Em:AA293827"
                 /evidence=not_experimental
repeat_region    13384..13694
                 /note="AluSx repeat: matches 1. .312 of consensus"
repeat_region    13868..14158
                 /note="AluSp repeat: matches 1. .309 of consensus"
repeat_region    14447..14752
                 /note="AluJb repeat: matches 3. .307 of consensus"
repeat_region    15010..15387
                 /note="MSTA repeat: matches 1. .426 of consensus"
repeat_region    15654..15790
                 /note="AluJo repeat: matches 1. .133 of consensus"
repeat_region    16192..16348
                 /note="AluJo repeat: matches 137. .296 of consensus"
CDS              join(16736. .16744,22015. .22080,44003. .44032)
                 /gene="dJ169023.2"
                 /note="5' UTR probably continues in bA66M4 (AL360079)
                 3rd exon misses correct 3' splice site"
                 /codon_start=1
                 /evidence=not_experimental
                 /product="dJ169023.2.1 (novel protein)"
                 /protein_id="CAC13157.1"
                 /db_xref="GI:10862734"
                 /db_xref="SPTREMBL:Q9H507"
                 /translation="MSMPLIQKPEGTHSPLRPSPTQQSQESDSGHRTW"
repeat_region    17434..17743
                 /note="AluSx repeat: matches 1. .309 of consensus"
misc_feature     complement(17768. .18077)
                 /note="match: GSS: Em:AQ80240"
repeat_region    17957..18057
                 /note="MER5A repeat: matches 10. .109 of consensus"
repeat_region    18254..18995
                 /note="L1MC2 repeat: matches 5582. .6328 of consensus"
repeat_region    19004..19128
                 /note="FAM repeat: matches 1. .124 of consensus"
repeat_region    19139..19511
                 /note="L1MC2 repeat: matches 5204. .5592 of consensus"
repeat_region    19567..19724
                 /note="MER63 repeat: matches 1. .783 of consensus"
repeat_region    19867..20140
                 /note="AluJo repeat: matches 1. .265 of consensus"
repeat_region    20141..20440
                 /note="FLAM_C repeat: matches 1. .132 of consensus"
repeat_region    20441..20476
                 /note="AluJb repeat: matches 2. .297 of consensus"
repeat_region    20531..20547
                 /note="AluJo repeat: matches 265. .301 of consensus"
repeat_region    20548..20844
                 /note="L1M4 repeat: matches 4735. .4751 of consensus"

repeat_region    20845..20978
                 /note="AluSx repeat: matches 1. .297 of consensus"
repeat_region    20979..21283
                 /note="L1M4 repeat: matches 4751. .4891 of consensus"
repeat_region    21284..21593
                 /note="AluSq repeat: matches 1. .306 of consensus"
repeat_region    21594..21892
                 /note="L1M4 repeat: matches 4891. .5163 of consensus"
repeat_region    21893..21968
                 /note="AluSp repeat: matches 1. .301 of consensus"
repeat_region    22116..22295
                 /note="L1M4 repeat: matches 5163. .5242 of consensus"
misc_feature     complement(22408. .23261)
                 /note="L1MEc repeat: matches 5319. .5503 of consensus"
repeat_region    22535..22832
                 /note="match: GSS: Em:AQ743836"
repeat_region    22849..23054
                 /note="AluJb repeat: matches 3. .312 of consensus"

Query Match             45.9%;  Score 272;  DB 9;  Length 98743;
Best Local Similarity   100.0%;  Pred. No. 2.8e-58;
Matches   272;  Conservative   0;  Mismatches   0;  Indels   0;  Gaps   0;

Qy         321 CTGACAAGGGAAGCTGGTGTGAGCAGCAGCTGTGTGCCTGTGACAAGGAGTGGCCTTCT 380
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       67401 CTGACAAGGGAAGCTGGTGTGAGCAGCAGCTGTGTGCCTGTGACAAGGAGTGGCCTTCT 67342

Qy         381 GCCTGAAGCGCAACCTGGACACCTACCAGAAGCGACTGCGTTCTTACTGGCGGCCCCACT 440
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       67341 GCCTGAAGCGCAACCTGGACACCTACCAGAAGCGACTGCGTTCTTACTGGCGGCCCCACT 67282

Qy         441 GCCGGGGGCAGACCCCTGGGTGCTAGAAGCCACACCCTCACCCTGTTCCTCAGCATGG 500
               |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       67281 GCCGGGGGCAGACCCCTGGGTGCTAGAAGCCACACCCTCACCCTGTTCCTCAGCATGG 67222

Qy         501 AGCTCTGGCATCCCACCTCAGTATCTAACCTGACCAGCCTGGCTTTTCAAACACTCCG 560
               |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       67221 AGCTCTGGCATCCCACCTCAGTATCTAACCTGACCAGCCTGGCTTTTCAAACACTCCG 67162

Qy         561 GGGGGAGGTAGTCCCAGCCTCCCCCGGAACCC 592
               ||||||||||||||||||||||||||||||||
Db       67161 GGGGGAGGTAGTCCCAGCCTCCCCCGGAACCC 67130

RESULT 13
E37202
LOCUS       E37202                 501 bp    DNA         linear       PAT 31-JAN-2002
DEFINITION  Mouse secretory phospholipase A2.
ACCESSION   E37202
VERSION     E37202.1  GI:18626612
KEYWORDS    JP 2000166544-A/1.
SOURCE      Mus musculus (house mouse)
            Mus musculus
  ORGANISM  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 501)
  AUTHORS   Ishizaki,J., Suzuki,N. and Hanasaki,K.
  TITLE     Mouse secretory phospholipase A2
  JOURNAL   Patent: JP 2000166544-A 1 20-JUN-2000;
            SHIONOGI & CO LTD
COMMENT     OS   Mus musculus (mouse)
            PN   JP 2000166544-A/1
            PD   20-JUN-2000
            PF   09-DEC-1998 JP 1998349602
            PR
            PI   JUN ISHIZAKI,NORIKO SUZUKI,KOJI HANASAKI
            PC   C12N9/16,C12N5/10,C12N15/09,C12Q1/44,G01N33/15//C12N9/16, PC
                 C12R1:91)
            PC   (C12N5/10,C12R1:91),(C12N15/09,C12R1:91),(C12N15/00,C12R1:91),
            PC   (C12N5/00,C12R1:91),(C12R1:91),(C12R1:91)
            CC
FH   Key             Location/Qualifiers
FT   source          1. .501
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CDS             54. .491
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                /codon_start=1
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                /protein_id="CAA57953.1"
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                /db_xref="GOA:P47711"
                /db_xref="SWISS-PROT:P47711"
                /translation="MKILLLLVVMASDLPQAHGHLKQFTEMIKLTTGKNGLTSYGAY
                GHCGVGGKGTPKDATDRCCVRHDCCYDRLMKRGCGTKFLNYRFTHKGSSITCSVKQN
                SCQKQLCECDKAAAYCFAANLKSYRRYQFYNGLCRGKTPSC"
sig_peptide     54. .113
mat_peptide     114. .488
                /product="unnamed"
polyA_signal    552. .557
polyA_signal    744. .749
ORIGIN

Query Match        22.6%;  Score 133.8;  DB 10;  Length 760;
Best Local Similarity  55.5%;  Pred. No. 3.7e-23;
Matches   258;  Conservative   0;  Mismatches  207;  Indels   0;  Gaps   0;

Qy    26  ATCATGGAACTTGCACTGCTGTGTGGCACTGCTGTGTGGCTGGTGGTGATGCTGGTGTGATTCCAATCCAG   85
Db    51  AGCATGAAGCTCCTGCTCCTGCTGGTTGTCATGGCCTCTGATCTGCCTCAAGCCCAC  110

Qy    86  GGCGGGATCCTGGAACCTGAACAAGATGGTCAAGCAAGTCACGGACTGGAAAATGCCCATCCTC  145
Db   111  GGACACTTGAAGCAATTCACAGAAATGATCAAGCTCACGACAGGAAAGAATGGACTTACA  170

Qy   146  TCCTACTGGCCCTACGGCTGTCACTGCGGACTAGGTGGCAGAGGCCAACCCAAAGATGCC  205
Db   171  AGTTATGGCCCTACGGCTGTCACTGTGGTGTGGTGGGTGGCAAAGGAACTCCCAAGATGCA  230

Qy   206  ACGGGACTGGTGCTGCCAGACCCCATGACTGTCGTCTATGACGCGGGGTGC  265
Db   231  ACAGATAGGTGCTGTGTCAGGCATGCATGACTGTGTGCTATGACCTGTGATGAAGCGTGGATGT  290

Qy   266  GGCATCTACAAGGACTATTACAGATACAACTTTCCCAGGGGAACATCCTGCTCTGAC  325
Db   291  GGCACGAAATTTCTGAACTACCGGTTTCCCATAAGGGGAGCTGTGACAAGGAGGTGGCCTTGACCTG  350

Qy   326  AAGGGAAGCTCGTGTGAGCAGCAGCTCTGTCAGATGTGATAAAGCTGCTGCCTACTGTTTT  385
Db   351  AAGCAGAACTCCTGTCAGAGCAGCTGTGTCGAGCAGCTGTGTCGAGCGCCCCACTGCGCCGG  410

Qy   386  AAGCGGCAACCTACCGACAACCTACCAGAGGCAGACGACTGGTTGCGTTTTCTACTGGCCCACTGCGCGG  445
Db   411  GCTGCAACCTGAAAGTTATAGCAGAAGGTACCAGTTTTATTACAATGACTGTGCCGC  470

Qy   446  GGGCAGACCCCTGGGTGCTAGAAGCCCACACCCTCTACCCTGTTC  490
Db   471  GGGAAGACCCCAGTTGCTGAGAGCCACCACCGGTGCACTGCTGAATCTTCTTC  515
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FEATURES       FT        Location/Qualifiers
               source    1. .501
                         /organism="Mus musculus"
                         /mol_type="genomic DNA"
                         /db_xref="taxon:10090"
ORIGIN

Query Match        45.4%;  Score 268.8;  DB 6;  Length 501;
Best Local Similarity  77.7%;  Pred. No. 2.2e-57;
Matches   324;  Conservative   0;  Mismatches  93;  Indels   0;  Gaps   0;

Qy    65  GCTGGTGTGATTCCAATCCAGGGCGGGATCCTGGAACCTGAACAAGATGGTCAAGCAAGTG  124
Db     1  GCGGNTATAACTGCAACCCAGGGAGGGCCTCCTGGAACCTGAACAAGATGGTCACCACACATG   60

Qy   125  ACTGGGAAAAATGCCCATCCTCCTCCTACTGGCCCTACGGCTGTCACTGCCGACTAGGTGGC  184
Db    61  ACGGGAGGGAAAGCCCTTCTTCAGCTACTGGCCCTACGGCTGTCACTGTCCGGACTGGTGGC  120

Qy   185  AGAGGCCAACCCAAAGATGCCACGGGACTGGTGCTGCCAGACCCCATGACTGTCGTCTATGAC  244
Db   121  AAAGGCCAACCCAAAGATGCCACCAGACTGGTCTCAGAAGCATGAGATTACAGATACAACTTTTCCCAG  180

Qy   245  CACCTGAAGACCCCAGGGTGCGGCAGCGGGATCTCAAGGACTATTACAAGGACTACAACTTTTCCCAG  304
Db   181  CACCTGAAGATCATGATGGATGCAAGGCCTGACAGAGACCTGACAGACAACTACAAATACAGCATCTCCCAG  240

Qy   305  GGGAACATCCACTGCTGCTTCTGACAAGGGAAGCTGGTGTGAGCAGCAGCTGTGTGCCTGTGAC  364
Db   241  GGCACTACTCCAGTGCTTCTGACAACGGAGCTGGTGTGAAAGGCAACTGTGTGCTTGTGAC  300

Qy   365  AAGGAGGTTGGCCTTCTGCCTGAAGCGCAACCTACCAGAGGCGACTGCGTTTC  424
Db   301  AAGGAGGTGGCCTTTGCTTGCTTGAAGCAAAATCTGATAGCTACAAATAAGCGCCTGCGTTAC  360

Qy   425  TACTGGCGGCCCACTGCGCGGGGGCAGACCCCTGGGTGCTGAGAAGCCCACACCCTCT  481
Db   361  TACTGGCGGCCCCGTTGCTGAGAGCAAGGACTCCAGCATGCTAAGGAGTCCACTCTGT  417
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RESULT 14
CPIIPHA2

```
LOCUS       CPIIPHA2       760 bp   mRNA    linear   ROD 25-FEB-2003
DEFINITION  C.porcellus mRNA for typeII phospholipase A2.
ACCESSION   X82631
VERSION     X82631.1  GI:951010
KEYWORDS    phospholipase a2.
SOURCE      Cavia porcellus (domestic guinea pig)
  ORGANISM  Cavia porcellus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.
REFERENCE   1
  AUTHORS   Vial,D., Senorale-Pose,M., Havet,N., Molio,L., Vargaftig,B.B. and
            Touqui,L.
  TITLE     Expression of the type-II phospholipase A2 in alveolar macrophages.
            Down-regulation by an inflammatory signal
  JOURNAL   J. Biol. Chem. 270 (29), 17327-17332 (1995)
  MEDLINE   95340522
  PUBMED    7615534
REFERENCE   2  (bases 1 to 760)
  AUTHORS   Vial,D.
  TITLE     Direct Submission
  JOURNAL   Submitted (10-NOV-1994) D. Vial, Institut Pasteur, 25 rue du Dr.
            Roux, 75015 Paris, FRANCE
FEATURES    Location/Qualifiers
  source    1. .760
            /organism="Cavia porcellus"
            /mol_type="mRNA"
            /strain="Hartley"
            /db_xref="taxon:10141"
            /cell_type="alveolar macrophage"
            /dev_stage="adult"
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RESULT 15
AR274880

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LOCUS       AR274880       1016 bp   DNA    linear   PAT 10-APR-2003
DEFINITION  Sequence 17 from patent US 6506607.
ACCESSION   AR274880
VERSION     AR274880.1  GI:29707430
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1016)
  AUTHORS   Shyjan,A.W.
  TITLE     Methods and compositions for the identification and assessment of
            prostate cancer therapies and the diagnosis of prostate cancer
  JOURNAL   Patent: US 6506607-A 17 14-JAN-2003;
FEATURES    Location/Qualifiers
  source    1. .1016
            /organism="unknown"
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ORIGIN   /mol_type="genomic DNA"

Query Match   20.2%; Score 119.6; DB 6; Length 1016;
Best Local Similarity 58.0%; Pred. No. 1.5e-19;
Matches 231; Conservative 0; Mismatches 164; Indels 3; Gaps 1;

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Qy    67 TGGTGTGATTCCAATCCAGGGCGGGATCCTGAACCTGAACAAGATGGTCAAGCAAGTGAC 126
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Db   171 TAGTGTGCCTGCTGTGCAAGGAGGCTTGCTGGACCTAAAAATCAATGATCGAGAAGGTGAC 230

Qy   127 TGGGAAAATGCCCATCCTCCTCCTACTGGCCCTACGGCTGTCACTGCGGACTAGGTGGCAG 186
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Db   231 AGGGAAGAACGCCCTGACAAACTACGGCTTCTACGGCTGTTACTGCGGCTGGGGCGGCCG 290

Qy   187 AGGCCAACCAAAGATGCCACGACTGGTGCTGCCAGACCCATGACTGCTGCTATGACCA 246
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Db   291 AGGAACCCCCAAGGATGGCACCGATTGGTGCTGTTGGGGCGCATGACCACTGCTATGGGCG 350

Qy   247 CCTGAAGACCCAGGGGTGCGGCATCTACAAGGACTATTACAGATACAACTTTTCCCAGG 306
            ||| |      ||  |||  |    |||      |||||| ||||||||
Db   351 GCTGGAGGAGGAGGGGCTGCAACATTCGCACACAGTCCTACACAGATTCGCGTGGGG 410

Qy   307 GAACATCCACTGCTCTGACAAGGGAAGCTGGTGTGAGCAGCAGCTGTGTGCCTGTGACAA 366
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Db   411 CGTGGTCACCTGC---GAGCCCGGGCCCTTCTGCCATGTGAACCTCTGCTGTGTGTGACCG 467

Qy   367 GGAGGTGGCCTTCTGCCTGAAGCGCAACCTGGACACCTACCAGGAAGCGACTGCGTTTCTA 426
            |||||  |||   ||||  |||||||| |||||   ||       ||||| |
Db   468 GAAGCTCGTCTACTGCCTCAAGAGAAAACCTACGGAGCTACAACCCACAGTACCAATACTT 527

Qy   427 CTGGCGGCCCCACTGCCGGGGCAGACCCCTGGGTGCT 464
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                    GenCore version 5.1.6
           Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on:    October  7, 2004, 11:14:15 ; Search time 251.748 Seconds
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Title:          US-09-830-321A-4
Perfect score:  592
Sequence:       1 tctgcctcactgctctgtg.........cccagcctccccggaaccc 592

Scoring table:  IDENTITY_NUC
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Searched:       3373863 seqs, 2124099041 residues

Total number of hits satisfying chosen parameters:       6747726

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
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Pred. No. is the number of results predicted by chance to have a
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                             SUMMARIES
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Result No.	Score	% Query Match	Length	DB	ID	Description		
1	592	100.0	592	3	AAA53269	Aaa53269 Human pho		
2	592	100.0	878	3	AAA60878	Aaa60878 Human sec		
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9	296	50.0	1233	3	AAA72076	Aaa72076 cDNA enco		
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26	284.2	48.0	496	8	ADB16125	Adb16125 Human PRO
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28	284.2	48.0	496	8	ACD68505	Acd68505 Novel hum
29	284.2	48.0	496	8	ADA67706	Ada67706 Human PRO
30	284.2	48.0	496	8	ADB30713	Adb30713 cDNA enco
31	284.2	48.0	496	8	ADA86009	Ada86009 Novel hum
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33	284.2	48.0	496	8	ADA79525	Ada79525 Human PRO
34	284.2	48.0	496	8	ADA87664	Ada87664 Novel hum
35	284.2	48.0	496	8	ADB16866	Adb16866 Human PRO
36	284.2	48.0	496	8	ADA91958	Ada91958 Novel hum
37	284.2	48.0	496	8	ADB15021	Adb15021 Human PRO
38	284.2	48.0	496	8	ADB18982	Adb18982 Novel hum
39	284.2	48.0	496	8	ADA94197	Ada94197 Human PRO
40	284.2	48.0	496	8	ADB20093	Adb20093 Novel hum
41	284.2	48.0	496	8	ADB13405	Adb13405 Human PRO
42	284.2	48.0	496	8	ACD98690	Acd98690 Novel hum
43	284.2	48.0	496	8	ADA74659	Ada74659 Novel hum
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```
                             ALIGNMENTS

RESULT 1
AAA53269
ID   AAA53269 standard; cDNA; 592 BP.
XX
AC   AAA53269;
XX
DT   05-OCT-2000  (first entry)
XX
DE   Human phospholipase 1 HPPL1 coding sequence.
XX
KW   Human; phospholipase 1; HPPL1; cancer; autoimmune disorder;
KW   inflammatory disorder; reproductive disorder; infection; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             29..466
FT                   /product= "HPPL1"
FT                   /tag= a
FT   sig_peptide     29..91
FT                   /tag= b
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FT   sig_peptide     29..76
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FT   mat_peptide     77..463
FT                   /tag= d
FT                   /note= "this is a putative mature HPPL1"
FT   mat_peptide     92..463
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XX
PN   WO200024911-A2.
XX
PD   04-MAY-2000.
XX
PF   27-OCT-1999;  99WO-US025021.
XX
PR   27-OCT-1998;  98US-00181317.
PR   21-JAN-1999;  99US-0234726.
XX
PA   (INCY-) INCYTE PHARM INC.
XX
PI   Hillman JL, Bandman O, Guegler KJ, Corley NC, Baughn MR,
PI   Azimzai Y, Lal P, Lu DAM;
XX
```

DR   WPI; 2000-350750/30.
DR   P-PSDB; AAB03627.
XX
PT   Human phospholipase genes and proteins useful to diagnose, prevent or
PT   treat cancer, autoimmune or inflammatory or reproductive disorders.
XX
PS   Claim 9; Page 74; 80pp; English.
XX
CC   The present sequence is the coding sequence of human phospholipase 1
CC   (HPPl1). The protein produced from this sequence is involved in the
CC   hydrolysis of membrane phospholipids. The protein and its coding sequence
CC   can be used to diagnose and treat the following: cancers such as
CC   prostate, breast and testicular cancers, autoimmune and inflammatory
CC   disorders such as AIDS, allergies, anaemia, asthma, atherosclerosis,
CC   Crohn's disease, diabetes mellitus, emphysema, Graves' disease, irritable
CC   bowel syndrome, multiple sclerosis, myasthenia gravis, psoriasis,
CC   rheumatoid arthritis and systemic lupus erythematosus, infection caused
CC   by viruses, fungi, bacteria, parasites and protozoa, and reproductive
CC   disorders including infertility, disruptions of the menstrual cycle,
CC   polycystic ovary syndrome, ectopic pregnancies, disruptions of
CC   spermatogenesis, cancers within the reproductive tract and impotence.
CC   This coding sequence was obtained from clone no.2641779, which was
CC   constructed using lung tumour tissue
XX
SQ   Sequence 592 BP; 126 A; 182 C; 165 G; 119 T; 0 U; 0 Other;

Query Match   100.0%; Score 592; DB 3; Length 592;
Best Local Similarity   100.0%; Pred. No. 2.9e-149;
Matches 592; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

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Qy    1 TCTGCCTCCACTGCTCTGTGCTGGATCATGGAACTTGCACTGCTGTGTGGGCTGGTGGT 60
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Qy   61 GATGGCTGGTGTGATTCAATCCAGGGGGGATCCGGACTCCTGAACCTGAACAAGATGGTCAAGCA 120
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Db  121 AGTGACTGGGAAAATGCCCATCCTCCTACTGGCCCTGCTCACTGCCGGACTAGG 180

Qy  181 TGGCAGAGGCCAACCAAAGATGCCACGGACTGGTGCTGCCACGACTGCTGCTA 240
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Db  181 TGGCAGAGGCCAACCAAAGATGCCACGGACTGGTGCTGCCACGACTGCTGCTA 240

Qy  241 TGACCACCTGAAGACCCAGGGGTGCGGCATCTACAAGGACTATTACAGATACAACTTTTC 300
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Qy  301 CCAGGGGAACATCCACTGCTCTGACAAGGGAAGCTGGTGTGAGCAGCTGTGTGCCTG 360
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Db  301 CCAGGGGAACATCCACTGCTCTGACAAGGGAAGCTGGTGTGAGCAGCTGTGTGCCTG 360

Qy  361 TGACAAGGAGGTGGCCTTCTGCCTGAAGCGCAACCTGGACACCTGGACGCTGCG 420
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  361 TGACAAGGAGGTGGCCTTCTGCCTGAAGCGCAACCTGGACACCTGGACGCTGCG 420

Qy  421 TTTCTACTGGCGGCCCCACTGCCGGGGCCCACTGCGGGGGCCCACTGCGGGGG 480
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy  481 TACCCTGTTCCTCAGCATGAGCTCTGGCATCCCCACCTCAGTATCTAACCTGAACCAGC 540
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Qy  541 CTGGCTTTTCAAACACTCCGGGGGGAGGTAGTCCCAGCCTCCCCCCGGAACCC 592
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ID   AAA60878 standard; cDNA; 878 BP.
XX
AC   AAA60878;
XX
DT   02-NOV-2000 (first entry)
XX
DE   Human secretory phospholipase A2 nucleotide sequence SEQ ID NO:26.
XX
KW   Secretory phospholipase A2; PLA2; antiallergic; antiinflammatory;
KW   antibacterial; immunosuppressive; tranquiliser; vulnerary; antirheumatic;
KW   antiarthritic; septic shock; trauma; pancreatitis; allergic rhinitis;
KW   chronic rheumatoid arthritis; ss.
OS   Homo sapiens.
XX
FH   Key   Location/Qualifiers
FT   CDS   29..466
FT   /tag= a
FT   /product= "secretory phospholipase A2 (PLA2)"
FT   sig_peptide   29..88
FT   /tag= b
FT   mat_peptide   89..463
FT   /tag= c
XX
PN   WO200034486-A1.
XX
PD   15-JUN-2000.
XX
PF   07-DEC-1999;   99WO-JP006844.
XX
PR   09-DEC-1998;   98JP-00349608.
XX
PA   (SHIO) SHIONOGI & CO LTD.
XX
PI   Ishizaki J, Suzuki N, Hanasaki K;
XX
DR   WPI; 2000-423429/36.
DR   P-PSDB; AAB12537.
XX
PT   Human secretory phospholipase A2 (PLA2) and its encoded gene for
PT   diagnosis and treatment of secretory PLA2-associated diseases e.g. septic
PT   shock, trauma, pancreatitis, allergic rhinitis and chronic rheumatoid
PT   arthritis.
XX
PS   Claim 5; Page 39-40; 45pp; Japanese.
XX
CC   The present invention describes human secretory phospholipase A2 (PLA2).
CC   PLA2 has antiallergic, antiinflammatory, antibacterial, tranquiliser,
CC   immunosuppressive, vulnerary, antirheumatic, antiarthritic activities.
CC   Human secretory phospholipase A2 (PLA2), the gene encoding it and
CC   antibodies against it are useful for the diagnosis and treatment of
CC   secretory PLA2-associated diseases e.g. septic shock, trauma,
CC   pancreatitis, allergic rhinitis and chronic rheumatoid arthritis. The
CC   present sequence encodes human PLA2
XX
SQ   Sequence 878 BP; 206 A; 257 C; 238 G; 177 T; 0 U; 0 Other;

Query Match   100.0%; Score 592; DB 3; Length 878;
Best Local Similarity   100.0%; Pred. No. 3.3e-149;
Matches 592; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

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Qy    1 TCTGCCTCCACTGCTCTGTGCTGGATCATGGAACTTGCACTGCTGTGTGGGCTGGTGGT 60
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Qy   61 GATGGCTGGTGTGATTCAATCCAGGGGGGATCCGGACTCCTGAACCTGAACAAGATGGTCAAGCA 120
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Db   61 GATGGCTGGTGTGATTCAATCCAGGGGGGATCCGGACTCCTGAACCTGAACAAGATGGTCAAGCA 120

Qy  121 AGTGACTGGGAAAATGCCCATCCTCCTACTGGCCCTGCTCACTGCCGGACTAGG 180
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RESULT 2
AAA60878

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Qy    241 TGACCACCTGAAGACCCAGGGTGCGGCATCTACAAGGACTATTACAGATACAACTTTTC 300
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Db    241 TGACCACCTGAAGACCCAGGGTGCGGCATCTACAAGGACTATTACAGATACAACTTTTC 300

Qy    301 CCAGGGAACATCCACTGCTTCTGACAAGGGAAGTGGTGTGAGCAGCAGCTGTGTGCCTG 360
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Db    301 CCAGGGAACATCCACTGCTTCTGACAAGGGAAGTGGTGTGAGCAGCAGCTGTGTGCCTG 360

Qy    361 TGACAAGGAGGTGGCCTTCTGCCTGAAGCGCAACCTACCAGAAGCGACTGCG 420
          |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 TGACAAGGAGGTGGCCTTCTGCCTGAAGCGCAACCTACCAGAAGCGACTGCG 420

Qy    421 TTTCTACTGGCGGCCCCACTGCGCCGGGGGCAGACCCCTGGTGCTGAGAAGCCCACCCCTC 480
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Db    421 TTTCTACTGGCGGCCCCACTGCGCCGGGGGCAGACCCCTGGTGCTGAGAAGCCCACCCCTC 480

Qy    481 TACCCTGTTCCTCAGCATGGAGCTCTGGCATCCCCACCCCAGTATCTAACCTGAACCAGC 540
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Db    481 TACCCTGTTCCTCAGCATGGAGCTCTGGCATCCCCACCCCAGTATCTAACCTGAACCAGC 540

Qy    541 CTGGCTTTTCAAACACTCCGGGGGGAGGTAGTCCCAGCCTCCCCCGGAACCC 592
          |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    541 CTGGCTTTTCAAACACTCCGGGGGGAGGTAGTCCCAGCCTCCCCCGGAACCC 592
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RESULT 3
ACC72857
ID   ACC72857 standard; cDNA; 2747 BP.
XX
AC   ACC72857;
XX
DT   09-JUL-2003 (first entry)
XX
DE   Human cancer related protein encoding cDNA SEQ ID NO:195.
XX
KW   Human; cancer; diagnosis; screening; modulator; leukaemia; ischaemia;
KW   heart disease; atherosclerosis; endometriosis; gene; ss.
XX
OS   Homo sapiens.
XX
XX
PN   WO200302138-A2.
XX
PD   27-MAR-2003.
XX
PF   17-SEP-2002; 2002WO-US029560.
XX
PR   17-SEP-2001; 2001US-0323469P.
PR   20-SEP-2001; 2001US-0328887P.
PR   13-NOV-2001; 2001US-0350666P.
PR   08-FEB-2002; 2002US-0355145P.
PR   08-FEB-2002; 2002US-0355257P.
PR   12-APR-2002; 2002US-0372246P.
XX
PA   (EOSB-) EOS BIOTECHNOLOGY INC.
XX
PI   Afar D, Aziz N, Gish KC, Hevezi PA, Mack DH, Wilson KE;
PI   Zlotnik A;
XX
DR   WPI; 2003-354600/33.
DR   P-PSDB; ABR58706.
XX
PT   New genes that are up-regulated or down-regulated in cancers, useful as
PT   markers for diagnosing e.g. cancer, ischemia or heart diseases, or as
PT   therapeutic targets for screening drugs for treating these diseases.
XX
PS   Claim 8; Page 733; 767pp; English.
XX
CC   The present invention describes an isolated nucleic acid molecule, which
CC   comprises the sequence of any of the genes that are up-regulated or down-
CC   regulated in specific cancers (e.g. about 1031 genes up-regulated in
CC   acute lymphocytic leukemia). ACC72641 to ACC72860 represent cancer
CC   related gene nucleotide sequences which encode the proteins given in
CC   ABR58521 to ABR58709. Also described: (1) determining the presence or
CC   absence of a pathological cell in a patient; (2) an expression vector
CC   comprising a nucleic acid molecule described above; (3) a host cell
CC   comprising the vector; (4) an isolated polypeptide, which is encoded by
CC   the nucleic acid; (5) an antibody that specifically binds the polypeptide
CC   of (4); (6) specifically targeting a compound to a pathological cell in a
CC   patient by administering to the patient the antibody above; and (7) a
CC   drug screening assay. The nucleic acid is useful as diagnostic markers or
CC   therapeutic targets. In particular, the nucleic acid is useful for
CC   diagnosing a pathology (e.g. cancer of the bone marrow,
CC   bladder, brain, breast, cervix, colon/rectum, kidney, lung, ovary,
CC   pancreas, prostate, skin and uterus), wounds, ischaemia, heart diseases,
CC   atherosclerosis and endometriosis. The nucleic acid is also useful in
CC   drug screening, particularly for identifying agents for treating these
CC   pathologies
XX
SQ   Sequence 2747 BP; 719 A; 762 C; 668 G; 598 T; 0 U; 0 Other;

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Query Match              97.9%;  Score 579.4;  DB 7;  Length 2747;
Best Local Similarity    99.8%;  Pred. No. 1.2e-145;
Matches  580;  Conservative   0;  Mismatches   0;  Indels  1;  Gaps   0;

Qy     12 TGCTCTGTGCTGGATCATGGAACTTGCACTGCTGCTGCTGTGGCTGGTGGTGATGGCTGGTG 71
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Qy     72 TGATTCCAATCCAGGGCGGGATCCTGAACCTGAACAAGATGGTCAAGCAAGTGACTGGGA 131
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 TGATTCCAATCCAGGGCGGGATCCTGAACCTGAACAAGATGGTCAAGCAAGTGACTGGGA 120

Qy    132 AAATGCCCATCCTCTCCTACTGGCCCTACGGCTGTCACTGCGGACTAGGTGGCGAGAGGCC 191
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Qy    192 AACCCAAAGATGCCACGGACTGTGCTGCCAGACCATGACTGCTGCTATGACCACCTGA 251
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 AACCCAAAGATGCCACGGACTGTGCTGCCAGACCATGACTGCTGCTATGACCACCTGA 240

Qy    252 AGACCCAGGGTGCGGCATCTACAAGGACTATTACAAGGACTACAACTTTCCCAGGGGAACA 311
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 AGACCCAGGGTGCAGCATCTACAAGGACTATTACAAGGACTACAACTTTCCCAGGGGAACA 300

Qy    312 TCCACTGCTTCTGACAAGGGAAGCGGTGTGAGCAGCAGCGGTGTGCCTGTGACAAGGAGG 371
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Qy    372 TGGCCTTCTGCCTGAAGCGCAACCTGGACACCTACCAGAAGCGGACTGCGGTTTCTACTGGC 431
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Db    361 TGGCCTTCTGCCTGAAGCGCAACCTGGACACCTACCAGAAGCGGACTGCGGTTTCTACTGGC 420

Qy    432 GGCCCCACTGCGCGGGGGCAGAGCCCCTGGGTGCTGAGAAGCCCACCACCCCTCTACCCTGTTCC 491
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Qy    492 TCAGCATGGAGCTCTGGCATCCCCACCCCAGTATCTAACCTGAACCAGCCTGGCTTTTCA 551
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Db    481 TCAGCATGGAGCTCTGGCATCCCCACCCCAGTATCTAACCTGAACCAGCCTGGCTTTTCA 540

Qy    552 AACACTCCGGGGGGAGGTAGTCCCAGCCTCCCCCGGAACCC 592
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Db    541 AACACTCCGGGGGGAGGTAGTCCCAGCCTCCCCCGGAACCC 581
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RESULT 4
AAS14884
ID   AAS14884 standard; cDNA; 854 BP.
XX
AC   AAS14884;
XX
DT   20-DEC-2001 (first entry)

XX
DE Human cDNA encoding novel human protein NHP #5.
XX
KW Human; novel human protein; NHP; ss; antidiabetic; antirheumatic;
KW antiarthritic; cytostatic; antiarteriosclerotic; vulnerary;
KW neuroprotective; nootropic; antiparkinsonian;
KW anti-human immunodeficiency virus; antiasthmatic; vasotropic; cardiant;
KW hypotensive; anorectic; antiinfertility; neuroleptic; anticonvulsant;
KW antimanic; immunosuppressive; cerebroprotective; antimicrobial;
KW antiinflammatory; antibacterial; antipsoriatic; thyromimetic;
KW immunomodulator; antiseborrheic; dermatological; vasoconstriction;
KW gastrointestinal disorder; cardiovascular disorder; hypertension;
KW coronary heart disease; arteriosclerosis; anorexia; obesity; bulimia;
KW cachexia; male infertility; impotence; testicular cancer; lung tumour;
KW hyperproliferative disorder; pulmonary system disorder;
KW central nervous system disorder; bone disorder;
KW neurodegenerative disease; Alzheimer's disease; Parkinson's disease;
KW Huntington's disease; schizophrenia; mania; dementia; paranoia;
KW panic disorder; learning disability; amyotropic lateral sclerosis;
KW psychosis; autism; sleep disorder; immune system disorder;
KW Hashimoto's thyroiditis; musculo-skeletal system disorders;
KW multiple sclerosis; ischaemic brain injury; stroke; infectious disease;
KW diabetes mellitus; immunological disorder; asthma; AIDS;
KW acquired immunodeficient syndrome; leukaemia; rheumatoid arthritis;
KW inflammatory bowel disease; sepsis; acne; psoriasis; lupus erythematosus;
KW neural system disorder; respiratory disorder; olfactory disorder;
KW wound healing.
XX
OS Homo sapiens.
XX
FH Key   Location/Qualifiers
FT CDS   22..459
FT   /tag= a
FT   /product= "NHP #5"
XX
PN WO200174896-A1.
XX
PD 11-OCT-2001.
XX
PF 02-APR-2001; 2001WO-US010542.
XX
PR 03-APR-2000; 2000US-0194118P.
PR 29-SEP-2000; 2000US-0236384P.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Moore PA, Ni J, Soppet DR, Coleman TA, Gentz RL, Endress GA;
PI Li Y, Dillon PJ;
XX
DR WPI; 2001-626394/72.
DR P-PSDB; AAU09096.
XX
PT New human proteins, useful for diagnosing, treating, preventing and/or
PT prognosing disorders related to the proteins, including cardiovascular
PT disorders, autoimmune disorders and reproductive disorders.
XX
PS Claim 1; Page 294; Page 318pp; English.
XX
CC The invention relates to novel human proteins (NHP) and the nucleic acids
CC that encode them and antibodies raised against them. The proteins,
CC antibodies and nucleic acids are useful in the diagnosis, prognosis,
CC prevention and/or treatment or diseases and/or disorders involving
CC vasoconstriction, gastrointestinal disorders, cardiovascular disorders
CC (e.g. hypertension, erectile dysfunction, high blood pressure, coronary
CC heart disease and arteriosclerosis), anorexia, obesity, bulimia,
CC cachexia, disorders of small intestine, disorders of reproductive system
CC (e.g. male infertility and/or impotence), testicular cancer, lung tumours
CC and other hyperproliferative disorders, disorders of pulmonary system,
CC central nervous system disorders, bone disorders, neurodegenerative
CC diseases, Huntington's disease, schizophrenia, mania, dementia, paranoia,
CC disease, Huntington's disease, schizophrenia, amyotropic lateral sclerosis,
CC panic disorder, learning disabilities, amyotropic lateral sclerosis,
CC psychoses, autism, sleep disorders, immune system disorders (e.g.

CC Hashimoto's thyroiditis), renal and musculo-skeletal system disorders,
CC central nervous system disorders (e.g. multiple sclerosis, ischaemic
CC brain injury and/or stroke), infectious diseases, diabetes mellitus,
CC immunological disorders (e.g. asthma, acquired immunodeficient syndrome
CC (AIDS), leukaemia, rheumatoid arthritis, inflammatory bowel disease,
CC sepsis, acne, psoriasis and lupus erythematosus), neural system
CC disorders, respiratory disorders, olfactory disorders and wound healing.
CC The present sequence encodes an NHP of the invention
XX
SQ Sequence 854 BP; 186 A; 254 C; 238 G; 176 T; 0 U; 0 Other;

Query Match   97.2%; Score 575.4; DB 4; Length 854;
Best Local Similarity   99.8%; Pred. No. 9.5e-145;
Matches 576;   Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy   16 CTGTGCTGGGATCATGAACTTGCACTGCTGTGTGGCTGGTGGTGATGGCTGGTGTGTGAT 75
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   9 CTGTGCTGGGATCATGAACTTGCACTGCTGTGTGGCTGGTGGTGATGGCTGGTGTGTGAT 68

Qy   76 TCCAATCCAGGGCGGATCCTGAACCTGAACAAGATGGTCAAGCAAGTGACTGGGAAAAT 135
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   69 TCCAATCCAGGGCGGATCCTGAACCTGAACAAGATGGTCAAGCAAGTGACTGGGAAAAT 128

Qy   136 GCCCATCCTCCTACTGGCCCTACGGCTGTCACTGCGGACTAGGTGGCAGAGGCCAACC 195
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   129 GCCCATCCTCCTACTGGCCCTACGGCTGTCACTGCGGACTAGGTGGCAGAGGCCAACC 188

Qy   196 CAAAGATGCCACGGACTGGTGCTGCGAGACCCATGACTGCTGCTATGACCACCTGAAGAC 255
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   189 CAAAGATGCCACGGACTGGTGCTGCGAGACCCATGACTGCTGCTATGACCACCTGAAGAC 248

Qy   256 CCAGGGGTGGCGCATCTACAAGGACTATTACAGATACAACTTTCCCAGGGGAACATCCA 315
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   249 CCAGGGGTGGCAGCATCTACAAGGACTATTACAGATACAACTTTCCCAGGGGAACATCCA 308

Qy   316 CTGCTCTGACAAGGGAAGCTGGTGTGAGCAGCAGCTGTGTGCCTGTGACAAGGAGGTGGC 375
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   309 CTGCTCTGACAAGGGAAGCTGGTGTGAGCAGCAGCTGTGTGCCTGTGACAAGGAGGTGGC 368

Qy   376 CTTCTGCCTGAAGCCCAACCTGGACACACTACCAGGAGCGACTGCGTTCTACTGGGCGCC 435
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   369 CTTCTGCCTGAAGCCCAACCTGGACACACTACCAGGAGCGACTGCGTTCTACTGGGCGCC 428

Qy   436 CCACTGCCGGGGCCAGACCCCCTGGGTGCTAGAAGCCCACACCCCTACCCTTCCTCAG 495
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   429 CCACTGCCGGGGCCAGACCCCCTGGGTGCTAGAAGCCCACACCCCTACCCTTCCTCAG 488

Qy   496 CATGGAGCTCTGGCATCCCACCTCAGTATCTAACCTGAACCAGCCTGGCTTTTCAAACA 555
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   489 CATGGAGCTCTGGCATCCCACCTCAGTATCTAACCTGAACCAGCCTGGCTTTTCAAACA 548

Qy   556 CTCCGGGGGAGGTAGTCCCAGCCTCCCCCCCGGAACCC 592
          ||||||||||||||||||||||||||||||||||||||
Db   549 CTCCGGGGGAGGTAGTCCCAGCCTCCCCCCCGGAACCC 585

RESULT 5
AAH98759
ID AAH98759 standard; cDNA; 1927 BP.
XX
AC AAH98759;
XX
DT 12-OCT-2001 (first entry)
XX
DE Human EST-derived coding sequence SEQ ID NO: 616.
XX
KW Human; sheep; pig; cow; fruit fly; yeast; hamster; macaque; horse;
KW tomato; monkey; dog; sea urchin; expressed sequence tag; EST;
KW diagnostics; forensic test; gene mapping; genetic disorder; biodiversity;
KW gene therapy; nutrition; ss.
XX
OS Homo sapiens.
XX

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PN    WO20154477-A2.
XX
PD    02-AUG-2001.
XX
PF    25-JAN-2001; 2001WO-US002687.
XX
PR    25-JAN-2000; 2000US-00491404.
PR    17-JUL-2000; 2000US-00617746.
PR    03-AUG-2000; 2000US-00631451.
PR    15-SEP-2000; 2000US-00663870.
XX
PA    (HYSE-) HYSEQ INC.
XX
PI    Tang YT, Liu C, Zhou P, Qian XB, Wang Z, Chen R, Asundi V;
PI    Cao Y, Drmanac RA, Zhang J, Werhman T;
XX
DR    WPI; 2001-476164/51.
DR    P-PSDB; AAM24100.
XX
PT    Isolated polypeptide for treatment of diseases, diagnostics, raising
PT    antibodies and research use.
XX
PS    Claim 1; Page 599-600; 1275pp; English.
XX
CC    The present invention provides the protein and coding sequences of novel
CC    proteins from a variety of organisms, including human, dog, cat, horse,
CC    cow, pig, hamster, monkey, macaque, yeast, bacteria, fruit fly, sea
CC    urchin and tomato. These were derived from expressed sequence tags (ESTs)
CC    from the organism of interest. They can be used in diagnostics,
CC    forensics, gene mapping, identification of mutations, to assess
CC    biodiversity and for nutritional purposes. The present sequence is a cDNA
CC    of the invention
XX
SQ    Sequence 1927 BP; 413 A; 598 C; 480 G; 436 T; 0 U; 0 Other;

Query Match       96.1%; Score 568.8; DB 4; Length 1927;
Best Local Similarity 98.8%; Pred. No. 7.4e-143;
Matches    573; Conservative    0; Mismatches    7; Indels    0; Gaps    0;

Qy      13 GCTCTGTGCTGGGATCATGGAACTTGCACTGCTGTGTGGGCTGGTGGTGATGGCTGGTGT 72
           |||||||||||||||||||| ||||||||||||||||| ||||| |||||||||||||||
Db       2 GCGGTGGAATTCGATCATGGAACTTGCACTGCTGTGTGTGGGCTGGTGGTGATGGCTGGTGT 61

Qy      73 GATTCCAATCCAGGGGCGGGATCCTGAACCTGAACAAGATGGTCAAGCAAGTGACTGGGAA 132
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      62 GATTCCAATCCAGGGGCGGGATCCTGAACCTGAACAAGATGGTCAAGCAAGTGACTGGGAA 121

Qy     133 AATGCCCATCCTCTCCTACTGCCCTACGGCTGTCACTGCGGACTAGGTGGCGAGAGCCA 192
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     122 AATGCCCATCCTCTCCTACTGCCCTACGGCTGTCACTGCGGACTAGGTGGCGAGAGCCA 181

Qy     193 ACCCAAAGATGCCACGGACTGGTGCTGCCAGACCCATGACTGCTGCTATGACCACCTGAA 252
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     182 ACCCAAAGATGCCACGGACTGGTGCTGCCAGACCCATGACTGCTGCTATGACCACCTGAA 241

Qy     253 GACCCAGGGGTGCGGCATCACAAGGACTATTACAGATACAACTTTTCCCAGGGAACAT 312
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     242 GACCCAGGGGTGCGGCATCACAAGGACTATTACAGATACAACTTTTCCCAGGGAACAT 301

Qy     313 CCACTGCTCTGACAAGGAAGCTGGTGTGAGCAGCAGCGTGTGCCTGTGACAAGGAGGT 372
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     302 CCACTGCTCTGACAAGGAAGCTGGTGTGAGCAGCAGCGTGTGCCTGTGACAAGGAGGT 361

Qy     373 GGCCTTCTGCCTGAAGCGCAACCTGGACACCTACCAGAAGCGACTGCGTTTCTACTGGCG 432
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     362 GGCCTTCTGCCTGAAGCGCAACCTGGACACCTACCAGAAGCGACTGCGTTTCTACTGGCG 421

Qy     433 GCCCCACTGCCGCGGGGCAGACCCCTGGGTGCTAGAAGCCCACACCCTCTACCCTGTTCCT 492
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     422 GCCCCACTGCCGCGGGGCAGACCCCTGGGTGCTAGAAGCCCACACCCTCTACCCTGTTCCT 481

Qy     493 CAGCATGGAGCTCTGCATCCCCACTCAGTATCTAACCTGAACCAGCCAGCCTGGCTTTTCAA 552
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
```

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Db     482 CAGCATGGAGCTCTGGCATCCCCACTCAGTATCTAACCTGAACCAGCCAGCCTGGCTTTTCAA 541
XX
Qy     553 ACACTCCGGGGGGAGGTAGTCCCAGCCTCCCCCGGAACCC 592
           |||||||||||||||||||||||||||||||||||||||||
Db     542 ACACTCCGGGGGGAGGTAGTCCCAGCCTCCCCCGGAACCC 581

RESULT 6
AAH99768
ID    AAH99768 standard; cDNA; 1927 BP.
XX
AC    AAH99768;
XX
DT    16-OCT-2001  (first entry)
XX
DE    Human protein encoding cDNA sequence SEQ ID NO:603.
XX
KW    Human; cancer; ulcer; HIV infection; human immunodeficiency virus;
KW    antiinflammatory; antirheumatic; antiarthritic; immunosuppressive;
KW    antibacterial; endocrine; cardiant; central nervous system; virucide;
KW    anti-HIV; fungicide; antimutagen; cardiovascular; antianaemic; anaemia;
KW    antiaggregant; haemostatic; vulnerary; antiulcer; osteopathic; eczema;
KW    dermatological; antiallergic; antiasthmatic; antidiabetic; cytostatic;
KW    neuroprotective; antidepressant; nootropic; antiparkinsonian; infection;
KW    immunostimulant; gene therapy; antisense therapy; vaccine; inflammation;
KW    antianaphylactic; rheumatoid arthritis; septic shock; pancreatitis;
KW    cardiac dysfunction; neuropathology; cardiac anaphylaxis; autoimmunity;
KW    genetic disease; haematopoietic disorder; platelet disorder; asthma;
KW    thrombocytopaenia; osteoporosis; severe combined immunodeficiency;
KW    allergic rhinitis; diabetes; multiple sclerosis; depression;
KW    Alzheimer's disease; Parkinson's disease; neurodegenerative disorder;
KW    neurological disorder; ss.
XX
OS    Homo sapiens.
XX
PN    WO200153455-A2.
XX
PD    26-JUL-2001.
XX
PF    22-DEC-2000; 2000WO-US035017.
XX
PR    23-DEC-1999;    99US-00471275.
PR    21-JAN-2000; 2000US-00488725.
PR    25-APR-2000; 2000US-00552317.
XX
PA    (HYSE-) HYSEQ INC.
XX
PI    Tang YT, Liu C,  Drmanac RT;
XX
DR    WPI; 2001-457603/49.
DR    P-PSDB; AAM25827.
XX
PT    Isolated human polynucleotides encoding polypeptides, useful for the
PT    treatment and diagnosis of e.g. cancer, ulcers and HIV infection.
XX
PS    Claim 1; Page 636; 1217pp; English.
XX
CC    AAH99166 to AAH99904 encode the human proteins given in AAM25225 to
CC    AAM25963. The proteins can have activities based on the tissues and cells
CC    they are expressed in, such as: antiinflammatory; antirheumatic;
CC    antiarthritic; immunosuppressive; antibacterial; endocrine; cardiant;
CC    central nervous system; virucide; anti-HIV; fungicide; antimutagen;
CC    cardiovascular; antianaemic; antiaggregant; haemostatic; vulnerary;
CC    antiulcer; osteopathic; dermatological; antiallergic; antiasthmatic;
CC    antidiabetic; cytostatic; neuroprotective; antidepressant; nootropic;
CC    antiparkinsonian; and immunostimulant. The proteins and polynucleotides
CC    encoding them can be used in gene therapy, antisense therapy and vaccine
CC    production. The proteins and polynucleotides are useful for screening for
CC    agonists or antagonists of a protein and for the treatment and diagnosis
CC    of disorders associated with the activity of a protein e.g. inflammation,
CC    rheumatoid arthritis, septic shock, pancreatitis, cardiac dysfunction,
CC    neuropathology, cardiac anaphylaxis, viral, bacterial, HIV and fungal
CC    infections, autoimmunity, genetic diseases, haematopoietic disorders,
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CC    anaemia, platelet disorders, thrombocytopaenia, wounds, burns, ulcers,
CC    osteoporosis, severe combined immunodeficiency, eczema, allergic
CC    rhinitis, asthma, diabetes, cancer, multiple sclerosis, depression,
CC    Alzheimer's disease, Parkinson's disease, neurodegenerative and
CC    neurological disorders
XX
SQ    Sequence 1927 BP; 413 A; 598 C; 480 T; 436 T; 0 U; 0 Other;

Query Match       96.1%;  Score 568.8;  DB 4;  Length 1927;
Best Local Similarity   98.8%;  Pred. No. 7.4e-143;
Matches  573;  Conservative    0;  Mismatches    7;  Indels    0;  Gaps    0;

Qy      13 GCTCTGTGCTGGGATCATGGAACTTGCACTGCTGTGTGGGCTGGTGTGTGATGGCTGGTGT 72
           ||||  |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2 GCGGTGGAATTCGATCATGGAACTTGCACTGCTGTGTGGGCTGGTGTGTGATGGCTGGTGT 61

Qy      73 GATTCCAATCCAGGGGCGGGGATCCTGAACCTGAACACAGATGGTCAAGCAAGTGACTGGGAA 132
           ||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||
Db      62 GATTCCAATCCAGGGGCGGGGATCCTGAACCTGAACACAGATGGTCAAGCAAGTGACTGGGAA 121

Qy     133 AATGCCCATCCTCTTCACTGGCCCTACGGCTGTCACTGCGGACTAGGTGGCAGAGGCCA 192
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     122 AATGCCCATCCTCTTCACTGGCCCTACGGCTGTCACTGCGGACTAGGTGGCAGAGGCCA 181

Qy     193 ACCCAAAGATGCCACGGACTGGTGCTGCCAGACCCATGACTGCTCATGACCACCTGAA 252
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     182 ACCCAAAGATGCCACGGACTGGTGCTGCCAGACCCATGACTGCTCATGACCACCTGAA 241

Qy     253 GACCCAGGGGGTGCGGCATCTACAAGGACTATTACAGATACAACTTTCCCAGGGGAACAT 312
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     242 GACCCAGGGGGTGCGGCATCTACAAGGACTATTACAGATACAACTTTCCCAGGGGAACAT 301

Qy     313 CCACTGCTCTGACAAGGGAAGCTGGTGTGAGCAGCAGCTGTGTGCCTGTGACAAGGAGGT 372
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     302 CCACTGCTCTGACAAGGGAAGCTGGTGTGAGCAGCAGCTGTGTGCCTGTGACAAGGAGGT 361

Qy     373 GGCCTTCGCCTGAAGCGCAACCTGACAACCTACCAGAGGCGACTGCGTTTCTACTGGCG 432
           ||| |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     362 GGCCTTCGCCTGAAGCGCAACCTGACAACCTACCAGAGGCGACTGCGTTTCTACTGGCG 421

Qy     433 GCCCCACTGCCCGGCGGCAGACCCCTGGGTGCTAGAAGCCCACACCCTACCCTGTTCCT 492
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     422 GCCCCACTGCCCGGCGGCAGACCCCTGGGTGCTAGAAGCCCACACCCTACCCTGTTCCT 481

Qy     493 CAGCATGGAGCTCTGGCATCCCACCCACTCAGTATCTAACCTGAACCAGCCTGGCTTTTCAA 552
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     482 CAGCATGGAGCTCTGGCATCCCACCCACTCAGTATCTAACCTGAACCAGCCTGGCTTTTCAA 541

Qy     553 ACACTCCGGGGGAGTAGTCCCAGCCTCCCCGGAACCC 592
           |||||||||||||||||||||||||||||||||||||
Db     542 ACACTCCGGGGGAGTAGTCCCAGCCTCCCCGGAACCC 581
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```
RESULT 7
AAD19218
ID   AAD19218 standard; DNA; 1931 BP.
XX
AC   AAD19218;
XX
DT   18-DEC-2001  (first entry)
XX
DE   Human CG95 (or C870) lipase DNA.
XX
KW   Human; apolipoprotein; lipase; lipoprotein receptor; ALlr; angina;
KW   cardiovascular disease; lipid metabolism; myocardial infarction;
KW   cerebral ischaemia; arterial thrombosis; thrombolytic; antilipaemic;
KW   coronary artery thrombosis; cerebral artery thrombosis; stroke;
KW   intracardiac thrombosis; gene therapy; cardiovascular; vasodilator;
KW   neuroprotectant; cerebroprotective; ds.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
```

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FT   CDS             18..455
FT                   /*tag= a
FT                   /product= "Human CG95 (or C870) lipase protein"
FT   sig_peptide     18..89
FT                   /*tag= b
FT   mat_peptide     90..452
FT                   /*tag= c
FT                   /product= "Human mature CG95 (or C870) protein"
XX
PN   WO200179446-A2.
XX
PD   25-OCT-2001.
XX
PF   16-APR-2001; 2001WO-US012529.
XX
PR   14-APR-2000; 2000US-0197137P.
PR   20-JUN-2000; 2000US-00598042.
PR   03-AUG-2000; 2000US-00631451.
PR   22-SEP-2000; 2000US-00667298.
PR   17-NOV-2000; 2000US-00714936.
XX
PA   (HYSB-) HYSEQ INC.
XX
PI   Ballinger DG, Loeb D, Montgomery JR, Tang TY, Zhou P, Goodrich R;
PI   Liu C, Asundi V, Zhao QA, Wehrman T, Drmanac RT, Ren F, Qian XB;
PI   Wang D;
XX
DR   WPI; 2001-611724/70.
DR   P-PSDB; AAE11924.
XX
PT   Nucleic acids encoding human apolipoproteins, lipases, and lipoprotein
PT   receptor polypeptides, useful for preventing diagnosing and treating
PT   lipid metabolism disorders, thrombosis and cardiovascular diseases.
XX
PS   Claim 1; Page 153-154; 266pp; English.
XX
CC   The invention relates to polynucleotides encoding proteins CG122, CG179,
CC   CG95, CG121, CG162, CG27, CG153 and CG168 which are related to proteins
CC   involved in lipid metabolism and cardiovascular disease such as human
CC   apolipoproteins, lipases and lipoprotein receptor proteins. These DNA and
CC   protein sequences are useful for treating or preventing disorders
CC   associated with apolipoproteins, lipases and lipoprotein receptor (ALlr)
CC   expression and for treating lipid metabolism, cardiovascular diseases and
CC   thrombosis. Antibodies against these proteins are useful for determining
CC   the presence or predisposition to a disease associated with altered
CC   levels of these sequences. ALlr polypeptides are also useful for
CC   identifying agents (agonists and antagonists) that bind to them and cells
CC   expressing ALlr proteins are useful for identifying a therapeutic agent
CC   for use in treatment of a pathology related to aberrant expression or
CC   physiological interactions of this polypeptide. Vectors comprising these
CC   DNA and protein sequences are also useful for producing ALlr proteins.
CC   The nucleic acids and polypeptides of the invention are also useful for
CC   the treatment of occlusive cardiovascular diseases, myocardial
CC   infarction, cerebral ischaemia, angina, arterial thrombosis, coronary
CC   artery thrombosis and cerebral artery thrombosis or intracardiac
CC   thrombosis and stroke. The nucleotides of the invention are used in gene
CC   therapy. The present sequence is human CG95 (or C870) lipase DNA
XX
SQ   Sequence 1931 BP; 417 A; 600 C; 479 G; 435 T; 0 U; 0 Other;

Query Match       95.8%;  Score 567.4;  DB 5;  Length 1931;
Best Local Similarity   99.8%;  Pred. No. 1.8e-142;
Matches  568;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      24 GGATCATGGAACTTGCACTGCTGTGTGGGCTGGTGTGTGATGGCTGGTGTGATTCCAATCC 83
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      13 GGACCATGGAACTTGCACTGCTGTGTGGGCTGGTGTGTGATGGCTGGTGTGATTCCAATCC 72

Qy      84 AGGGGCGGGATCCTGAACCTGAACAAGATGGTCAAGCAAGTGACTGGGAAAATGCCCATCC 143
           ||||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||
Db      73 AGGGGCGGGATCCTGAACCTGAACAAGATGGTCAAGCAAGTGACTGGGAAAATGCCCATCC 132

Qy     144 TCTCCTACTGGCCCTACGGCTGTCACTGCGGACTAGGTGCGGAGGGGCAACCCAAAGATG 203
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PT   Human secretory phospholipase A2 (PLA2) and its encoded gene for
PT   diagnosis and treatment of secretory PLA2-associated diseases e.g. septic
PT   shock, trauma, pancreatitis, allergic rhinitis and chronic rheumatoid
PT   arthritis.
XX
PS   Example 3; Page 35-36; 45pp; Japanese.
XX
CC   The present invention describes human secretory phospholipase A2 (PLA2).
CC   PLA2 has antiallergic, antiinflammatory, antibacterial, tranquiliser,
CC   immunosuppressive, vulnerary, antirheumatic and antiarthritic activities.
CC   Human secretory phospholipase A2 (PLA2), the gene encoding it and
CC   antibodies against it are useful for the diagnosis and treatment of
CC   secretory PLA2-associated diseases e.g. septic shock, trauma,
CC   pancreatitis, allergic rhinitis and chronic rheumatoid arthritis. The
CC   present sequence encodes mouse PLA2, which is used in an example from the
CC   present invention
XX
SQ   Sequence 1233 BP; 279 A; 337 C; 307 G; 310 T; 0 U; 0 Other;

Query Match             50.0%;  Score 296;  DB 3;  Length 1233;
Best Local Similarity   77.5%;  Pred. No. 1.7e-69;
Matches  372;  Conservative    0;  Mismatches  105;  Indels    3;  Gaps    1;

Qy         2 CTGCCTCCACTGCTCTGTGCTGGGATCATGGAACTTGCACTGCTCGTGTGGGCTGGTGGTG 61
             |||||| || |||||||  ||| |||  ||||| |||| ||  ||||| ||||||| |||
Db         9 CTGCCTGCCTTGCTCTGGGCTGGCTGGAACTATGAGACTTCGCCCCTGCTGTGGGCTGCGC-- 66

Qy        62 ATGGCTGGTGGATTCCAATCCAGGGCGGGATCCTGGAACCTGAACAAGATGGTCAAGCAA 121
             ||| | ||| |  ||||| ||||||| ||| |||||||||||||||||||| || |||
Db        67 -TGGCCGGTATAACTGCAACCCAGGGAGGGCTCCTGAACCTGAACAAGATGTCACACAC 125

Qy       122 GTGACTGGGAAAATGCCCATCCTTCCTCACTGGCCCTACGGCTGTCACTGCGGACTAGGT 181
             ||||| ||| |  |||||  || || ||||||||||||||||||||||||| |||| ||
Db       126 ATGACGGGGAAGAAAGCCCTTCTTCAGCTACTGGCCCTACGGCTGTCACTGTGGACTTGGT 185

Qy       182 GGCAGAGGCCAACCCAAAGATGCCACGGACTGGTGCTGCCAGACCCATGACTGCTGCTAT 241
             ||||  || ||||||||||||||||||||||||||||||||||  ||||| ||||||||
Db       186 GGCAAAGGGCAACCCAAAGATGCCACGGACTGGTGCTGCCAGAGCATGATTGTTGCTAT 245

Qy       242 GACCACCTGAAGACCCAGGGGTGCGGCATCTACAAGGACTATTACAGATACAACTTTTCC 301
             | |||||||||| |   || ||| |||||||| |||| |  || |||||| ||  || ||
Db       246 GCCCACCTGAAGATCGATGGATGCAAGAGCCTGACAGACAACTACAAATACAGACATCTCC 305

Qy       302 CAGGGGAACATCCACTGCTCTGACAAGGAGGTGGTGTGAGCAGTGTGAGCAGTGTGCCTGT 361
             ||||| ||||||| |||||||||||  ||||  ||||| ||| ||||| ||||| | ||||
Db       306 CAGGGCACTATCCAGTGCTCTGACAACGGAGCGGAGTGGTGTGAAAGGCAACTGTGTGCTTGT 365

Qy       362 GACAAGGAGGTGGCCTTCTGCCTGAAGCGGCAACCTACCAGAAGCGACCACTGCGCT 421
             |||||||||||||||| |  ||||||||  ||| ||  | ||| ||  || ||| ||
Db       366 GACAAGGAGGTGGCCTTGCTTGCTTGAAGCAAAACCTGGATAGCTACAATAAGCGCCTGCGT 425

Qy       422 TTCTACTGGCGCGCCCACTGCCGCGGGGGGCAGACCCCTCGGGTGCTGTAGAAGCCCACACCCTCT 481
             | ||||||||| ||||| ||| | ||| ||||||||  |||||||| || ||||||||||| | |
Db       426 TACTACTGGCGGCGCCCCGTTGCAAAGGCAAGACTCCAGCATGTCAAGGGAGTCCACTCTGT 485
```

```
Db       133 TCTCCTACTGCCCTACGGCTGTCACTGCGGACTAGGTGGCAGAGGCCAACCCAAAGATG 192
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy       204 CCACGGACTGGTGCTGCCAGACCCATGACTGCTGCTATGACCACCTGAAGACCCAGGGGT 263
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       193 CCACGGACTGGTGCTGCCAGACCCATGACTGCTGCTATGACCACCTGAAGACCCAGGGGT 252

Qy       264 GCGGCATCTACAAGGACTATTACAGATACAACTTTTCCAGGGGAACATCCACTGCTCTG 323
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       253 GCGGCATCTACAAGGACTATTACAGATACAACTTTTCCAGGGGAACATCCACTGCTCTG 312

Qy       324 ACAAGGGAAGCTGGTGTGAGCAGCAGCAGCTGTGCCTGTGACAAGGAGGTGGCCTTCTGCC 383
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       313 ACAAGGGAAGCTGGTGTGAGCAGCAGCAGCTGTGCCTGTGACAAGGAGGTGGCCTTCTGCC 372

Qy       384 TGAAGCGCAACCTGACAACCTACCAGAAGCGACTGCGTTTCTACTGGGCGGCCCACTGCC 443
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       373 TGAAGCGCAACCTGACAACCTACCAGAAGCGACTGCGTTTCTACTGGGCGGCCCACTGCC 432

Qy       444 GGGGGCGGCAGACCCCTGGGTGCTAGAAGCCCACACCCTCACCCTGTTCCTGAGCATGGAGC 503
             ||||||||||||||||||||||||||||||||||||||||||||||||||||| |||||||
Db       433 GGGGGCGGCAGACCCCTGGGTGCTAGAAGCCCACACCCTCACCCTGTTCCTCAGCATGGAGC 492

Qy       504 TCTGGCATCCCCACCTCAGTATCTAACCTGAACCAGCCTGGCTTTCAAACACTCCGGGG 563
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       493 TCTGGCATCCCCACCTCAGTATCTAACCTGAACCAGCCTGGCTTTCAAACACTCCGGGG 552

Qy       564 GGAGGTAGTCCCAGCCTCCCCCGGAACCC 592
             |||||||||||||||||||||||||||||
Db       553 GGAGGTAGTCCCAGCCTCCCCCGGAACCC 581
```

```
RESULT 8
AAA60866
ID   AAA60866 standard; cDNA; 1233 BP.
XX
AC   AAA60866;
XX
DT   02-NOV-2000 (first entry)
XX
DE   Mouse secretory phospholipase A2 nucleotide sequence SEQ ID NO:13.
XX
KW   Secretory phospholipase A2; PLA2; antiallergic; antiinflammatory;
KW   antibacterial; immunosuppressive; tranquilser; vulnerary; antirheumatic;
KW   antiarthritic; septic shock; trauma; pancreatitis; allergic rhinitis;
KW   chronic rheumatoid arthritis; ss.
XX
OS   Mus musculus.
XX
FH   Key             Location/Qualifiers
FT   CDS             36..470
FT                   /*tag= a
FT                   /product= "secretory phospholipase A2 (PLA2)"
FT   sig_peptide     36..92
FT                   /*tag= b
FT   mat_peptide     93..467
FT                   /*tag= c
XX
PN   WO200034486-A1.
XX
PD   15-JUN-2000.
XX
PF   07-DEC-1999; 99WO-JP006844.
XX
PR   09-DEC-1998; 98JP-00349608.
XX
PA   (SHIO ) SHIONOGI & CO LTD.
XX
PI   Ishizaki J, Suzuki N, Hanasaki K;
XX
DR   WPI; 2000-423429/36.
DR   P-PSDB; AAB12536.
XX
```

```
RESULT 9
AAA72076
ID   AAA72076 standard; cDNA; 1233 BP.
XX
AC   AAA72076;
XX
DT   24-NOV-2000 (first entry)
XX
DE   cDNA encoding mouse secreted phospholipase A2.
XX
KW   Secreted phospholipase A2; PLA2; mouse; murine; recombinant production;
KW   antibody; diagnosis; expressed sequence tag; EST; drug screening; ss.
XX
OS   Mus musculus.
XX
FH   Key             Location/Qualifiers
FT   CDS             36..470
```

```
FT                  /*tag= a
FT                  /product= "Mouse secreted phospholipase A2"
FT   sig_peptide    36..92
FT                  /*tag= b
FT   mat_peptide    93..467
FT                  /*tag= c
FT                  /product= "Mouse mature secreted phospholipase A2"
XX
PN   JP2000165544-A.
XX
PD   20-JUN-2000.
XX
PF   09-DEC-1998;   98JP-00349602.
XX
PR   09-DEC-1998;   98JP-00349602.
XX
PA   (SHIO ) SHIONOGI & CO LTD.
XX
DR   WPI; 2000-458171/40.
DR   P-PSDB; AAB11994.
XX
PT   Mouse secretion type phospholipase A2.
XX
PS   Claim 5; Page 8-10; 12pp; Japanese.
XX
CC   This sequence represents cDNA encoding a mouse secreted phospholipase A2
CC   (secreted PLA2). This was initially identified in an EST (expressed
CC   sequence tag) database, and a fragment (AAA72077) was isolated from cDNA
CC   derived from several mouse tissue types using primers AAA72078-A72081).
CC   The full length cDNA was generated using primers AAA72082-A72088. The
CC   invention relates to the novel secreted PlA2, nucleic acids encoding it,
CC   and variants of the protein which retain phospholipase A2 activity. It
CC   also encompasses an expression vector and host cells comprising DNA
CC   encoding murine secreted PlA2, a method for the recombinant production of
CC   the protein, a method of screening potential inhibitors of the protein
CC   and the compounds thus identified, and an antibody specific for murine
CC   PLA2. The antibody can be used for the diagnosis of a variety of diseases
XX
SQ   Sequence 1233 BP; 279 A; 337 C; 307 G; 310 T; 0 U; 0 Other;

Query Match             50.0%;  Score 296;  DB 3;  Length 1233;
Best Local Similarity   77.5%;  Pred. No. 1.7e-69;
Matches  372;  Conservative   0;  Mismatches 105;  Indels   3;  Gaps    1;

Qy          2 CTGCCTCCACTGCTCTGTGCTGGGATCATGGAACTTGCACTGCTGTGGCTGGTGGTG 61
              ||||||||||| |||||||||||| |||||| ||||| |||||| |||||||||||
Db          9 CTGCCTGCCTTGCTCTGGGGCTGGAACTATGGAGACTCGCCCCGCTGTGTGGGCTGGCTGCTGC-- 66

Qy         62 ATGGCTGGTGTGATTCCAATCCAGGGCGGATCCTGAACCTGAACAAGATGGTCAAGCAA 121
              |||||||||||||||||||| ||||||| |||||||||| ||||||| |||||||||||
Db         67 -TGGCCGGTATTAACTGCAACCCAGGGAGGCGCTCCAGGCAGGAGGACAAGAAGATGGTCACACAC 125

Qy        122 GTGACTGGGAAAAATGCCCATCCTCCTCCTACTGGCCCTACGGCTGTCACTGCGGACTAGGT 181
              |||||  |||||| |||||||||| |||||||||||| |||||||
Db        126 ATGACGGGGAAGAAAGCCTTTCACTAGCTACTGGCCGCCTCCTACGGGCTGTCACTGGGGACTTGGT 185

Qy        182 GGCAGAGGCCAACCAAAGATGCCACGACGGACTGGTGTGCCAGGACCCATGACTGCTGTCTAT 241
              ||||||||||||||||||||||  ||||||||||||||||||||||||| |||||||||||
Db        186 GGCAAAGGGCAACCAAAGATGCCACCAGACTGCTGTCAGAAGCATGATTGTTGCTAT 245

Qy        242 GACCACCTGAAGACCCAGGGTGCGGCATCTACAAGGACTATTACAGACGAACTTTTCC 301
              |||| |||||||||||||||| | ||||||| ||||||| ||||| |||||||||||||
Db        246 GCCCACCTGAAGACCCGATGGATGCAAGAGAGCCTGACAGAGCAAGCTACACATCTCC 305

Qy        302 CAGGGGAACATCCACTGCTCTGACAAGGGAGGCTGGTGTGAGCAGCAGCAGCTGTTGCCTGT 361
              ||||| |||||||||||||||||||| || |||||||| |||| ||||||| |||||||||
Db        306 CAGGGCACTATCCAGTGCTCTGACAACGGGAGCTGGTGTGAAAGGCAACTGTGTCCTTGT 365

Qy        362 GACAAGGAGGTGGCCTTCTGCCTGAAGGCGCAACCTGACAACCTACCAGAAGCGACTGCGT 421
              |||| ||||||||  |||||||||||||| |||||||| |||||||||||||||||||||
Db        366 GACAAGGAGGTGGCCTTGCCCTTGTGCTTGAACGCAAAACCTGGTCACATAAGCGCCTGCGT 425

Qy        422 TTCTACTGGCGCGCCCACTGCCGCGGGGGGCAGACCCCTCGGGTGCTAGAAGCCCACACCCTCT 481
```

```
RESULT 10
AAA77684
ID   AAA77684 standard; cDNA; 496 BP.
XX
AC   AAA77684;
XX
DT   07-NOV-2000  (first entry)
XX
DE   Human PRO1561 cDNA sequence SEQ ID NO:221.
XX
KW   Human; PRO; promotion; inhibition; angiogenesis; cardiovascularisation;
KW   diagnosis; trauma; wound; cancer; atherosclerosis; cardiac hypertrophy;
KW   angiogenic; proliferative; cardiant; cardiovascular; antiatherosclerotic;
KW   cytostatic; gene therapy; vaccine; ss.
XX
OS   Homo sapiens.
XX
PN   WO200032221-A2.
XX
PD   08-JUN-2000.
XX
PF   30-NOV-1999;   99WO-US028313.
XX
PR   01-DEC-1998;   98WO-US025108.
PR   16-DEC-1998;   98US-0112850P.
PR   12-JAN-1999;   99US-0115554P.
PR   08-MAR-1999;   99WO-US005028.
PR   12-MAR-1999;   99US-0123957P.
PR   28-APR-1999;   99US-0131445P.
PR   14-MAY-1999;   99US-0134287P.
PR   02-JUN-1999;   99WO-US012252.
PR   23-JUN-1999;   99US-0141037P.
PR   20-JUL-1999;   99US-0144758P.
PR   26-JUL-1999;   99US-0145698P.
PR   01-SEP-1999;   99WO-US020111.
PR   08-SEP-1999;   99WO-US020594.
PR   13-SEP-1999;   99WO-US020944.
PR   15-SEP-1999;   99WO-US021090.
PR   15-SEP-1999;   99WO-US021547.
PR   05-OCT-1999;   99WO-US023089.
PR   29-OCT-1999;   99US-0162506P.
XX
PA   (GETH ) GENENTECH INC.
XX
PI   Ashkenazi AJ,  Baker KP,  Ferrara N,  Gerber H,  Hillan KJ;
PI   Goddard A,  Godowski PJ,  Gurney AL,  Klein RD,  Kuo SS,  Paoni NF;
PI   Smith V,  Watanabe CK,  Williams PM,  Wood WI;
XX
DR   WPI; 2000-412154/35.
DR   P-PSDB; AAB24434.
XX
PT   Nucleic acids encoding PRO polypeptides useful for preventing, diagnosing
PT   and treating diagnosing a cardiovascular, endothelial or angiogenic
PT   disorders in mammals.
XX
PS   Claim 61; Fig 93; 315pp; English.
XX
CC   The present invention describes nucleic acids encoding PRO polypeptides
CC   useful for preventing, diagnosing and treating diagnosing a
CC   cardiovascular, endothelial or angiogenic disorder in mammals by
CC   modulating cell proliferation, angiogenesis and cardiovascularisation,
CC   and for identifying agonists and antagonists of these processes. The
CC   nucleic acids and the proteins they encode may be used in the prevention,
CC   treatment and diagnosis of diseases associated with inappropriate PRO
CC   expression such as cardiovascular, endothelial or angiogenic disorders in
CC   mammals (e.g. atherosclerosis, cancers and cardiac hypertrophy). For
CC   example, the nucleic acids (NCs) and vectors containing them and the PRO
CC   polypeptide may be used to treat disorders associated with decreased PRO
CC   expression. AAA77510 to AAA77721 and AAB24388 to AAB24435 represent
```

CC   nucleotide and protein sequences used in the exemplification of the
CC   present invention
XX
SQ   Sequence 496 BP; 200 A; 95 C; 104 G; 95 T; 0 U; 2 Other;

Query Match   48.0%; Score 284.2; DB 3; Length 496;
Best Local Similarity   97.3%; Pred. No. 1.9e-66;
Matches 289; Conservative   0; Mismatches   8; Indels   0; Gaps   0;

Qy   1 TCTGCCTCCACTGCTCTGTGCTGGATCATGGAACTTGCACTGCTGTGGGCTGGTGGT 60
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 TCTGCCTCCACTGCTCTGTGCTGGATCATGGAACTTGCACTGCTGTGGGCTGGTGGT 60

Qy   61 GATGGCTGGTGTGATTCCAATCCAGGGCGGGATCCTGAACCTGAACAAGATGGTCAAGCA 120
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 GATGGCTGGTGTGATTCCAATCCAGGGCGGGATCCTGAACCTGAACAAGATGGTCAAGCA 120

Qy   121 AGTGACTGGGAAAATGCCCATCCTCCTACTGGCCCTACGGCTGTCACTGCGGACTAGG 180
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121 AGTGACTGGGAAAATGCCCATCCTCCTACTGGCCCTACGGCTGTCACTGCGGACTAGG 180

Qy   181 TGGCAGAGGCCAACCCAAAGATGCCACGGACTGGTGCTGCCAGACCCATGACTGCTGCTA 240
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181 TGGCAGAGGCCAACCCAAAGATGCCACGGACTGGTGCTGCCAGACCCATGACTGCTGCTA 240

Qy   241 TGACCACCTGAAGACCCAGGGGGTGCGGCATCTACAAGGACTATTACAGATACAACTT 297
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241 TGACCACCTGAAGACCCAGGGGGTGCGGCATCTACAAGGACTACAAGGACAACAAAAGCAGCAT 297

RESULT 11
AAF54466
ID   AAF54466 standard; DNA; 496 BP.
XX
AC   AAF54466;
XX
DT   02-APR-2001 (first entry)
XX
DE   DNA encoding protein of the invention #109.
XX
KW   Secreted; transmembrane; gene therapy; ss.
XX
OS   Unidentified.
XX
PN   WO200078961-A1.
XX
PD   28-DEC-2000.
XX
PF   18-FEB-2000; 2000WO-US004342.
XX
PR   23-JUN-1999;   99US-0141037P.
PR   20-JUL-1999;   99US-0144758P.
PR   26-JUL-1999;   99US-0145698P.
PR   01-SEP-1999;   99WO-US020011.
PR   29-OCT-1999;   99US-0162506P.
PR   30-NOV-1999;   99WO-US028313.
PR   02-DEC-1999;   99WO-US028551.
PR   16-DEC-1999;   99WO-US030095.
PR   05-JAN-2000;   2000WO-US000219.
PR   06-JAN-2000;   2000WO-US000376.
XX
PA   (GETH) GENENTECH INC.
XX
PI   Baker KP, Botstein D, Desnoyers L, Eaton DL, Ferrara N, Fong S;
PI   Gao W, Goddard A, Godowski PJ, Grimaldi CJ, Gurney AL, Hillan KJ;
PI   Pan J, Paoni NF, Roy MA, Smith V, Stewart TA, Tumas D, Watanabe CK;
PI   Williams PM, Wood WI;
XX
DR   WPI; 2001-071395/08.
XX
PT   Secreted and transmembrane proteins and nucleic acids designated PRO,
PT   useful as hybridization probes, in chromosome and gene mapping and gene
PT   therapy.

XX
PS   Claim 2; Fig 217; 787pp; English.
XX
CC   The present invention relates to secreted and transmembrane proteins.
CC   These proteins and the DNA encoding them may be used as hybridization
CC   probes, in chromosome and gene mapping and in the generation of anti-
CC   sense RNA and DNA. They may also be used to generate either
CC   transgenic animals or knockout animals which are in turn useful for
CC   development and screening of therapeutically useful reagents. The nucleic
CC   acids may also be used in gene therapy
XX
SQ   Sequence 496 BP; 200 A; 95 C; 104 G; 95 T; 0 U; 2 Other;

Query Match   48.0%; Score 284.2; DB 4; Length 496;
Best Local Similarity   97.3%; Pred. No. 1.9e-66;
Matches 289; Conservative   0; Mismatches   8; Indels   0; Gaps   0;

Qy   1 TCTGCCTCCACTGCTCTGTGCTGGATCATGGAACTTGCACTGCTGTGGGCTGGTGGT 60
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 TCTGCCTCCACTGCTCTGTGCTGGATCATGGAACTTGCACTGCTGTGGGCTGGTGGT 60

Qy   61 GATGGCTGGTGTGATTCCAATCCAGGGCGGGATCCTGAACCTGAACAAGATGGTCAAGCA 120
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 GATGGCTGGTGTGATTCCAATCCAGGGCGGGATCCTGAACCTGAACAAGATGGTCAAGCA 120

Qy   121 AGTGACTGGGAAAATGCCCATCCTCCTACTGGCCCTACGGCTGTCACTGCGGACTAGG 180
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121 AGTGACTGGGAAAATGCCCATCCTCCTACTGGCCCTACGGCTGTCACTGCGGACTAGG 180

Qy   181 TGGCAGAGGCCAACCCAAAGATGCCACGGACTGGTGCTGCCAGACCCATGACTGCTGCTA 240
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181 TGGCAGAGGCCAACCCAAAGATGCCACGGACTGGTGCTGCCAGACCCATGACTGCTGCTA 240

Qy   241 TGACCACCTGAAGACCCAGGGGGTGCGGCATCTACAAGGACTATTACAGATACAACTT 297
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241 TGACCACCTGAAGACCCAGGGGGTGCGGCATCTACAAGGACAACAAAAGCAGCAT 297

RESULT 12
AAS21510
ID   AAS21510 standard; cDNA; 496 BP.
XX
AC   AAS21510;
XX
DT   24-OCT-2001 (first entry)
XX
DE   Human cDNA sequence encoding for PRO1561 polypeptide.
XX
KW   Human secretory and transmembrane; PRO; mammalian; cancer; lung; breast;
KW   prostate; cervical; tumour necrosis factor-alpha; TNF-alpha; cartilage;
KW   ear; proliferation; glucose; free fatty acid; skeletal muscle; adipocyte;
KW   A-peptide; factor VIIA; gene therapy; ss.
XX
OS   Homo sapiens.
XX
PN   WO200140466-A2.
XX
PD   07-JUN-2001.
XX
PF   01-DEC-2000; 2000WO-US032678.
XX
PR   01-DEC-1999;   99WO-US028301.
PR   01-DEC-1999;   99WO-US028634.
PR   02-DEC-1999;   99WO-US028551.
PR   02-DEC-1999;   99WO-US028564.
PR   02-DEC-1999;   99WO-US028565.
PR   09-DEC-1999;   99US-0170262P.
PR   16-DEC-1999;   99WO-US030095.
PR   20-DEC-1999;   99WO-US030911.
PR   20-DEC-1999;   99WO-US030999.
PR   30-DEC-1999;   99WO-US031243.
PR   30-DEC-1999;   99WO-US031274.
PR   05-JAN-2000;   2000WO-US000219.

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PR   06-JAN-2000; 2000WO-US000277.
PR   06-JAN-2000; 2000WO-US000376.
PR   11-FEB-2000; 2000WO-US003565.
PR   18-FEB-2000; 2000WO-US004341.
PR   18-FEB-2000; 2000WO-US004342.
PR   22-FEB-2000; 2000WO-US004414.
PR   24-FEB-2000; 2000WO-US004914.
PR   24-FEB-2000; 2000WO-US005004.
PR   01-MAR-2000; 2000WO-US005601.
PR   02-MAR-2000; 2000WO-US005841.
PR   03-MAR-2000; 2000US-0187202P.
PR   10-MAR-2000; 2000WO-US006319.
PR   15-MAR-2000; 2000WO-US006884.
PR   20-MAY-2000; 2000WO-US007377.
PR   21-MAR-2000; 2000WO-US007532.
PR   30-MAR-2000; 2000WO-US008439.
PR   17-MAY-2000; 2000WO-US013705.
PR   22-MAY-2000; 2000WO-US014042.
PR   30-MAY-2000; 2000WO-US014941.
PR   02-JUN-2000; 2000WO-US015264.
PR   05-JUN-2000; 2000US-0209832P.
PR   28-JUL-2000; 2000WO-US020710.
PR   11-AUG-2000; 2000WO-US022031.
PR   23-AUG-2000; 2000WO-US023522.
PR   24-AUG-2000; 2000WO-US023328.
PR   08-NOV-2000; 2000WO-US030952.
PR   10-NOV-2000; 2000WO-US030873.
XX
PA   (GETH ) GENENTECH INC.
XX
PI   Baker KP, Beresini M, Deforge L, Desnoyers L, Filvaroff E, Gao W;
PI   Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S;
PI   Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;
XX
DR   WPI; 2001-408281/43.
DR   P-PSDB; AAU12438.
XX
PT   Isolated , secretory and transmembrane PRO polypeptide used to detect
PT   other PRO polypeptides, link bioactive molecules to cells expressing PRO
PT   polypeptides, and detect the presence of mammalian tumors e.g. lung,
PT   breast, prostate, cervical.
XX
PS   Claim 3; Fig 533; 813pp; English.
XX
CC   AAS21244-AAS21518 encode for novel human secretory and transmembrane PRO
CC   polypeptides. The PRO polypeptides are useful to detect other PRO
CC   polypeptides, to link bioactive molecules to cells expressing PRO
CC   polypeptides, to modulate biological activities of cells expressing PRO
CC   polypeptides, and to detect the presence of mammalian lung, colon,
CC   breast, prostate, rectal, cervical or liver tumours by comparing PRO
CC   polypeptide expression in a cell sample to that in a control sample. Some
CC   of the 275 sequences are also useful to stimulate the release of tumour
CC   necrosis factor-alpha (TNF-alpha) from human blood, the proliferation or
CC   differentiation of chondrocytes, the proliferation or gene expression in
CC   pericyte cells, the release of proteoglycans from cartilage, the
CC   proliferation of inner ear utricular supporting cells or of T-
CC   lymphocytes, the release of a cytokine from peripheral blood monocytes
CC   (PBMCs), or the proliferation of endothelial cells. Some of the PRO
CC   polypeptides may modulate glucose or free fatty acid uptake by skeletal
CC   muscle cells or by adipocytes; or inhibit binding of A-peptide to factor
CC   VIIA. The PRO polypeptides can be used in assays to identify molecules
CC   involved in binding interactions. The polynucleotides encoding PRO
CC   polypeptides can be used to generate probes, antisense RNA/DNA,
CC   transgenic or knock out animals and can be used in gene therapy
XX
SQ   Sequence 496 BP; 200 A; 95 C; 104 G; 95 T; 0 U; 2 Other;
```

```
Query Match       48.0%;  Score 284.2;  DB 4;  Length 496;
Best Local Similarity  97.3%;  Pred: No. 1.9e-66;
Matches  289;  Conservative  0;  Mismatches  8;  Indels  0;  Gaps  0;

Qy   1 TCTGCCTCCACTGCTCTGTGCTGGGATCATGAACTTGCACTGCTGTGTGGGCTGGTGGT 60
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
```

```
Db   1 TCTGCCTCCACTGCTCTGTGCTGGGATCATGAACTTGCACTGCTGTGTGGGCTGGTGGT 60
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  61 GATGGCTGGTGTGTGATTCCAATCCAGGGCGCGGATCTCGAACCTGAACAAGATGGTCAAGCA 120
         ||||||||||||||||||||||||||||||||||||| ||||||||||||||||||||||||
Db  61 GATGGCTGGTGTGTGATTCCAATCCAGGGCGCGGATCCTGAACCTGAACAAGATGGTCAAGCA 120
Qy 121 AGTGACTGGGAAAATGCCCATCCTCTTCACTGCGTGTCACTGCCGGACTAGG 180
         |||||||||||||||||||||||||||||   |||||||||||||||||||
Db 121 AGTGACTGGGAAAATGCCCATCCTCTTCTCTACTGCCGTGTCACTGCCGGACTAGG 180
Qy 181 TGGCAGAGGCCAACCCAAAGATGCCACGGACTGGTGCGTGCCAGACCCATGCTGCTA 240
         ||||||||||||||||||||||||||||||||||||    |||||||||||||||||
Db 181 TGGCAGAGGCCAACCCAAAGATGCCACGGACTGGTGCTGCCATGCCCATGACTGCTGCTA 240
Qy 241 TGACCACCTGAAGACCCAGGGGTGCGGCATCTACAAGGACTATTACAGATACAACTT 297
         ||||||||||||||||||||||||||||||||||||||    |||
Db 241 TGACCACCTGAAGACCCAGGGGTGCGGCATCTACAAGGACAACACAAAAGCAGCAT 297
```

```
RESULT 13
ACD24119
ID   ACD24119 standard; cDNA; 496 BP.
XX
AC   ACD24119;
XX
DT   26-AUG-2003 (first entry)
XX
DE   Novel human secreted and transmembrane protein PRO1561 cDNA.
XX
KW   Human; secreted and transmembrane protein; PRO; antiinflammatory;
KW   antiarteriosclerotic; cardiant; anti-infertility; anti-HIV; cytostatic;
KW   antidiabetic; gene therapy; tumour necrosis factor (TNF)-alpha release;
KW   TNF-alpha release; cell proliferation; cell differentiation;
KW   gene expression modulator; proteoglycan release; cytokine release;
KW   tumour; inflammatory disease; organ failure; atherosclerosis;
KW   cardiac injury; infertility; birth defect; premature aging; AIDS;
KW   acquired immunodeficiency syndrome; cancer; diabetic complication;
KW   chromosome mapping; gene mapping; pharmaceutical; diagnostic; biosensor;
KW   bioreactor; tissue typing; gene; ss.
XX
OS   Homo sapiens.
XX
PN   US2003032156-A1.
XX
PD   13-FEB-2003.
XX
PF   06-MAY-2002; 2002US-00140474.
XX
PR   31-MAR-1997; 97WO-US005230.
PR   12-JUN-1998; 98WO-US012456.
PR   14-JUL-1998; 98WO-US014552.
PR   28-AUG-1998; 98WO-US017888.
PR   10-SEP-1998; 98WO-US018824.
PR   14-SEP-1998; 98WO-US019093.
PR   14-SEP-1998; 98WO-US019094.
PR   14-SEP-1998; 98WO-US019177.
PR   16-SEP-1998; 98WO-US019330.
PR   17-SEP-1998; 98WO-US019437.
PR   07-OCT-1998; 98WO-US021141.
PR   29-OCT-1998; 98WO-US022991.
PR   29-OCT-1998; 98WO-US022992.
PR   20-NOV-1998; 98WO-US024855.
PR   01-DEC-1998; 98WO-US025108.
PR   05-JAN-1999; 99WO-US000106.
PR   08-MAR-1999; 99WO-US005028.
PR   10-MAR-1999; 99WO-US005190.
PR   20-APR-1999; 99WO-US008615.
PR   14-MAY-1999; 99WO-US010733.
PR   02-JUN-1999; 99WO-US012252.
PR   01-SEP-1999; 99WO-US020111.
PR   08-SEP-1999; 99WO-US020594.
PR   13-SEP-1999; 99WO-US020944.
PR   15-SEP-1999; 99WO-US021090.
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PR   15-SEP-1999;   99WO-US021547.
PR   05-OCT-1999;   99WO-US023089.
PR   29-NOV-1999;   99WO-US028214.
PR   30-NOV-1999;   99WO-US028313.
PR   01-DEC-1999;   99WO-US028409.
PR   01-DEC-1999;   99WO-US028634.
PR   02-DEC-1999;   99WO-US028551.
PR   02-DEC-1999;   99WO-US028561.
PR   02-DEC-1999;   99WO-US028565.
PR   16-DEC-1999;   99WO-US030095.
PR   20-DEC-1999;   99WO-US030911.
PR   20-DEC-1999;   99WO-US030999.
PR   22-DEC-1999;   99WO-US030720.
PR   30-DEC-1999;   99WO-US031243.
PR   30-DEC-1999;   99WO-US031274.
PR   05-JAN-2000;   2000WO-US000219.
PR   06-JAN-2000;   2000WO-US000277.
PR   06-JAN-2000;   2000WO-US000376.
PR   11-FEB-2000;   2000WO-US003565.
PR   18-FEB-2000;   2000WO-US004341.
PR   18-FEB-2000;   2000WO-US004342.
PR   22-FEB-2000;   2000WO-US004414.
PR   24-FEB-2000;   2000WO-US004914.
PR   24-FEB-2000;   2000WO-US005004.
PR   01-MAR-2000;   2000WO-US005601.
PR   02-MAR-2000;   2000WO-US005746.
PR   02-MAR-2000;   2000WO-US005841.
PR   10-MAR-2000;   2000WO-US006319.
PR   15-MAR-2000;   2000WO-US006884.
PR   20-MAR-2000;   2000WO-US007377.
PR   21-MAR-2000;   2000WO-US007532.
PR   30-MAR-2000;   2000WO-US008419.
PR   17-MAY-2000;   2000WO-US013705.
PR   22-MAY-2000;   2000WO-US014042.
PR   30-MAY-2000;   2000WO-US014941.
PR   02-JUN-2000;   2000WO-US015264.
PR   28-JUL-2000;   2000WO-US020710.
PR   11-AUG-2000;   2000WO-US022031.
PR   23-AUG-2000;   2000WO-US023522.
PR   24-AUG-2000;   2000WO-US023328.
PR   08-NOV-2000;   2000WO-US030952.
PR   10-NOV-2000;   2000WO-US030873.
PR   01-DEC-2000;   2000WO-US032678.
PR   20-DEC-2000;   2000US-00747259.
PR   20-DEC-2000;   2000WO-US034956.
PR   28-FEB-2001;   2001WO-US005520.
PR   28-FEB-2001;   2001WO-US006666.
PR   01-MAR-2001;   2001WO-US006666.
PR   09-MAR-2001;   2001US-00802706.
PR   14-MAR-2001;   2001US-00808689.
PR   22-MAR-2001;   2001US-00816744.
PR   05-APR-2001;   2001US-00828366.
PR   10-MAY-2001;   2001US-00854208.
PR   10-MAY-2001;   2001US-00854280.
PR   18-MAY-2001;   2001US-00860216.
PR   25-MAY-2001;   2001US-00866028.
PR   25-MAY-2001;   2001US-00866034.
PR   25-MAY-2001;   2001WO-US017092.
PR   01-JUN-2001;   2001US-00872035.
PR   01-JUN-2001;   2001WO-US017800.
PR   05-JUN-2001;   2001US-00874503.
PR   14-JUN-2001;   2001US-00882636.
PR   19-JUN-2001;   2001US-00886342.
PR   20-JUN-2001;   2001US-00919692.
PR   21-JUN-2001;   2001US-00887879.
PR   22-JUN-2001;   2001WO-US020116.
PR   29-JUN-2001;   2001US-00921066.
PR   09-JUL-2001;   2001WO-US021735.
PR   18-JUL-2001;   2001US-00908827.
PR   06-AUG-2001;   2001US-00924419.
PR   09-AUG-2001;   2001US-00927796.
PR   16-AUG-2001;   2001US-00931836.

PR   19-DEC-2001; 2001US-00028072.
XX
PA   (GETH) GENENTECH INC.
XX
PI   Baker KP,   Beresini M,   Deforge L,   Desnoyers L,   Filvaroff E,   Gao W;
PI   Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S;
PI   Smith V,   Stewart TA,   Tumas D,   Watanabe CK,   Wood WI,   Zhang Z;
XX
DR   WPI; 2003-341980/32.
DR   P-PSDB; ABO17882.
XX
PT   New secreted and transmembrane PRO nucleic acids, for treating
PT   inflammation, organ failure, atherosclerosis, cardiac injury,
PT   infertility, birth defects, premature aging, axquired immunodeficiency
PT   syndrome (AIDS), or cancer.
XX
PS   Claim 2; Fig 533; 660pp; English.
XX
CC   The invention describes an isolated nucleic acid (I) comprising, or which
CC   has 80 % sequence identity to, or the full-length coding sequence of, one
CC   of 275 nucleotide sequences, and which encodes a corresponding
CC   polypeptide selected from 275 amino acid sequences, where all sequences
CC   are given in the specification. The polypeptide encoded by (I) is used to
CC   detect PRO polypeptides, link a bioactive molecule to a cell expressing a
CC   PRO polypeptide, modulate a biological activity of a cell, stimulate the
CC   release of tumour necrosis factor (TNF)-alpha from human blood, modulate
CC   the uptake of glucose or free fatty acid by cells, stimulate or inhibit
CC   the proliferation or differentiation of cells or gene expression,
CC   stimulate the release of proteoglycans, stimulate the release of cytokine
CC   from peripheral blood mononuclear cells, inhibit the binding of A-peptide
CC   to factor VIIA, or detect the presence of tumour in a mammal. The nucleic
CC   acid and polypeptide encoded by it, are useful for treating inflammatory
CC   diseases, organ failure, atherosclerosis, cardiac injury, infertility,
CC   birth defects, premature aging, acquired immunodeficiency syndrome
CC   (AIDS), cancer, or diabetic complications. The nucleic acid is useful as
CC   hybridisation probes, in chromosome and gene mapping, and in generating
CC   antisense RNA or DNA. The polypeptides are useful as pharmaceuticals,
CC   diagnostics, biosensors or bioreactors. Both are useful in tissue typing.
CC   This sequence encodes a novel human secreted and transmembrane PRO
CC   polypeptide
XX
SQ   Sequence 496 BP; 200 A; 95 C; 104 G; 95 T; 0 U; 2 Other;

Query Match   48.0%; Score 284.2; DB 7; Length 496;
Best Local Similarity   97.3%; Pred. No. 1.9e-66;
Matches 289;   Conservative   0; Mismatches   8;   Indels   0; Gaps   0;

Qy   1 TCTGCCTCCACTGCTCTGTGCTGGGATCATGGACTTGCACTGCTGCTGTGTGGGCTGGTCGT 60
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 TCTGCCTCCACTGCTCTGTGCTGTGCTGGGATCATGGACTTGCACTGCTGTGTGGGCTGGTGT 60

Qy   61 GATGGCTGGTGTGATTCCAATCCAGGGCGGGATCCTGAACCTGAACCAAGATGGTCAAGCA 120
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 GATGGCTGGTGTGATTCCAATCCAGGGCGGGATCCTGAACCTGAACCAAGATGGTCAAGCA 120

Qy   121 AGTGACTGGGAAAATGCCCATCCTCTCCACTGGCCCTACGGCGTGTCACTGCGGACTAGG 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121 AGTGACTGGGAAAATGCCCATCCTCTCCACTGGCCCTACGGCGTGTCACTGCGGACTAGG 180

Qy   181 TGGCAGAGGCCAACCCAAAGATGCCACGGACTGGTGCTGCCAGACCCATGACTGCTGCTA 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181 TGGCAGAGGCCAACCCAAAGATGCCACGGACTGGTGCTGCCAGACCCATGACTGCTGCTA 240

Qy   241 TGACCACTGAAGACCCAGGGGTGCGCATCACAAGGACTATTACAGATACAACTT 297
          |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241 TGACCACTGAAGACCCAGGGGTGCGCATCACAAGGACAACAACAAAAGCAGCAT 297

RESULT 14
ACA67260
ID   ACA67260 standard; cDNA; 496 BP.
XX
AC   ACA67260;

XX
DT   23-JUN-2003   (first entry)
XX
DE   cDNA encoding human PRO polypeptide #267.
XX
KW   Human; PRO polypeptide; secreted and transmembrane protein;
KW   anti-PRO antibody; diagnostic assay; gene expression; diabetes;
KW   bone disorder; cartilage disorder; rheumatoid arthritis; obesity;
KW   sports injury; osteoarthritis; hyper-insulinaemia; hypo-insulinaemia;
KW   hearing loss; coagulation disorder; stroke; heart attack; cardiant;
KW   antidiabetic; anorectic; vulnerary; antiarthritic; osteopathic;
KW   antirheumatic; auditory; cerebroprotective; angiogenic; gene; ss.
XX
OS   Homo sapiens.
XX
PN   US2003004311-A1.
XX
PD   02-JAN-2003.
XX
PF   19-DEC-2001; 2001US-00028072.
XX
PR   18-JUN-1997;   97US-0049911P.
PR   26-AUG-1997;   97US-0056974P.
PR   17-SEP-1997;   97US-0059113P.
PR   17-SEP-1997;   97US-0059115P.
PR   17-SEP-1997;   97US-0059117P.
PR   17-SEP-1997;   97US-0059122P.
PR   17-SEP-1997;   97US-0059184P.
PR   18-SEP-1997;   97US-0059263P.
PR   19-SEP-1997;   97US-0059352P.
PR   19-SEP-1997;   97US-0059588P.
PR   24-SEP-1997;   97US-0059836P.
PR   17-OCT-1997;   97US-0062250P.
PR   17-OCT-1997;   97US-0062285P.
PR   17-OCT-1997;   97US-0062287P.
PR   17-OCT-1997;   97US-0063755P.
PR   24-OCT-1997;   97US-0062814P.
PR   24-OCT-1997;   97US-0062816P.
PR   24-OCT-1997;   97US-0063045P.
PR   24-OCT-1997;   97US-0063082P.
PR   24-OCT-1997;   97US-0063127P.
PR   27-OCT-1997;   97US-0063327P.
PR   27-OCT-1997;   97US-0063329P.
PR   28-OCT-1997;   97US-0063550P.
PR   28-OCT-1997;   97US-0063561P.
PR   29-OCT-1997;   97US-0063704P.
PR   29-OCT-1997;   97US-0063733P.
PR   29-OCT-1997;   97US-0063735P.
PR   29-OCT-1997;   97US-0063738P.
PR   03-NOV-1997;   97US-0064248P.
PR   07-NOV-1997;   97US-0064809P.
PR   12-NOV-1997;   98US-0065186P.
PR   17-NOV-1997;   97US-0065846P.
PR   21-NOV-1997;   98US-0063364P.
PR   24-NOV-1997;   97US-0066453P.
PR   24-NOV-1997;   97US-0066511P.
PR   24-NOV-1997;   97US-0066770P.
PR   01-DEC-1997;   97US-0069212P.
PR   11-DEC-1997;   97US-0069278P.
PR   11-DEC-1997;   97US-0069334P.
PR   16-DEC-1997;   97US-0069694P.
PR   23-JAN-1998;   98US-0072320P.
PR   04-FEB-1998;   98US-0073612P.
PR   09-FEB-1998;   98US-0074086P.
PR   12-NOV-1998;   98US-0074092P.
PR   17-NOV-1998;   98US-0077791P.
PR   20-MAR-1998;   98US-0078910P.
PR   25-MAR-1998;   98US-0072294P.
PR   27-MAR-1998;   98US-0079663P.
PR   27-MAR-1998;   98US-0079728P.
PR   31-MAR-1998;   98US-0080165P.
PR   12-JUN-1998;   98WO-US012456.
PR   14-JUL-1998;   98WO-US014552.
PR   28-AUG-1998;   98WO-US017888.
PR   10-SEP-1998;   98WO-US018824.
PR   14-SEP-1998;   98WO-US019093.
PR   14-SEP-1998;   98WO-US019094.
PR   14-SEP-1998;   98WO-US019177.
PR   16-SEP-1998;   98WO-US019330.
PR   17-SEP-1998;   98WO-US019437.
PR   07-OCT-1998;   98WO-US021141.
PR   29-OCT-1998;   98WO-US022991.
PR   29-OCT-1998;   98WO-US022992.
PR   01-DEC-1998;   98WO-US024855.
PR   01-DEC-1998;   98WO-US025108.
PR   05-JAN-1999;   99WO-US000106.
PR   08-MAR-1999;   99WO-US005028.
PR   10-MAR-1999;   99WO-US005190.
PR   20-APR-1999;   99WO-US008615.
PR   14-MAY-1999;   99WO-US010733.
PR   02-JUN-1999;   99WO-US012252.
PR   01-SEP-1999;   99WO-US020111.
PR   08-SEP-1999;   99WO-US020594.
PR   13-SEP-1999;   99WO-US020944.
PR   15-SEP-1999;   99WO-US021090.
PR   15-SEP-1999;   99WO-US021547.
PR   05-OCT-1999;   99WO-US023089.
PR   29-NOV-1999;   99WO-US028214.
PR   30-NOV-1999;   99WO-US028313.
PR   01-DEC-1999;   99WO-US028409.
PR   01-DEC-1999;   99WO-US028301.
PR   02-DEC-1999;   99WO-US028634.
PR   02-DEC-1999;   99WO-US028551.
PR   02-DEC-1999;   99WO-US028564.
PR   02-DEC-1999;   99WO-US028565.
PR   16-DEC-1999;   99WO-US030095.
PR   20-DEC-1999;   99WO-US030911.
PR   20-DEC-1999;   99WO-US030999.
PR   30-DEC-1999;   99WO-US031243.
PR   30-DEC-1999;   99WO-US031274.
PR   05-JAN-2000;   2000WO-US000219.
PR   06-JAN-2000;   2000WO-US000277.
PR   06-JAN-2000;   2000WO-US000376.
PR   11-FEB-2000;   2000WO-US003565.
PR   18-FEB-2000;   2000WO-US004341.
PR   18-FEB-2000;   2000WO-US004342.
PR   22-FEB-2000;   2000WO-US004414.
PR   24-FEB-2000;   2000WO-US004914.
PR   24-FEB-2000;   2000WO-US005004.
PR   01-MAR-2000;   2000WO-US005601.
PR   02-MAR-2000;   2000WO-US005746.
XX
PA   (GETH) GENENTECH INC.
XX
PI   Baker KP, Beresini M, Deforge L, Desnoyers L, Filvaroff E, Gao W;
PI   Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S;
PI   Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;
XX
DR   WPI; 2003-352836/33.
DR   P-PSDB; ABU81136.
XX
PT   New isolated PRO polypeptide useful for treating diabetes, rheumatoid
PT   arthritis, sports injuries, obesity, hearing loss in mammals, stroke, or
PT   heart attack.
XX
PS   Claim 2; Fig 533; 643pp; English.
XX
CC   The present invention relates to the isolation of novel human PRO
CC   polypeptides, and the polynucleotide sequences encoding them. The PRO
CC   polypeptides are secreted and transmembrane proteins. The PRO
CC   polypeptides and polynucleotides are useful for preparing a medicament
CC   useful in the treatment of diabetes, bone and/or cartilage disorders
CC   (e.g. rheumatoid arthritis, sports injuries, osteoarthritis), obesity,
CC   hyper- or hypo-insulinaemia, hearing loss, and coagulation disorders
CC   (e.g. stroke, heart attack). Anti-PRO antibodies are useful in diagnostic
CC   assays for PRO, by detecting its expression in specific cells, tissues or

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CC   serum, and for affinity purification of PRO from recombinant cell culture
CC   or natural sources. ACA66994-ACA67268 represent cDNA sequences encoding
CC   the human PRO polypeptides of the invention. Note: The sequence data for
CC   this patent was obtained in electronic format directly from the USPTO web
CC   site at seqdata.uspto.gov/psipsDIDentry.html
XX
SQ   Sequence 496 BP; 200 A; 95 C; 104 G; 95 T; 0 U; 2 Other;

Query Match             48.0%;  Score 284.2; DB 7;  Length 496;
Best Local Similarity   97.3%;  Pred. No. 1.9e-66;
Matches   289;  Conservative   0;  Mismatches   8;  Indels   0;  Gaps   0;

Qy     1 TCTGCCTCCACTGCTCTGTGCTGGGATCATGGAACTTGCACTGCTTGTGTGGGCTGGTGGT 60
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1 TCTGCCTCCACTGCTCTGTGCTGGGATCATGGAACTTGCACTGCTTGTGTGGGCTGGTGGT 60

Qy    61 GATGGCTGGTGTGATTCCAATCCAGGGCGGGATCCTGAACCTGAACAAGATGGTCAAGCA 120
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Db    61 GATGGCTGGTGTGATTCCAATCCAGGGCGGGATCCTGAACCTGAACAAGATGGTCAAGCA 120

Qy   121 AGTGACTGGGAAAATGCCCATCCTCTCCTACTGCCCTACGGCTGTCACTGCCGCGACTAGG 180
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121 AGTGACTGGGAAAATGCCCATCCTCTCCTACTGCCCTACGGCTGTCACTGCCGCGACTAGG 180

Qy   181 TGGCAGAGGCCAACCCAAAGATGCCACGGACTGGTGCTGCCAGACCCATGACTGCTGCTA 240
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Db   181 TGGCAGAGGCCAACCCAAAGATGCCACGGACTGGTGCTGCCAGACCCATGACTGCTGCTA 240

Qy   241 TGACCACCTGAAGACCCAGGGGTGCGGCATCTACAAGGACTATTACAGATACAACTT 297
         |||||||| |||||||||||||||||||||||| ||| ||| |||||||||||
Db   241 TGACCACCTGAAGACCCAGGGGTGCGGCATCTACAAGGACTACAAGGACAACAAAAGCAGCAT 297


RESULT 15
ACA03869
ID   ACA03869 standard; cDNA; 496 BP.
XX
AC   ACA03869;
XX
DT   23-MAY-2003  (first entry)
XX
DE   cDNA encoding human PRO polypeptide #267.
XX
KW   Human; PRO polypeptide; secreted and transmembrane protein;
KW   tumour necrosis factor-alpha; TNF-alpha; blood; proliferation;
KW   differentiation; chondrocyte; tumour; genetic disorder; cytostatic; gene;
KW   ss.
XX
OS   Homo sapiens.
XX
PN   US2003036180-A1.
XX
PD   20-FEB-2003.
XX
PF   09-MAY-2002; 2002US-00143114.
XX
PR   31-MAR-1997;  97WO-US005230.
PR   12-JUN-1998;  98WO-US012456.
PR   14-JUL-1998;  98WO-US014552.
PR   28-AUG-1998;  98WO-US017888.
PR   10-SEP-1998;  98WO-US018824.
PR   14-SEP-1998;  98WO-US019093.
PR   14-SEP-1998;  98WO-US019094.
PR   16-SEP-1998;  98WO-US019177.
PR   17-SEP-1998;  98WO-US019330.
PR   07-OCT-1998;  98WO-US019437.
PR   29-OCT-1998;  98WO-US021141.
PR   29-OCT-1998;  98WO-US022991.
PR   20-NOV-1998;  98WO-US022992.
PR   01-DEC-1998;  98WO-US024855.
PR   05-JAN-1999;  98WO-US025108.
PR   08-MAR-1999;  99WO-US000106.
                  99WO-US005028.
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PR   10-MAR-1999;  99WO-US005190.
PR   20-APR-1999;  99WO-US008615.
PR   14-MAY-1999;  99WO-US010733.
PR   02-JUN-1999;  99WO-US012252.
PR   01-SEP-1999;  99WO-US020111.
PR   08-SEP-1999;  99WO-US020594.
PR   13-SEP-1999;  99WO-US020944.
PR   15-SEP-1999;  99WO-US021090.
PR   15-SEP-1999;  99WO-US021547.
PR   05-OCT-1999;  99WO-US023089.
PR   29-NOV-1999;  99WO-US023214.
PR   30-NOV-1999;  99WO-US028313.
PR   30-NOV-1999;  99WO-US028409.
PR   01-DEC-1999;  99WO-US028301.
PR   01-DEC-1999;  99WO-US028634.
PR   02-DEC-1999;  99WO-US028551.
PR   02-DEC-1999;  99WO-US028564.
PR   16-DEC-1999;  99WO-US028565.
PR   20-DEC-1999;  99WO-US030095.
PR   20-DEC-1999;  99WO-US030911.
PR   22-DEC-1999;  99WO-US030999.
PR   30-DEC-1999;  99WO-US030720.
PR   05-JAN-2000;  99WO-US031243.
PR   06-JAN-2000;  99WO-US031274.
PR   06-JAN-2000;  2000WO-US000219.
PR   11-FEB-2000;  2000WO-US000277.
PR   18-FEB-2000;  2000WO-US000376.
PR   18-FEB-2000;  2000WO-US003565.
PR   22-FEB-2000;  2000WO-US004341.
PR   24-FEB-2000;  2000WO-US004342.
PR   01-MAR-2000;  2000WO-US004414.
PR   02-MAR-2000;  2000WO-US004914.
PR   02-MAR-2000;  2000WO-US005004.
PR   10-MAR-2000;  2000WO-US005601.
PR   15-MAR-2000;  2000WO-US005746.
PR   21-MAR-2000;  2000WO-US005841.
PR   30-MAR-2000;  2000WO-US006319.
PR   17-MAY-2000;  2000WO-US006884.
PR   22-MAY-2000;  2000WO-US007377.
PR   30-MAY-2000;  2000WO-US007532.
PR   02-JUN-2000;  2000WO-US008439.
PR   28-JUL-2000;  2000WO-US013705.
PR   11-AUG-2000;  2000WO-US014042.
PR   23-AUG-2000;  2000WO-US014941.
PR   24-AUG-2000;  2000WO-US015264.
PR   08-NOV-2000;  2000WO-US020710.
PR   10-NOV-2000;  2000WO-US022031.
PR   01-DEC-2000;  2000WO-US023522.
PR   20-DEC-2000;  2000WO-US023328.
PR   28-FEB-2001;  2000WO-US030952.
PR   01-MAR-2001;  2000WO-US030873.
PR   09-MAR-2001;  2000WO-US032678.
PR   14-MAR-2001;  2000US-00747259.
PR   22-MAR-2001;  2000WO-US034956.
PR   05-APR-2001;  2001US-00796498.
PR   10-MAY-2001;  2001WO-US006520.
PR   10-MAY-2001;  2001WO-US006666.
PR   18-MAY-2001;  2001US-00802706.
PR   25-MAY-2001;  2001US-00808689.
PR   25-MAY-2001;  2001US-00816744.
PR   01-JUN-2001;  2001US-00828366.
PR   01-JUN-2001;  2001US-00854208.
PR   05-JUN-2001;  2001US-00854280.
PR   14-JUN-2001;  2001US-00860216.
PR   19-JUN-2001;  2001US-00866028.
PR   20-JUN-2001;  2001US-00866034.
                   2001WO-US017092.
                   2001US-00017092.
                   2001US-00872035.
                   2001WO-US017800.
                   2001US-00874503.
                   2001US-00882636.
                   2001US-00886342.
                   2001WO-US019692.
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PR    21-JUN-2001;  2001US-00887879.
PR    22-JUN-2001;  2001WO-US020116.
PR    29-JUN-2001;  2001WO-US021066.
PR    09-JUL-2001;  2001WO-US021735.
PR    18-JUL-2001;  2001US-00908827.
PR    06-AUG-2001;  2001US-00924419.
PR    09-AUG-2001;  2001US-00927796.
PR    16-AUG-2001;  2001US-00931836.
PR    19-DEC-2001;  2001US-00028072.
XX
PA   (GETH ) GENENTECH INC.
XX
PI    Baker KP,  Beresini M,  Deforge L,  Desnoyers L,  Filvaroff E,  Gao W;
PI    Gerritsen ME, Goddard A,  Godowski PJ,  Gurney AL,  Sherwood S;
PI    Smith V,  Stewart TA,  Tumas D,  Watanabe CK,  Wood WI,  Zhang Z;
XX
DR    WPI; 2003-332040/31.
DR    P-PSDB; ABU66836.
XX
PT    New secreted and transmembrane PRO nucleic acids, useful for gene
PT    therapy, in chromosome and gene mapping, as chromosome markers, in tissue
PT    typing, and in chromosome identification.
XX
PS    Claim 2; Fig 533; 660pp; English.
XX
CC    The present invention relates to the isolation of novel human PRO
CC    polypeptides, and the polynucleotide sequences encoding them. The PRO
CC    polypeptides are secreted and transmembrane proteins. The PRO
CC    polypeptides are useful for detecting other PRO polypeptides, for linking
CC    bioactive molecules to cells expressing PRO polypeptides, for modulating
CC    biological activities of cells expressing PRO polypeptides, and for for
CC    identifying agonists or antagonists. The PRO polypeptides are useful for
CC    for stimulating the release of tumour necrosis factor (TNF)-alpha from
CC    human blood, for stimulating the proliferation or differentiation of
CC    chondrocytes, and detecting the presence of tumours. The polynucleotide
CC    sequences encoding PRO polypeptides are useful as hybridisation probes,
CC    in chromosome and gene mapping, in the generation of antisense RNA and
CC    DNA, in the preparation of PRO polypeptides, for generating transgenic
CC    animals or knockout animals, for the genetic analysis of individuals with
CC    genetic disorders, and in gene therapy. ACA03603-ACA03877 represent cDNAs
CC    encoding the human PRO polypeptides of the invention. Note: The sequence
CC    data for this patent was obtained in electronic format directly from the
CC    USPTO web site at seqdata.uspto.gov/psipsDIEntry.html
XX
SQ    Sequence 496 BP; 200 A; 95 C; 104 G; 95 T; 0 U; 2 Other;
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Query Match             48.0%;  Score 284.2;  DB 7;  Length 496;
Best Local Similarity   97.3%;  Pred. No. 1.9e-66;
Matches 289;  Conservative   0;  Mismatches   8;  Indels   0;  Gaps   0;

Qy         1 TCTGCCTCCACTGCTCTGTGCTGGGATCATGGAACTTGCACTGCTGTGGGCTGGTGGT   60
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         1 TCTGCCTCCACTGCTCTGTGCTGGGATCATGGAACTTGCACTGCTGTGGGCTGGTGGT   60

Qy        61 GATGGCTGGTGTGATTCAATCCAGGGCGGGATCCTGGCCTGAACCTGAACAAGATGGTCAAGCA   120
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Db        61 GATGGCTGGTGTGATTCAATCCAGGGCGGGATCCTGGCCTGAACCTGAACAAGATGGTCAAGCA   120

Qy       121 AGTGACTGGGAAAAATGCCCATCCTCTCCTACTGGCCTACGGCTGTCACTGCGGACTAGG   180
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       121 AGTGACTGGGAAAAATGCCCATCCTCTCCTACTGGCCTACGGCTGTCACTGCGGACTAGG   180

Qy       181 TGGCAGAGGCCAACCCAAAGATGCCACGGACTGGTGCTGCCAGACCCATGACTGCTGCTA   240
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       181 TGGCAGAGGCCAACCCAAAGATGCCACGGACTGGTGCTGCCAGACCCATGACTGCTGCTA   240

Qy       241 TGACCACCTGAAGAGCCCAGGGGTGCGGCATCTACAAGGACTATTACAGATACAACTT   297
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Db       241 TGACCACCTGAAGAGCCCAGGGGTGCGGCATCTACAAGGACTACACAAGGACAACAACAAAAGCAGCAT   297
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Search completed: October 7, 2004, 13:34:27
Job time : 258.748 secs

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                    Copyright   GenCore version 5.1.6
                    Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on:        October  7, 2004, 13:04:44 ; Search time 46.7926 Seconds
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Title:        US-09-830-321A-4
Perfect score: 592
Sequence:      1 tctgcctccactgtctgtg.........cccagcctccccggaaccc 592

Scoring table: IDENTITY_NUC
               Gapop 10.0 , Gapext 1.0

Searched:      682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters:     1365418

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :    Issued_Patents NA:*
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              5: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
              6: /cgn2_6/ptodata/2/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
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SUMMARIES

Result No.	Score	% Match	Query Match Length	DB	ID	Description
1	119.6	20.2	1016	4	US-09-220-132-17	Sequence 17, Appl
2	118	19.9	1014	2	US-08-888-497-31	Sequence 31, Appl
3	118	19.9	1014	2	US-09-362-230-31	Sequence 31, Appl
4	118	19.9	1014	5	PCT-US94-07926-31	Sequence 31, Appl
5	112.4	19.0	479	1	US-08-186-895-9	Sequence 9, Appli
6	110.8	18.7	854	4	US-09-023-655-1207	Sequence 1207, Ap
7	101.8	17.2	375	2	US-09-740-569-1	Sequence 1, Appli
8	98.4	16.6	1828	2	US-08-888-497-29	Sequence 29, Appl
9	98.4	16.6	1828	4	US-09-362-230-29	Sequence 29, Appl
10	98.4	16.6	1828	5	PCT-US94-07926-29	Sequence 29, Appl
11	92.6	15.6	4325	2	US-08-888-497-21	Sequence 21, Appl
12	92.6	15.6	4325	4	US-09-362-230-21	Sequence 21, Appl
13	92.6	15.6	4325	5	PCT-US94-07926-21	Sequence 21, Appl
14	63.2	10.7	742	3	US-08-966-317-2	Sequence 2, Appli
15	63.2	10.7	742	4	US-09-489-770-2	Sequence 2, Appli
16	62.6	10.6	562	2	US-09-023-655-1200	Sequence 1200, Ap
17	52.6	8.9	15328	2	US-08-888-497-33	Sequence 33, Appl
18	52.6	8.9	15328	4	US-09-362-230-33	Sequence 33, Appl
19	52.6	8.9	15328	5	PCT-US94-07926-33	Sequence 33, Appl
20	51	8.6	151	2	US-08-888-497-26	Sequence 26, Appl
21	51	8.6	151	4	US-09-362-230-26	Sequence 26, Appl
22	51	8.6	151	5	PCT-US94-07926-26	Sequence 26, Appl
23	50.4	8.5	151	2	US-08-888-497-25	Sequence 25, Appl
24	50.4	8.5	151	4	US-09-362-230-25	Sequence 25, Appl
25	50.4	8.5	151	5	PCT-US94-07926-25	Sequence 25, Appl
26	38.2	6.5	167	2	US-08-888-497-28	Sequence 28, Appl
27	38.2	6.5	167	4	US-09-362-230-28	Sequence 28, Appl
28	38.2	6.5	167	5	PCT-US94-07926-28	Sequence 28, Appl
29	36.8	6.2	1511	2	US-08-809-763-3	Sequence 3, Appli
30	36.8	6.2	1511	3	US-08-956-253-3	Sequence 3, Appli
31 c	36.6	6.2	505	4	US-09-621-976-15639	Sequence 15639, A
32	36.6	6.2	5511	2	US-08-928-361B-2	Sequence 2, Appli
33	36.6	6.2	5511	3	US-09-588-995A-2	Sequence 2, Appli
34	36.6	6.0	7334	3	US-08-928-361B-1	Sequence 1, Appli
35	36.6	6.0	7334	3	US-09-588-995A-1	Sequence 1, Appli
36 c	35.6	6.0	7615	4	US-09-620-312D-330	Sequence 330, App
37 c	35.6	6.0	7657	4	US-09-620-312D-353	Sequence 353, App
38	35.4	6.0	867	4	US-09-216-393B-340	Sequence 340, App
39	35.4	6.0	867	4	US-09-216-393B-342	Sequence 342, App
40	35.4	6.0	1397	4	US-09-216-393B-343	Sequence 343, App
41 c	35.2	5.9	1397	4	US-09-216-393B-345	Sequence 345, App
42	35.2	5.9	744	4	US-09-252-991A-7521	Sequence 7521, Ap
43	34.8	5.9	2285	4	US-09-230-225B-1	Sequence 1, Appli
44	34.6	5.8	364	4	US-09-621-976-17202	Sequence 17202, A
45	34.4	5.8	430	4	US-09-621-976-16656	Sequence 16656, A

ALIGNMENTS

RESULT 1
US-09-220-132-17

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; Sequence 17, Application US/09220132
; Patent No. 6506607
; GENERAL INFORMATION:
; APPLICANT: Shyjan, Andrew W.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE IDENTIFICATION AND ASSESSMENT
; TITLE OF INVENTION: OF PROSTATE CANCER THERAPIES AND THE DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 07334-074001
; CURRENT APPLICATION NUMBER: US/09/220,132
; CURRENT FILING DATE: 1998-12-23
; PRIOR APPLICATION NUMBER: US 60/079,303
; PRIOR FILING DATE: 1998-03-25
; PRIOR APPLICATION NUMBER: US 60/068,821
; PRIOR FILING DATE: 1997-12-24
; NUMBER OF SEQ ID NOS: 191
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 17
; LENGTH: 1016
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-220-132-17

Query Match             20.2%;  Score 119.6;  DB 4;  Length 1016;
Best Local Similarity   58.0%;  Pred. No. 1e-23;
Matches 231;  Conservative  0;  Mismatches 164;  Indels  3;  Gaps  1;

Qy   67 TGGTGTGATTCCAATCCAGGGCGGGATCCTGAACCTGAACACAGATGGTCAAGCAAGTGAC 126
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Qy  127 TGGGAAAATGCCCATCCTCTCCTGGCCCTACGCGCTGTCACTCGCCGACTAGGTGGCAG 186
Db  231 AGGGAAGAAACGCCCTGACAAACTACGGCTTCTACGGCTGTGTTACTCGCGCTGGGGCGCCG 290

Qy  187 AGGCCAACCCAAAGATGCCACGGACTCGGTGCTGCCAGACCCATGCTGCTGCTATGACCA 246
Db  291 AGGAACCCCCAGGGATGGCACCGATTGGTGCGTGTTGGGCCGCATGACCACTGCTATGGGCG 350

Qy  247 CCTGAAGACCCAGGGTGCGGCATCTACAAGGACTATTACAGATACAAACTTTTCCCAGGG 306
Db  351 GCTGGAGGAGAAGGGCTTCAACATTCGCACACAGTCCTACAAATACAGATTCGCGTGGG 410

Qy  307 GAACATCCACTGCTTCTGACAAGGAGGAAGTGGTGTGAGCAGCAGCGCTGTTGTGCCTGACAA 366
Db  411 CGTGGTCACCTGC---GAGCCCGGGCCCTTGTGACAACTGGACATGGAACCTCGTGCCTGTGACCG 467

Qy  367 GGAGGTGGCCTTCTGCCTGAAGCGCAACCTGACAACTACCACCGAAGCGACTGCGTTTCTA 426
Db  468 GAAGCTCGTCACTGCTTCAAGAGAAACCTACGGAGCTACAACCCCACCAGTACCAATACTT 527
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Db      AGGAACCCCAAGGATGGCACCGATTGGTGTCTGTTGGGCGCATGACCACTGCTATGGGCG 348
Qy  289 AGGAACCCCAAGGATGGCACCGATTGGTGTCTGTTGGGCGCATGACCACTGCTATGGGG  306
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Db  247 CCTGAAGACCCAGGGGTGCGGCATCTACAAGGACTATTACAGATAACTTTCCCAGGG   306
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Qy  349 GCTGGAGGAGAGAGGGCTGCAACATTCGCAACAGTCCTACAAATACAGATTCGCTGGGG   408
           ||||                  ||||    |||||||||
Db  307 GAACATCCACTGCTCTGACAAGGGAAGCTGGTGTGAGCAGCAGCTGTGTGCCTGTGACAA   366
           ||  |||||  ||         ||||
Qy  409 CGTGGTCACCTGC---GAGCCGCGGCCCTTCTGACGCATGTCAACCTTCTGTGCCTGTGACCG 465
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Qy  367 GGAGGTGGCCTTCTGCCTGAAGCGCAACCTGGACACCACCTACCGAGCGACTGCGTTTCTA 426
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Db  466 GAAGCTCGTCTACTGCCTCAAGAGAAACCTACCGAGCTTACAACCCACAGTACCAATACTT 525

Qy  427 CTGGCGGCGCCCACTGCCGCGGGGCGCAGACCCCTGGGTGCT 464
           |||||||  ||      |||||||||||||||||
Db  526 TCCCAACATCCTCTGCTCCTAGGCCTCCCCAGCGAGCT 563
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RESULT 3
US-09-362-230-31
; Sequence 31, Application US/09362230
; Patent No. 6352849
; GENERAL INFORMATION:
;   APPLICANT: Tischfield, Jay A.
;   APPLICANT: Seilhamer, Jeffrey J.
;   TITLE OF INVENTION: Mammalian Phospholipase A2 Nucleotide
;   TITLE OF INVENTION: Sequences and Low Molecular Weight Amino Acid Sequences
;   TITLE OF INVENTION: Encoded Thereby, Antisense Sequences and Nucleotide
;   TITLE OF INVENTION: Sequences Having Internal Ribosome Binding Sites
;   NUMBER OF SEQUENCES: 44
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE: Ruden, Barnett, McClosky, Smith, Schuster &
;   ADDRESSEE: Russell PA
;   STREET: 200 East Broward Boulevard
;   CITY: Fort Lauderdale
;   STATE: FL
;   COUNTRY: USA
;   ZIP: 33301
;   COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: PatentIn Release #1.0, Version #1.25
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/09/362,230
;   FILING DATE:
;   CLASSIFICATION:
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: 08/888,497
;   FILING DATE:
;   APPLICATION NUMBER: US 08/097,354
;   FILING DATE: 26-JUL-1993
;   ATTORNEY/AGENT INFORMATION:
;   NAME: Manso, Peter J.
;   REGISTRATION NUMBER: 32,264
;   REFERENCE/DOCKET NUMBER: IN21044-5
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE: 305-527-2498
;   TELEFAX: 305-764-4996
; INFORMATION FOR SEQ ID NO: 31:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH: 1014 base pairs
;   TYPE: nucleic acid
;   STRANDEDNESS: single
;   TOPOLOGY: linear
;   MOLECULE TYPE: cDNA
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: 131..544
US-09-362-230-31

Query Match   19.9%;   Score 118; DB 4; Length 1014;
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Qy  427 CTGGCGGCGCCCACTGCCGCGGGGCGCAGACCCCTGGGTGCT 464
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Db  528 TCCCAACATCCTCTGCTCCTAGGCCTCCCCAGCGAGCT 565
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RESULT 2
US-08-888-497-31
; Sequence 31, Application US/08888497
; Patent No. 5972677
; GENERAL INFORMATION:
;   APPLICANT: Tischfield, Jay A.
;   APPLICANT: Seilhamer, Jeffrey J.
;   TITLE OF INVENTION: Mammalian Phospholipase A2 Nucleotide
;   TITLE OF INVENTION: Sequences and Low Molecular Weight Amino Acid Sequences
;   TITLE OF INVENTION: Encoded Thereby, Antisense Sequences and Nucleotide
;   TITLE OF INVENTION: Sequences Having Internal Ribosome Binding Sites
;   NUMBER OF SEQUENCES: 44
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE: Ruden, Barnett, McClosky, Smith, Schuster &
;   ADDRESSEE: Russell PA
;   STREET: 200 East Broward Boulevard
;   CITY: Fort Lauderdale
;   STATE: FL
;   COUNTRY: USA
;   ZIP: 33301
;   COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: PatentIn Release #1.0, Version #1.25
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/08/888,497
;   FILING DATE:
;   CLASSIFICATION:
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: US/08/651,405
;   FILING DATE:
;   APPLICATION NUMBER: US 08/097,354
;   FILING DATE: 26-JUL-1993
;   ATTORNEY/AGENT INFORMATION:
;   NAME: Manso, Peter J.
;   REGISTRATION NUMBER: 32,264
;   REFERENCE/DOCKET NUMBER: IN21044-5
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE: 305-527-2498
;   TELEFAX: 305-764-4996
; INFORMATION FOR SEQ ID NO: 31:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH: 1014 base pairs
;   TYPE: nucleic acid
;   STRANDEDNESS: single
;   TOPOLOGY: linear
;   MOLECULE TYPE: cDNA
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: 131..544
US-08-888-497-31

Query Match   19.9%;   Score 118; DB 2; Length 1014;
Best Local Similarity   57.8%;   Pred. No. 2.8e-23;
Matches 230; Conservative   0; Mismatches 165; Indels 3; Gaps 1;

Qy   67 TGGTGTGATTCCAATCCAGGCGGCGGGATCCTGAACCTGAACCAGATGGTCAAGCAAGTGAC 126
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Db 169 TAGTGTGCCTGCTGCTGCGTGCAAGGAGGCGCTTGCTGGACCTAAAATCAATGATCGAAGAAGGTGAC 228
Qy 127 TGGGAAAATGCCCATCCTCTCCTACTGGCCCTACTGGCCTCTCCTACGGCTGCACTGGGGACTAGGTGGCAG 186
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Db 229 AGGGAAGAACGCCCTGACAAACTACGGCTTCTACGGCTGTTTACTGCGGCTGTTGGGGCGGCCG 288
Qy 187 AGGCCAACCCAAAGATGCCACGACTGGTGCTGCCAGACCCATGACCTGCTGCTATGACCA 246
           || ||| ||| ||| || |||||||||
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;  TYPE: nucleic acid
;  STRANDEDNESS: single
;  TOPOLOGY: linear
;  MOLECULE TYPE: cDNA
;  FEATURE:
;     NAME/KEY: CDS
;     LOCATION: 131..544
PCT-US94-07926-31

Query Match              19.9%;  Score 118;  DB 5;  Length 1014;
Best Local Similarity    57.8%;  Pred. No. 2.8e-23;
Matches  230;  Conservative    0;  Mismatches  165;  Indels    3;  Gaps    1;

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Db   169  TAGTGTGCCTGCTGTGCAAGGAGGCTTGCTGGACCTAAAATCAATGATCGAGAAGGTGAC  228

Qy   127  TGGGAAAATGCCCATCCTCTCCTACTGGCCCTACGGCTGTCACTGCGGACTAGGTGGCAG  186
              ||||| |||| |  |||  ||||||| || || |||   |||| ||  || |||||
Db   229  AGGGAAGAACGCCCTGACAAACTACGGCTTCTACGGCTGTTACTGCGGGCTGGGGCGCCG  288

Qy   187  AGGCCAACCCAAAGATGCCACGGACTGGTGCTGCCAGACCCATGACTGCTGCTATGACCA  246
              ||| |    |  |||||| ||||    |    ||||||  |  | ||| |||||||||
Db   289  AGGAACCCCCAAGGATGGCACCGATTGGTGCTGGTGTTGGGCCGCATGACCACCTGCTATGGGCG  348

Qy   247  CCTGAAGACCCAGGGTGCGGCATCTACAAGGACTATTACAGATACAACTTTTCCCAGGG  306
              |||||||| |||   ||  |||| |  ||||  |  |||  || |||   |||||||
Db   349  GCTGGAGGAGAAGGGCTGCAACATTCGCACACAGTCCTACAAATACAGATTCGCGTGGGG  408

Qy   307  GAACATCCACTGCTTCTGACAAGGGAAGCTTGTGTGCATGTGACAA  366
              |||||||  ||| ||||||   |||  |  |  | |||  |||||
Db   409  CGTGGTCACCTGC---GAGCCCGGGCCCTTCTGCATGTCAACCTCTGTGCCTGTGACCG  465

Qy   367  GGAGGTGGCCTTCTGCCTGAAGCGCAACCTACCAGAGCGACTGCGTTTCTA  426
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Db   466  GAAGCTCGTCTACTGCCTCAAGAGAAAACTACGGAGCTACAACCCACAGTACCAATACTT  525

Qy   427  CTGGCGCGCCCCACTGCGCGGGGGCAGACCCCTGGGTGCT  464
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Db   526  TCCCAACATCCTCTGCTCCTAGGCCTCCCCAGCGAGCT  563


RESULT 4
PCT-US94-07926-31
; Sequence 31, Application PC/TUS9407926
;  GENERAL INFORMATION:
;  APPLICANT: Tischfield, Jay A.
;  APPLICANT: Seilhamer, Jeffrey J.
;  TITLE OF INVENTION: Mammalian Phospholipase A2 Nucleotide
;  TITLE OF INVENTION: Sequences and Low Molecular Weight Amino Acid Sequences
;  TITLE OF INVENTION: Encoded Thereby, Antisense Sequences and Nucleotide
;  TITLE OF INVENTION: Sequences Having Internal Ribosome Binding Sites
;  NUMBER OF SEQUENCES: 44
;  CORRESPONDENCE ADDRRSS:
;     ADDRESSEE: Ruden, Barnett, McClosky, Smith, Schuster &
;     ADDRESSEE: Russell PA
;     STREET: 200 East Broward Boulevard
;     CITY: Fort Lauderdale
;     STATE: FL
;     COUNTRY: USA
;     ZIP: 33301
;  COMPUTER READABLE FORM:
;     MEDIUM TYPE: Floppy disk
;     COMPUTER: IBM PC compatible
;     OPERATING SYSTEM: PC-DOS/MS-DOS
;     SOFTWARE: PatentIn Release #1.0, Version #1.25
;  CURRENT APPLICATION DATA:
;     APPLICATION NUMBER: PCT/US94/07926
;     FILING DATE: 15-JUL-1994
;  CLASSIFICATION:
;  PRIOR APPLICATION DATA:
;     APPLICATION NUMBER: US 08/097,354
;     FILING DATE: 26-JUL-1993
;  ATTORNEY/AGENT INFORMATION:
;     NAME: Manso, Peter J.
;     REGISTRATION NUMBER: 32,264
;     REFERENCE/DOCKET NUMBER: IN21044-5
;  TELECOMMUNICATION INFORMATION:
;     TELEPHONE: 305-527-2498
;     TELEFAX: 305-764-4996
; INFORMATION FOR SEQ ID NO: 31:
;  SEQUENCE CHARACTERISTICS:
;     LENGTH: 1014 base pairs
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Best Local Similarity    57.8%;  Pred. No. 2.8e-23;
Matches  230;  Conservative    0;  Mismatches  165;  Indels    3;  Gaps    1;

Qy    67  TGGTGTGATTCCAATCCAGGGCGGATCCTGAACCTGAACAAGATGGTCAAGCAAGTGAC  126
              ||||||||||||||||||||| |||||||| || ||| || ||| |||| |||| |||
Db   169  TAGTGTGCCTGCTGTGCAAGGAGGCTTGCTGGACCTAAAATCAATGATCGAGAAGGTGAC  228

Qy   127  TGGGAAAATGCCCATCCTCTCCTACTGGCCCTACGGCTGTCACTGCGGACTAGGTGGCAG  186
              ||||| |||| |  |||  ||||||| || || |||   |||| ||  || |||||
Db   229  AGGGAAGAACGCCCTGACAAACTACGGCTTCTACGGCTGTTACTGCGGGCTGGGGCGCCG  288

Qy   187  AGGCCAACCCAAAGATGCCACGGACTGGTGCTGCCAGACCCATGACTGCTGCTATGACCA  246
              ||| |    |  |||||| ||||    |    ||||||  |  | ||| |||||||||
Db   289  AGGAACCCCCAAGGATGGCACCGATTGGTGCTGGTGTTGGGCCGCATGACCACCTGCTATGGGCG  348

Qy   247  CCTGAAGACCCAGGGTGCGGCATCTACAAGGACTATTACAGATACAACTTTTCCCAGGG  306
              |||||||| |||   ||  |||| |  ||||  |  |||  || |||   |||||||
Db   349  GCTGGAGGAGAAGGGCTGCAACATTCGCACACAGTCCTACAAATACAGATTCGCGTGGGG  408

Qy   307  GAACATCCACTGCTTCTGACAAGGGAAGCTTGTGTGCATGTGACAA  366
              |||||||  ||| ||||||   |||  |  |  | |||  |||||
Db   409  CGTGGTCACCTGC---GAGCCCGGGCCCTTCTGCATGTCAACCTCTGTGCCTGTGACCG  465

Qy   367  GGAGGTGGCCTTCTGCCTGAAGCGCAACCTACCAGAGCGACTGCGTTTCTA  426
              ||||||||||||||||||||||||||||||||||||||||
Db   466  GAAGCTCGTCTACTGCCTCAAGAGAAAACTACGGAGCTACAACCCACAGTACCAATACTT  525

Qy   427  CTGGCGCGCCCCACTGCGCGGGGGCAGACCCCTGGGTGCT  464
              ||||||||||||||||||||||||
Db   526  TCCCAACATCCTCTGCTCCTAGGCCTCCCCAGCGAGCT  563


RESULT 5
US-08-186-895-9
; Sequence 9, Application US/08186895
; Patent No. 5538885
;  GENERAL INFORMATION:
;  APPLICANT: Hollis, Melvyn
;  APPLICANT: Needham, Maurice R.C.
;  APPLICANT: Gooding, Clare
;  APPLICANT: Grosveld, Franklin G.
;  TITLE OF INVENTION: Expression Systems
;  NUMBER OF SEQUENCES: 10
;  CORRESPONDENCE ADDRESS:
;     ADDRESSEE: Cushman, Darby & Cushman
;     STREET: 1615 L Street, N.W.
;     CITY: Washington
;     STATE: D.C.
;     COUNTRY: U.S.A.
;     ZIP: 20036-5601
;  COMPUTER READABLE FORM:
;     MEDIUM TYPE: Floppy disk
;     COMPUTER: IBM PC compatible
;     OPERATING SYSTEM: PC-DOS/MS-DOS
;     SOFTWARE: PatentIn Release #1.0, Version #1.25
;  CURRENT APPLICATION DATA:
;     APPLICATION NUMBER: US/08/186,895
;     FILING DATE: 27-JAN-1994
;     CLASSIFICATION: 435
;  PRIOR APPLICATION DATA:
;     APPLICATION NUMBER: US/08/046,383
;     FILING DATE: 09-APR-1993
;     APPLICATION NUMBER: US/07/810,414
```

ATTORNEY/AGENT INFORMATION:
    NAME: Kokulis, Paul N.
    REGISTRATION NUMBER: 16,773
    REFERENCE/DOCKET NUMBER: PNK/3893/93802/MJW
TELECOMMUNICATION INFORMATION:
    TELEPHONE: 202-861-3000
    TELEFAX: 202-822-0944
    TELEX: 6714627 CUSH
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
    LENGTH: 479 base pairs
    TYPE: nucleic acid
    STRANDEDNESS: single
    TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
    NAME/KEY: CDS
    LOCATION: 24..455
US-08-186-895-9

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Query Match          19.0%;   Score 112.4;  DB 1;  Length 479;
Best Local Similarity  54.4%;  Pred. No. 7.6e-22;
Matches 249;   Conservative  0;   Mismatches 206;  Indels  3;  Gaps  1;

Qy    21 CTGGGATCATGGAACTTGCACTGCTGTGTGGCTGGTCTGGTGTGATGGCTCGGTGTGATTCCAA 80
         ||||  || ||||||   |||||||   ||| ||||||||||| |||||   |||||
Db    16 CTCTTACCATGAAGACCCCTCCTACTGTTGGCCTACTGTTCTTGGCCTACTGCAGG 75

Qy    81 TCCAGGGCGGGATCCTGAACCTGAACAAGATGGTCAAGCAAGTGACTGGGAAAATGCCCA 140
         ||| |||||||   ||    ||||||| |||  |||||||||||||||||||||
Db    76 CCCATGGGAATTTGGTGAATTTCCACAGAATGATCAAGTTGACGACAGAAAGGAAGCCG 135

Qy   141 TCCTCTCCTACTGGCCCTACGGCTGTCACTGCGGACTAGGTGCGCAGAGGCCAACCCAAAG 200
         ||| ||||||||||||  || |||||||||||| ||||||  ||||||| ||||||||||
Db   136 CACTCAGTTATGGCTTCTACGGCTGCCACTGTGGCGTGGGTGGCAGAGACCCCCAGG 195

Qy   201 ATGCCACGACTGGTGCTGCCAGACCCATGACTGCTGTCTATGGACCACCTGAAGACCCAGG 260
         |||||||||| ||||| || |||||||||||||| ||  |  |  ||||||||||||||
Db   196 ATGCAACGACATCGGCTGCTGCTGTGTCACTGACTGTTGCTCACAGCGTCTGGAGAAAACGTG 255

Qy   261 GGTGCCGGCATCTACAAGGACTATTACAGATACAAACTTTTCCCAGGGAACATCCACTGCT 320
         ||||||||||  ||  ||||||| ||| ||||||||||||||   |||||||||||||||
Db   256 GATGTGGCACCAAATTTCTGAGCTACAAGTTAGCAACTC---GGGGAGCAGAATCACCT 312

Qy   321 CTGACAAGGGAAGCTGGTGTGAGCAGCAGCTGCTGTGCCTGTGACAAGGAGGTGCCTTCT 380
         ||   |||||||  |||||||| || |||   |||| |||| |||||||||||||||||
Db   313 GTGCAAAACAGGACTCCTGCAGAAGTCAACTGTGTGAGTGTGATAAGGCTGCTGCCAGG 372

Qy   381 GCCTGAAGCGCAACCTGACACTTACCAGAGAGCGACTGCGTTCTACTGGCGGCCCCCACT 440
         ||||| || || |  ||||||||| ||  ||||||||||||||||||||||||||
Db   373 GTTTTGCTAGAAACAAGAACGACCTACAATAAAAAGTACCAGTACTAATTCCAATAAAACACT 432

Qy   441 GCCGGGGGCAGACCCCTGGGTGCTAGAAGCCCACACCC 478
         ||||||||||||||| || ||| |||||||||||||||
Db   433 GCAGAGGGAGCACCCCCTGCTTGCTGAGTCCCCTCTTCC 470
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RESULT 6
US-09-023-655-1207
; Sequence 1207, Application US/09023655
; Patent No. 6607879
GENERAL INFORMATION:
    APPLICANT: Cocks, Benjamin G.
    APPLICANT: Susan G. Stuart
    APPLICANT: Jeffrey J. Seilhamer
    TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL GENE
    TITLE OF INVENTION: EXPRESSION
    NUMBER OF SEQUENCES: 1508
CORRESPONDENCE ADDRESS:
    ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
    STREET: 3174 PORTER DRIVE
    CITY: PALO ALTO
    STATE: CALIFORNIA
    COUNTRY: USA
    ZIP: 94304
COMPUTER READABLE FORM:
    MEDIUM TYPE: Floppy disk
    COMPUTER: IBM PC compatible
    OPERATING SYSTEM: PC-DOS/MS-DOS
    SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
CURRENT APPLICATION DATA:
    APPLICATION NUMBER: US/09/023,655
    FILING DATE: HEREWITH
    CLASSIFICATION:
PRIOR APPLICATION DATA:
    APPLICATION NUMBER:
    FILING DATE:
    CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
    NAME: Zeller, Karen J.
    REGISTRATION NUMBER: 37,071
    REFERENCE/DOCKET NUMBER: PA-0001 US
TELECOMMUNICATION INFORMATION:
    TELEPHONE: (650) 845-4166
    TELEFAX: (650) 855-0555
INFORMATION FOR SEQ ID NO: 1207:
SEQUENCE CHARACTERISTICS:
    LENGTH: 854 base pairs
    TYPE: nucleic acid
    STRANDEDNESS: single
    TOPOLOGY: linear
IMMEDIATE SOURCE:
    LIBRARY: GENBANK
    CLONE: g190888
US-09-023-655-1207

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Query Match          18.7%;   Score 110.8;  DB 4;  Length 854;
Best Local Similarity  54.1%;  Pred. No. 2.6e-21;
Matches 248;   Conservative  0;   Mismatches 207;  Indels  3;  Gaps  1;

Qy    21 CTGGGATCATGGAACTTGCACTGCTGTGTGGCTGGTCTGGTGTGATGGCTCGGTGTGATTCCAA 80
         ||||  || ||||||   |||||||   ||| ||||||||||| |||||   |||||
Db   128 CTCTTACCATGAAGACCCCTCCTACTGTTGGCCTACTGTTCTTGGCCTACTGCAGG 187

Qy    81 TCCAGGGCGGGATCCTGAACCTGAACAAGATGGTCAAGCAAGTGACTGGGAAAATGCCCA 140
         ||| |||||||   ||    ||||||| |||  |||||||||||||||||||||
Db   188 CCCATGGGAATTTGGTGAATTTCCACAGAATGATCAAGTTGACGACAGAAAGGAAGCCG 247

Qy   141 TCCTCTCCTACTGGCCCTACGGCTGTCACTGCGGACTAGGTGCGCAGAGGCCAACCCAAAG 200
         ||| ||||||||||||  || |||||||||||| ||||||  ||||||| ||||||||||
Db   248 CACTCAGTTATGGCTTCTACGGCTGCCACTGTGGCGTGGGTGGCAGAGACCCCCAGG 307

Qy   201 ATGCCACGACTGGTGCTGCCAGACCCATGACTGCTGTCTATGGACCACCTGAAGACCCAGG 260
         |||||||||| ||||| || |||||||||||||| ||  |  |  ||||||||||||||
Db   308 ATGCAACGACATCGGCTGCTGCTGTGTCACTGACTGTTGCTCACAGCGTCTGGAGAAAACGTG 367

Qy   261 GGTGCCGGCATCTACAAGGACTATTACAGATACAAACTTTTCCCAGGGAACATCCACTGCT 320
         ||||||||||  ||  ||||||| ||| ||||||||||||||   |||||||||||||||
Db   368 GATGTGGCACCAAATTTCTGAGCTACAAGTTAGCAACTC---GGGGAGCAGAATCACCT 424

Qy   321 CTGACAAGGGAAGCTGGTGTGAGCAGCAGCTGCTGTGCCTGTGACAAGGAGGTGCCTTCT 380
         ||   |||||||  |||||||| || |||   |||| |||| |||||||||||||||||
Db   425 GTGCAAAACAGGACTCCTGCAGAAGTCAACTGTGTGAGTGTGATAAGGCTGCTGCCACCT 484

Qy   381 GCCTGAAGCGCAACCTGACACTTACCAGAGAGCGACTGCGTTCTACTGGCGGCCCCCACT 440
         ||||| || || |  ||||||||| ||  ||||||||||||||||||||||||||
Db   485 GTTTTGCTAGAAACAAGACGACCTACAATAAAAAGTACCAGTACTATTCCAATAAAACACT 544

Qy   441 GCCGGGGGCAGACCCCTGGGTGCTAGAAGCCCACACCC 478
         ||||||||||||||| || ||| |||||||||||||||
Db   545 GCAGAGGGAGCACCCCCTCGTTGCTGAGTCCCCTCTTCC 582
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RESULT 7
US-09-740-569-1
; Sequence 1, Application US/09740569

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; Patent No. 6475484
; GENERAL INFORMATION:
;   APPLICANT: Weiss, Jerrold
;   APPLICANT: Elsbach, Peter
;   APPLICANT: Liang, Ning-Sheng
;   TITLE OF INVENTION: ANTIBACTERIAL GROUP IIA PHOSPHOLIPASE A2 AND METHODS OF USE THERE
;   FILE REFERENCE: 5936/1E917US1
;   CURRENT APPLICATION NUMBER: US/09/740,569
;   CURRENT FILING DATE: 2000-12-18
;   PRIOR APPLICATION NUMBER: US 60/172,467
;   PRIOR FILING DATE: 1999-12-17
;   NUMBER OF SEQ ID NOS: 5
;   SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
;   LENGTH: 375
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-740-569-1

Query Match             17.2%;  Score 101.8;  DB 4;  Length 375;
Best Local Similarity   56.6%;  Pred. No. 6e-19;
Matches  209;  Conservative   0;  Mismatches  157;  Indels   3;  Gaps   1;

Qy     96  TGAACCTGAACAAGATGGTCAAGCAAGTGACTGGGAAAATGCCCATCCTCCTCCTACTCGGC  155
           ||||  ||  |||  ||||||||||||||||||| ||||||| |||||| |||||||||||
Db      8  TGAATTTCCACAGACTACAAGTTGACGACACAGGAAAGGAAGCCGCACTCAGTTATGCGT   67

Qy    156  CCTACGGCTGTGCTGCGGACTAGGTGCAGAGGCCAACCCAAAGATGCCACCGACTCGT  215
           |||||||||||||||||| ||||||||||||||||  ||||||  |||||| |||||||
Db     68  TCTTACGGCTGCCACTGTGCGTGGGTGCAGAGGATGCAACGGATCGCT  127

Qy    216  GCTGCCAGACCCATGACTGCTGCTATGACCACCTGAAGACCCAGGGGTGCGGCATCTACA  275
           || |||||||||||||||||||  ||||||||||||||||||||||||||| |||||||
Db    128  GCTGTGTCACTCATGACTGTTGCTACAAAACGTCTGGAGAAAACGTGGATGTGGCACCAAAT  187

Qy    276  AGGACTATTACAGATACAAACTTTTCCCAGGGGAACATCCACTGCTCTGACAAGGGAAGCT  335
           ||||  || |  ||||||||
Db    188  TTCTGAGCTACAAGTTTAGCAACTCGAAGAGCAGAATCACCTGTGCAAAAACAGG--ACT  244

Qy    336  GGTGTGAGCAGCAGCTGTGTGCCTGTGACAAGGAGGTGGCCTTCTGCCTGAAGCGCAACC  395
           |    ||||||||||||||||||
Db    245  CCTGCGAGAAGTCAACTGTGTGAGTGTGTGATAAGGCTGCTCGTGCCACCTGTTTTGCTAGAAACA  304

Qy    396  TGGACACCTACCAGAGAGCGACTGCGTTTCTACTGCGGGGCCCCACTGCGGGGGCAGACCC  455
           ||||  || || ||
Db    305  AGAAGACCTACAATAAAAGTACCAGTACTATTCCAATAAACACTGCAGAGGGAGCACCC  364

Qy    456  CTGGGTGCT  464
           ||  |||||
Db    365  CTCGTTGCT  373
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RESULT 8
US-08-888-497-29
; Sequence 29, Application US/08888497
; Patent No. 5972677
; GENERAL INFORMATION:
;   APPLICANT: Tischfield, Jay A.
;   APPLICANT: Seilhamer, Jeffrey J.
;   TITLE OF INVENTION: Mammalian Phospholipase A2 Nucleotide
;   TITLE OF INVENTION: Sequences and Low Molecular Weight Amino Acid Sequences
;   TITLE OF INVENTION: Encoded Thereby, Antisense Sequences and Nucleotide
;   TITLE OF INVENTION: Sequences Having Internal Ribosome Binding Sites
;   NUMBER OF SEQUENCES: 44
; CORRESPONDENCE ADDRESS:
;   ADDRESSEE: Ruden, Barnett, McClosky, Smith, Schuster &
;   ADDRESSEE: Russell PA
;   STREET: 200 East Broward Boulevard
;   CITY: Fort Lauderdale
;   STATE: FL
;   COUNTRY: USA
;   ZIP: 33301
;   COMPUTER READABLE FORM:
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;     MEDIUM TYPE: Floppy disk
;     COMPUTER: IBM PC compatible
;     OPERATING SYSTEM: PC-DOS/MS-DOS
;     SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
;     APPLICATION NUMBER: US/08/888,497
;     FILING DATE:
;     CLASSIFICATION:
; PRIOR APPLICATION DATA:
;     APPLICATION NUMBER: US/08/651,405
;     FILING DATE:
;     APPLICATION NUMBER: US 08/097,354
;     FILING DATE: 26-JUL-1993
; ATTORNEY/AGENT INFORMATION:
;     NAME: Manso, Peter J.
;     REGISTRATION NUMBER: 32,264
;     REFERENCE/DOCKET NUMBER: IN21044-5
; TELECOMMUNICATION INFORMATION:
;     TELEPHONE: 305-527-2498
;     TELEFAX: 305-764-4996
; INFORMATION FOR SEQ ID NO: 29:
;     SEQUENCE CHARACTERISTICS:
;     LENGTH: 1828 base pairs
;     TYPE: nucleic acid
;     STRANDEDNESS: single
;     TOPOLOGY: linear
;   MOLECULE TYPE: cDNA
;   FEATURE:
;     NAME/KEY: CDS
;     LOCATION: 233..643
US-08-888-497-29

Query Match              16.6%;  Score 98.4;  DB 2;  Length 1828;
Best Local Similarity    57.6%;  Pred. No. 9e-18;
Matches  196;  Conservative   0;  Mismatches  141;  Indels   3;  Gaps   1;

Qy     69  GTGTGATTCCAATCCAGGGCGGGATCCTGAACCTGAACAAGAGATGGTCAAGCAAGTGACTG  128
           |||||     |||||||||||||||   |||||||||||   |||||||||||||||||||
Db    273  GTGTGCCTGCCAGTCCCAGGGGCTTGCTAGAACTGAAGTCCATGATTGAGAAGGTGACTG  332

Qy    129  GGAAAATGCCCATCCTCCTCCTACTGGCCCTACGGCTGTCACTGCGGACTAGGTGCGAGAG  188
           |||||   ||||  |||||||  ||||  |||||||||||  |||||||||||||||||
Db    333  GGAAGAATGCCGTAAAGAACTATGGCTTCTACGGCTGCCGGCGCTGGTGCTGGGGGCCCACG  392

Qy    189  GCCAACCCAAAGATGCCACGGACTGGTGCTGCCAGACCCATGACTGCTGCTATGACCACC  248
           |||   ||||||||||||||||||||||||||||||||||||||  |||| |||| |||||
Db    393  GGACCCCTAAGGATGGCACTGATTGGTGCTGCGGATGCACGACCGTTGTTATGGGCTAC  452

Qy    249  TGAAGACCCAGGGGTGCGGCATCTACAAGGACTATTACAGATACAAACTTTTCCCAGGGGA  308
           |||||||||||||   |||||||||||||||||| ||||||||  ||||||||||||
Db    453  TGGAGGAGAAACACTGTGCCATCCGGACCAGTCCTATGACTACAGATTCACACAGG---  509

Qy    309  ACATCCACTGCTCTGACAAGGGAAGCTGGTGTGAGCAGCAGCTGTGTGCCTGTGACAAGG  368
           ||||| |||||| |||||||||||||||||||||||||||||||||||||||||||||||
Db    510  ACTTAGTCATCTGCGAACACGACTCCTTCTGTCCCAGTGAGGCTTGTTGTGCTTGTGACCCGA  569

Qy    369  AGGTGGCCTTCTGCCTGGAAGCGCAACCTGGACACCTACCA  408
           ||||
Db    570  AGCTGGTCTACTGCCTCGAGGAGAAACCTCTGGAGTTACAA  609
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RESULT 9
US-09-362-230-29
; Sequence 29, Application US/09362230
; Patent No. 6352849
; GENERAL INFORMATION:
;   APPLICANT: Tischfield, Jay A.
;   APPLICANT: Seilhamer, Jeffrey J.
;   TITLE OF INVENTION: Mammalian Phospholipase A2 Nucleotide
;   TITLE OF INVENTION: Sequences and Low Molecular Weight Amino Acid Sequences
;   TITLE OF INVENTION: Encoded Thereby, Antisense Sequences and Nucleotide
;   TITLE OF INVENTION: Sequences Having Internal Ribosome Binding Sites
;   NUMBER OF SEQUENCES: 44
```

GENERAL INFORMATION:
APPLICANT: Tischfield, Jay A.
APPLICANT: Seilhamer, Jeffrey J.
TITLE OF INVENTION: Mammalian Phospholipase A2 Nucleotide
TITLE OF INVENTION: Sequences and Low Molecular Weight Amino Acid Sequences
TITLE OF INVENTION: Encoded Thereby, Antisense Sequences and Nucleotide
TITLE OF INVENTION: Sequences Having Internal Ribosome Binding Sites
NUMBER OF SEQUENCES: 44
CORRESPONDENCE ADDRESS:
ADDRESSEE: Ruden, Barnett, McClosky, Smith, Schuster &
ADDRESSEE: Russell PA
STREET: 200 East Broward Boulevard
CITY: Fort Lauderdale
STATE: FL
COUNTRY: USA
ZIP: 33301
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/07926
FILING DATE: 15-JUL-1994
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/097,354
FILING DATE: 26-JUL-1993
ATTORNEY/AGENT INFORMATION:
NAME: Manso, Peter J.
REGISTRATION NUMBER: 32,264
REFERENCE/DOCKET NUMBER: IN21044-5
TELECOMMUNICATION INFORMATION:
TELEPHONE: 305-527-2498
TELEFAX: 305-764-4996
INFORMATION FOR SEQ ID NO: 29:
SEQUENCE CHARACTERISTICS:
LENGTH: 1828 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 233..643
PCT-US94-07926-29

```
Query Match             16.6%;   Score 98.4;  DB 5;  Length 1828;
Best Local Similarity   57.6%;   Pred. No. 9e-18;
Matches   196;  Conservative    0;  Mismatches  141;  Indels    3;  Gaps    1;

Qy     69 GTGTGATTCCAATCCAGGCGGGATCCTGAACCAAGATGGTCAAGCAAGTGACTG 128
             ||||  ||| |||| |||||   || | |||||  ||||| |   ||||||||||
Db    273 GTGTGCCTGCAGTCCCCAGGGGCGGCTTGCTAGGAACTGAAGTCCATGAGAAGTGAGAAGTGACTG 332

Qy    129 GGAAAATGCCCATCCTCCTCCTACTGGCCGCCAGACCCATGACTG 188
             ||||  ||||| |  ||| ||| ||||     |||||| ||||||
Db    333 GGAAGAATGCCGTAAAGAACTATGGCTTCTACGGTGCTACTGTGCTGGGCCGCCACG 392

Qy    189 GCCAACCCAAAGATGCCACGGACTGGTGCTGCCAGACCCATGACTGCCTGCTATGACCACC 248
             ||||| |||||||||| |||| |||||||| ||||||| |||||| || ||| |||||||
Db    393 GGACCCCTAAGGATGGCACTGATTGGTGCTGTGCGTCGTGCACCGGTTGTTATGGGCTAC 452

Qy    249 TGAAGACCCAGGGGTGCGGCATCTACAAGGACTATTACAGATACAACTTTTCCCAGGGGA 308
             || || || || |||| | ||| |||| |||  ||  || |||| | || | || |||
Db    453 TGGAGGAGAAAACACTGTCCATCCGGACACGACTCCTATGACTACAGATTCACACAGG--- 509

Qy    309 ACATCCACTGCTTCTGCCTGACAAGGAAGCTGGTGTGAGCAGCTGTGTGCCTGTGCTGTGACAAGG 368
             ||||||||||||||| | |||  |||||  | || ||| |  || | || || |||||||| ||||
Db    510 ACTTAGTCATCTGCGAACACGACTCCTTGTCCAGTGAGGCTTTGTGTGTCTTGTGTGACCGGA 569

Qy    369 AGGTGGCCTTCTGCTGACAACTGGCCAACCTGGACACCTACCA 408
             | ||||||| | |||| |  || |||| ||||||||| |||||||
Db    570 AGCTGGTCTACTGCTTGAGGAGAAACCTCTGAGTTACAA 609
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Db   570 AGCTGGTCTACTGCCTGAGGAGAAACCTCTGGAGTTACAA 609

RESULT 11
US-08-888-497-21
; Sequence 21, Application US/08888497
; Patent No. 5972677
; GENERAL INFORMATION:
;   APPLICANT: Tischfield, Jay A.
;   APPLICANT: Seilhamer, Jeffrey J.
;   TITLE OF INVENTION: Mammalian Phospholipase A2 Nucleotide
;   TITLE OF INVENTION: Sequences and Low Molecular Weight Amino Acid Sequences
;   TITLE OF INVENTION: Encoded Thereby, Antisense Sequences and Nucleotide
;   TITLE OF INVENTION: Sequences Having Internal Ribosome Binding Sites
;   NUMBER OF SEQUENCES: 44
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE: Ruden, Barnett, McClosky, Smith, Schuster &
;   ADDRESSEE: Russell PA
;   STREET: 200 East Broward Boulevard
;   CITY: Fort Lauderdale
;   STATE: FL
;   COUNTRY: USA
;   ZIP: 33301
;   COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: PatentIn Release #1.0, Version #1.25
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/08/888,497
;   FILING DATE:
;   CLASSIFICATION:
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: US/08/651,405
;   FILING DATE:
;   APPLICATION NUMBER: US 08/097,354
;   FILING DATE: 26-JUL-1993
;   ATTORNEY/AGENT INFORMATION:
;   NAME: Manso, Peter J.
;   REGISTRATION NUMBER: 32,264
;   REFERENCE/DOCKET NUMBER: IN21044-5
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE: 305-527-2498
;   TELEFAX: 305-764-4996
; INFORMATION FOR SEQ ID NO: 21:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH: 4325 base pairs
;   TYPE: nucleic acid
;   STRANDEDNESS: single
;   TOPOLOGY: linear
;   MOLECULE TYPE: cDNA
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: 722..1195
US-08-888-497-21

Query Match   15.6%; Score 92.6; DB 2; Length 4325;
Best Local Similarity   56.9%; Pred. No. 4.9e-16;
Matches 195; Conservative   0; Mismatches 139; Indels   9; Gaps   1;

Qy   78 CAATCCAGGGCGGGGATCCTGAACCTGAACAAGATGGTCAAGCAAGTGACTGGGAAAATGC 137
          ||||||||||||| ||||||||||| | | || |||||||||||||||||||||||||||||
Db   795 CCACCCTCAGCAGCTTCTGGCAGTTCCAGAGATGGTCAAACACATCACGGGGCGCAGCG 854

Qy   138 CCATCCTCCTCCTACTGGCCTCACGGCTGTCACTGCGGACTAGGTGGCAGAGGCCAACCCA 197
          |||| || | ||||||||||||||||||
Db   855 CCTTCTTCTCCTATTACGGATATGGCTGCTCACTGTGGGGCCGAGGGGATCCCTG 914

Qy   198 AAGATGCCACGGACTGTGCTGCCAGCCATGACTGCTGCTATGACCACCTGAAGACCC 257
          |||||| ||||| ||||| |||||||||
Gap   915 TGGACGCCCAGACAGCAGGTGCTGCTGGCCTCATGACTTGCTACCACAACTTTAAGGAAT 974

Qy   258 AGGGGTGCGGCATCACAAGGACTATTACAGATAACAACTTTTCCCAGGGAACATCCACT 317

RESULT 12
US-09-362-230-21
; Sequence 21, Application US/09362230
; Patent No. 6352849
; GENERAL INFORMATION:
;   APPLICANT: Tischfield, Jay A.
;   APPLICANT: Seilhamer, Jeffrey J.
;   TITLE OF INVENTION: Mammalian Phospholipase A2 Nucleotide
;   TITLE OF INVENTION: Sequences and Low Molecular Weight Amino Acid Sequences
;   TITLE OF INVENTION: Encoded Thereby, Antisense Sequences and Nucleotide
;   TITLE OF INVENTION: Sequences Having Internal Ribosome Binding Sites
;   NUMBER OF SEQUENCES: 44
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE: Ruden, Barnett, McClosky, Smith, Schuster &
;   ADDRESSEE: Russell PA
;   STREET: 200 East Broward Boulevard
;   CITY: Fort Lauderdale
;   STATE: FL
;   COUNTRY: USA
;   ZIP: 33301
;   COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: PatentIn Release #1.0, Version #1.25
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/09/362,230
;   FILING DATE:
;   CLASSIFICATION:
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: 08/888,497
;   FILING DATE:
;   APPLICATION NUMBER: US 08/097,354
;   FILING DATE: 26-JUL-1993
;   ATTORNEY/AGENT INFORMATION:
;   NAME: Manso, Peter J.
;   REGISTRATION NUMBER: 32,264
;   REFERENCE/DOCKET NUMBER: IN21044-5
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE: 305-527-2498
;   TELEFAX: 305-764-4996
; INFORMATION FOR SEQ ID NO: 21:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH: 4325 base pairs
;   TYPE: nucleic acid
;   STRANDEDNESS: single
;   TOPOLOGY: linear
;   MOLECULE TYPE: cDNA
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: 722..1195
US-09-362-230-21

Query Match   15.6%; Score 92.6; DB 4; Length 4325;
Best Local Similarity   56.9%; Pred. No. 4.9e-16;
Matches 195; Conservative   0; Mismatches 139; Indels   9; Gaps   1;

Qy   78 CAATCCAGGGCGGGGATCCTGAACCTGAACAAGATGGTCAAGCAAGTGACTGGGAAAATGC 137
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Db   795 CCACCCTCAGCAGCTTCTGGCAGTTCCAGAGATGGTCAAACACATCACGGGGCGCAGCG 854

Db   975 ATGGGCTGCCAGCCATCTTGAATGCCTATCATCAGTTGCCATTGTCAACGGGACCGTGACCT 1034
              | ||||| ||||||||||||||||||||||||||||
Qy   318 G--------CTCTGACAAGGAAGCTGGTGTGAGCAGCAGCTGTGTCCTGTGACAAGG 368

Db   1035 GTGGATGCACCATGGGTGCGGCTGCTTGTGCGGGCAGAAAGCCTGTGAGTGTGACAAAC 1094
              |||||||||||||||||||||||||| ||||||| |||||||||||||||||||||
Qy   369 AGGTGGCCTTCTGCTGAAGCCAACCGACACCTACCAGAA 411

Db   1095 TGTCTGTGTACTGCTTCAAGGAGAACCTGGCCACCTACGAGAA 1137

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                   Matches  195;  Conservative   0;  Mismatches 139;  Indels    9;  Gaps     1;

Qy      138  CCATCCTCCTACTGGCCTCACGGCTGTCACTGCGGACTAGGTGGCAGAGGCCAACCCA  197
             ||| |||||||||||||    |  || || ||| ||||||||| || ||  ||  ||
Db       78  CAATCCAGGGCGGGATCCTGAACCTGAACAAGATGGTCAAGCAAGTGACTGGGAAAATGC  137

Qy           CCTTCTTCTCCTTATTACGGATATGGCTGCTACTGTGGGCTTGGGGGCCGAGGGATCCCTG  914
Db      795  CCACCCTCAGCAGCTTCTGGCAGTTCCAGAGGATGGTCAAACACATCACGGGCGCGCAGCG  854

Qy      198  AAGATGCCACGGACTGGTGCTGCCAGACCCATGACTGCTGCTATGACCACCTGAAGACCC  257
             |||| ||  |||  | ||| || ||||||||||||| | | | ||||| |||| ||||
Db      915  TGGACGCCACAGACAGAGTGCTGCTGGGCTTGGGGCTTGGGGGCCCAGGGATCCCTG  914

Qy      258  AGGGGTGCGGCATCTACAAGGACTATTACAGATACAACTTTTCCAGGGGAACATCCACT  317
             ||||  | |||||||| ||||||     ||||||| ||| || ||||| |||||||
Db      975  ATGGCTGCCAGCCCATCTGAATGCCTATCAGTTTGCCATTGCTGCTACCACAAGCTTAAGGAAT  1034

Qy      318  G--------CCTGACAAGGAAGCTGGTGTGAGCAGCAGCGTGTGCCTGTGACAAGG  368
             |        |||||||||||||||||||||  ||||| ||| |||||| |||||||
Db     1035  GTGGATGCACCATGGTGCGGGCTGCTTGTGCGGGCCAGAGAAAGCCTGTGAGTGTGACAAAC  1094

Qy      369  AGGTGGCCTTCTGCCTGAAGCGCAACCTGGACACCTACCAGAA  411
             ||| ||||||||||||||||||||||||||||| ||||||||
Db     1095  TGTCTGTGTACTGCTTCAAGGAGAACCTGGCCACCTACGAGAA  1137
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RESULT 13
PCT-US94-07926-21

; Sequence 21, Application PCT/US9407926

GENERAL INFORMATION:
,, APPLICANT: Tischfield, Jay A.
,, APPLICANT: Seilhamer, Jeffrey J.
,, TITLE OF INVENTION: Mammalian Phospholipase A2 Nucleotide
,, TITLE OF INVENTION: Sequences and Low Molecular Weight Amino Acid Sequences
,, TITLE OF INVENTION: Encoded Thereby, Antisense Sequences and Nucleotide
,, TITLE OF INVENTION: Sequences Having Internal Ribosome Binding Sites
,, NUMBER OF SEQUENCES: 44
,, CORRESPONDENCE ADDRESS:
,,   ADDRESSEE: Ruden, Barnett, McClosky, Smith, Schuster &
,,   ADDRESSEE: Russell PA
,,   STREET: 200 East Broward Boulevard
,,   CITY: Fort Lauderdale
,,   STATE: FL
,,   COUNTRY: USA
,,   ZIP: 33301
,, COMPUTER READABLE FORM:
,,   MEDIUM TYPE: Floppy disk
,,   COMPUTER: IBM PC compatible
,,   OPERATING SYSTEM: PC-DOS/MS-DOS
,,   SOFTWARE: PatentIn Release #1.0, Version #1.25
,, CURRENT APPLICATION DATA:
,,   APPLICATION NUMBER: PCT/US94/07926
,,   FILING DATE: 15-JUL-1994
,,   CLASSIFICATION:
,, PRIOR APPLICATION DATA:
,,   APPLICATION NUMBER: US 08/097,354
,,   FILING DATE: 26-JUL-1993
,, ATTORNEY/AGENT INFORMATION:
,,   NAME: Manso, Peter J.
,,   REGISTRATION NUMBER: 32,264
,,   REFERENCE/DOCKET NUMBER: IN21044-5
,, TELECOMMUNICATION INFORMATION:
,,   TELEPHONE: 305-527-2498
,,   TELEFAX: 305-764-4996
,, INFORMATION FOR SEQ ID NO: 21:
,, SEQUENCE CHARACTERISTICS:
,,   LENGTH: 4325 base pairs
,,   TYPE: nucleic acid
,,   STRANDEDNESS: single
,,   TOPOLOGY: linear
,,   MOLECULE TYPE: cDNA
,, FEATURE:
,,   NAME/KEY: CDS
,,   LOCATION: 722..1195
PCT-US94-07926-21

Query Match   15.6%; Score 92.6; DB 5; Length 4325;
Best Local Similarity   56.9%; Pred. No. 4.9e-16;

RESULT 14
US-08-966-317-2

; Sequence 2, Application US/08966317

; Patent No. 6103469

GENERAL INFORMATION:
,, APPLICANT: Hawkins, Phillip R.
,, APPLICANT: Bandman, Olga
,, APPLICANT: Guegler, Karl J.
,, APPLICANT: Shah, Purvi
,, APPLICANT: Corley, Neil C.
,, TITLE OF INVENTION: HUMAN PHOSPHOLIPASE A2 PROTEIN
,, NUMBER OF SEQUENCES: 4
,, CORRESPONDENCE ADDRESS:
,,   ADDRESSEE: Incyte Pharmaceuticals, Inc.
,,   STREET: 3174 Porter Dr.
,,   CITY: Palo Alto
,,   STATE: CA
,,   COUNTRY: USA
,,   ZIP: 94304
,, COMPUTER READABLE FORM:
,,   MEDIUM TYPE: Diskette
,,   COMPUTER: IBM Compatible
,,   OPERATING SYSTEM: DOS
,,   SOFTWARE: FastSEQ for Windows Version 2.0
,, CURRENT APPLICATION DATA:
,,   APPLICATION NUMBER: US/08/966,317
,,   FILING DATE: Filed Herewith
,, PRIOR APPLICATION DATA:
,,   APPLICATION NUMBER:
,,   FILING DATE:
,, ATTORNEY/AGENT INFORMATION:
,,   NAME: Billings, Lucy J.
,,   REGISTRATION NUMBER: 36,749
,,   REFERENCE/DOCKET NUMBER: PF-0403 US
,, TELECOMMUNICATION INFORMATION:
,,   TELEPHONE: 650-855-0555
,,   TELEFAX: 650-845-4166
,, INFORMATION FOR SEQ ID NO: 2:
,, SEQUENCE CHARACTERISTICS:
,,   LENGTH: 742 base pairs
,,   TYPE: nucleic acid
,,   STRANDEDNESS: single
,,   TOPOLOGY: linear
,, IMMEDIATE SOURCE:
,,   LIBRARY: OVARTUT01
,,   CLONE: 816403

US-08-966-317-2

Query Match   10.7%;   Score 63.2;   DB 3;   Length 742;
Best Local Similarity   51.8%;   Pred. No. 3.5e-08;
Matches 143;   Conservative   0;   Mismatches 133;   Indels   0;   Gaps   0;

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Db  197 CCCCCATCGCCTATATGAAATATGGTTGCTTTTGTGCTTGGCTGGGAGGCCATGGCCAGCCCC 256

Qy  198 AAGATGCCACGGACTGGTGCTGCCAGACCCATGACTGCTGCTATGACCACCTGAAGACCC 257
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Db  257 GCGATGCCATTGACTGGTGCTGCCACATGGCCACGACTGTTGTTACACTCGAGCTGAGGAGG 316

Qy  258 AGGGGTGCGGCATCTACACAGGACTATTACAGATACAACTTTTCCCAGGGGAACATCCACT 317
          |    ||| |    |  ||||       |||||    || ||  ||||  |||||||
Db  317 CCGGCTGCAGCCCCAAGACAGAGCGCTACTCCTGGCAGTGCGTCAATCAGAGCGTCCTGT 376

Qy  318 GCTCTGACAAGGGAAGCTGGTGTGAGCAGCTGTGTGCCTGTGACAAGGAGGTGGCCT 377
          |  |||| |      | |    | ||| ||||| ||   |||| ||||  |||||
Db  377 GCGGACCGGCAGAGAGAACAAATGCCAAGAACTGTTGTGCAAGTGTGACCAGAGATTGCTA 436

Qy  378 TCTGCCTGAAGCGCAACCTGGACACCTACCAGAAGC 413
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Db  437 ACTGCTTAGCCCAAACTGAGTACAACTTAAAGTACC 472
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RESULT 15
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; Sequence 2, Application US/09489770
; Patent No. 6399301
GENERAL INFORMATION:
  APPLICANT: Hawkins, Phillip R.
  APPLICANT: Bandman, Olga
  APPLICANT: Guegler, Karl J.
  APPLICANT: Shah, Purvi
  APPLICANT: Corley, Neil C.
  TITLE OF INVENTION: HUMAN PHOSPHOLIPASE A2 PROTEIN
  NUMBER OF SEQUENCES: 4
  CORRESPONDENCE ADDRESS:
    ADDRESSEE: Incyte Pharmaceuticals, Inc.
    STREET: 3174 Porter Dr.
    CITY: Palo Alto
    STATE: CA
    COUNTRY: USA
    ZIP: 94304
  COMPUTER READABLE FORM:
    MEDIUM TYPE: Diskette
    COMPUTER: IBM Compatible
    OPERATING SYSTEM: DOS
    SOFTWARE: FastSEQ for Windows Version 2.0
  CURRENT APPLICATION DATA:
    APPLICATION NUMBER: US/09/489,770
    FILING DATE:
  PRIOR APPLICATION DATA:
    APPLICATION NUMBER: 08/966,317
    FILING DATE:
  ATTORNEY/AGENT INFORMATION:
    NAME: Billings, Lucy J.
    REGISTRATION NUMBER: 36,749
    REFERENCE/DOCKET NUMBER: PF-0403 US
  TELECOMMUNICATION INFORMATION:
    TELEPHONE: 650-855-0555
    TELEFAX: 650-845-4166
INFORMATION FOR SEQ ID NO: 2:
  SEQUENCE CHARACTERISTICS:
    LENGTH: 742 base pairs
    TYPE: nucleic acid
    STRANDEDNESS: single
    TOPOLOGY: linear
  IMMEDIATE SOURCE:
    LIBRARY: OVARTUT01
    CLONE: 816403

US-09-489-770-2

Query Match   10.7%;   Score 63.2;   DB 4;   Length 742;
Best Local Similarity   51.8%;   Pred. No. 3.5e-08;
Matches 143;   Conservative   0;   Mismatches 133;   Indels   0;   Gaps   0;

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Qy  138 CCATCCTCTCCTACTGGCCCTACGGCTGTCACTGCGGACTAGGTGGCAGAGGCCAACCCA 197
            |   |    |||      ||||     ||      ||||||    ||||| ||||
Db  197 CCCCCATCGCCTATATGAAATATGGTTGCTTTTGTGCTTGGCTGGGAGGCCATGGCCAGCCCC 256

Qy  198 AAGATGCCACGGACTGGTGCTGCCAGACCCATGACTGCTGCTATGACCACCTGAAGACCC 257
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Qy  258 AGGGGTGCGGCATCTACACAGGACTATTACAGATACAACTTTTCCCAGGGGAACATCCACT 317
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Qy  318 GCTCTGACAAGGGAAGCTGGTGTGAGCAGCTGTGTGCCTGTGACAAGGAGGTGGCCT 377
          |  |||| |      | |    | ||| ||||| ||   |||| ||||  |||||
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Qy  378 TCTGCCTGAAGCGCAACCTGGACACCTACCAGAAGC 413
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Job time : 49.7926 secs

OM nucleic - nucleic search, using sw model

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          Copyright (c) 1993 - 2004 Compugen Ltd.
          GenCore version 5.1.6
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Title: US-09-830-321A-4
Perfect score: 592
Sequence: 592
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                Gapop 10.0 , Gapext 1.0

Searched: 3340653 seqs, 2534783454 residues

Total number of hits satisfying chosen parameters: 6681306

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

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     2: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
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     7: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*
     8: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*
     9: /cgn2_6/ptodata/2/pubpna/US09A_PUBCOMB.seq:*
    10: /cgn2_6/ptodata/2/pubpna/US09B_PUBCOMB.seq:*
    11: /cgn2_6/ptodata/2/pubpna/US09C_PUBCOMB.seq:*
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    13: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq2:*
    14: /cgn2_6/ptodata/2/pubpna/US10A_PUBCOMB.seq:*
    15: /cgn2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq:*
    16: /cgn2_6/ptodata/2/pubpna/US10C_PUBCOMB.seq:*
    17: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*
    18: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*
    19: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	575.4	97.2	854	9	US-09-969-384-6	Sequence 6, Appli
2	568.8	96.1	1927	13	US-10-296-115-603	Sequence 603, App
3	567.4	95.8	1931	10	US-09-835-996A-5	Sequence 5, Appli
4	284.2	48.0	496	12	US-10-015-395A-377	Sequence 377, App
5	284.2	48.0	496	13	US-10-147-493-533	Sequence 533, App
6	284.2	48.0	496	13	US-10-145-127-533	Sequence 533, App
7	284.2	48.0	496	13	US-10-160-503-533	Sequence 533, App
8	284.2	48.0	496	13	US-10-143-118-533	Sequence 533, App
9	284.2	48.0	496	13	US-10-144-993-533	Sequence 533, App
10	284.2	48.0	496	13	US-10-158-787-533	Sequence 533, App
11	284.2	48.0	496	13	US-10-140-024-533	Sequence 533, App
12	284.2	48.0	496	13	US-10-140-808-533	Sequence 533, App
13	284.2	48.0	496	13	US-10-006-485A-377	Sequence 377, App
15	284.2	48.0	496	13	US-10-013-907A-377	Sequence 377, App
16	284.2	48.0	496	13	US-10-015-499A-377	Sequence 377, App
17	284.2	48.0	496	13	US-10-152-405-533	Sequence 533, App
18	284.2	48.0	496	13	US-10-127-852A-533	Sequence 533, App
19	284.2	48.0	496	13	US-10-127-900A-533	Sequence 533, App
20	284.2	48.0	496	13	US-10-128-685A-533	Sequence 533, App
21	284.2	48.0	496	13	US-10-226-254A-377	Sequence 377, App
22	284.2	48.0	496	13	US-10-131-820A-533	Sequence 533, App
23	284.2	48.0	496	13	US-10-142-886-533	Sequence 533, App
24	284.2	48.0	496	13	US-10-146-728-533	Sequence 533, App
25	284.2	48.0	496	13	US-10-146-786-533	Sequence 533, App
26	284.2	48.0	496	13	US-10-147-499-533	Sequence 533, App
27	284.2	48.0	496	13	US-10-157-798-533	Sequence 533, App
28	284.2	48.0	496	15	US-10-028-072-533	Sequence 533, App
29	284.2	48.0	496	15	US-10-121-049-533	Sequence 533, App
30	284.2	48.0	496	15	US-10-123-904-533	Sequence 533, App
31	284.2	48.0	496	15	US-10-140-470-533	Sequence 533, App
32	284.2	48.0	496	15	US-10-175-746-533	Sequence 533, App
33	284.2	48.0	496	15	US-10-176-918-533	Sequence 533, App
34	284.2	48.0	496	15	US-10-176-921-533	Sequence 533, App
35	284.2	48.0	496	15	US-10-137-865-533	Sequence 533, App
36	284.2	48.0	496	15	US-10-140-474-533	Sequence 533, App
37	284.2	48.0	496	15	US-10-142-431-533	Sequence 533, App
38	284.2	48.0	496	15	US-10-143-114-533	Sequence 533, App
39	284.2	48.0	496	15	US-10-140-002-533	Sequence 533, App
40	284.2	48.0	496	15	US-10-006-856A-377	Sequence 377, App
41	284.2	48.0	496	15	US-10-142-419-533	Sequence 533, App
42	284.2	48.0	496	15	US-10-123-262-533	Sequence 533, App
43	284.2	48.0	496	15	US-10-142-423-533	Sequence 533, App
44	284.2	48.0	496	15	US-10-006-818A-377	Sequence 377, App
45	284.2	48.0	496	15	US-10-121-050-533	Sequence 533, App

ALIGNMENTS

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RESULT 1
US-09-969-384-6
; Sequence 6, Application US/09969384
; Publication No. US20020192749A1
; GENERAL INFORMATION:
; APPLICANT: Moore, et al.
; TITLE OF INVENTION: Human Gene Polynucleotides, Polypeptides, and Antibodies
; FILE REFERENCE: PT055P1
; CURRENT APPLICATION NUMBER: US/09/969,384
; CURRENT FILING DATE: 2001-10-03
; PRIOR APPLICATION NUMBER: PCT/US01/10542
; PRIOR APPLICATION NUMBER: 60/236,384
; PRIOR FILING DATE: 2001-04-02
; PRIOR FILING DATE: 2000-09-29
; PRIOR APPLICATION NUMBER: 60/194,118
; PRIOR FILING DATE: 2000-04-03
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
; LENGTH: 854
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-969-384-6

Query Match          97.2%;  Score 575.4;  DB 9;  Length 854;
Best Local Similarity  99.8%;  Pred. No. 8.9e-171;
Matches  576;  Conservative  0;  Mismatches  1;  Indels  0;  Gaps  0;

Qy   16  CTGTGCTGGGATCATGGAACTTGCCACTCGTGTCGTGGGCTCGTGGTCGTGGTGTGGTGAT   75
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Db    9  CTGTGCTGGGATCATGGAACTTGCCACTCGTGTCGTGGGCTCGTGGTCGTGGTGTGGTGAT   68

Qy   76  TCCAATCCAGGGCGGGATCCTGAACCTGAACAAGATGTCAGCAAGTGACTGGGAAAT  135
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Qy  136  GCCCATCCTCTCCTACTGGCCCTACCGCGTGTCACTGCGGACTAGGTGGCGAGAGGCCAACC  195
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Qy   196 CAAAGATGCCACGGACTGGTGCTGCCAGACCCATGACTGCTCTATGACCACCTGAAGAC 255
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Db   189 CAAAGATGCCACGGACTGGTGCTGCCAGACCCATGACTGCTCTATGACCACCTGAAGAC 248

Qy   256 CCAGGGGTGCGGCATCTACAAGGACTATTACAGATACAACTTTTCCCAGGGAACATCCA 315
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Qy   316 CTGCTCTGACAAGGAAGCTGGTGTGAGCAGCGTGTGTGCCTGTGACAAGGAGGTGGC 375
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Db   309 CTGCTCTGACAAGGAAGCTGGTGTGAGCAGCGTGTGTGCCTGTGACAAGGAGGTGGC 368

Qy   376 CTTCTGCCTGAAGCGCAACCTACCAGAAGCGACTGCGTTTCTACTGGCGGCC 435
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Db   369 CTTCTGCCTGAAGCGCAACCTGACAACCTACCAGAAGCGACTGCGTTTCTACTGGCGGCC 428

Qy   436 CCACTGCCGCGGGGGCAGACCCCTGGGTGCTAGAAGCCCACACCCTCTACCCTGTTCCTCAG 495
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Db   429 CCACTGCCGCGGGGGCAGACCCCTGGGTGCTAGAAGCCCACACCCTCTACCCTGTTCCTCAG 488

Qy   496 CATGGAGCTCTGGCATCCCACCTCAGTAGTCAACTGAACCAGCCTGGCTTTTCAAACA 555
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RESULT 2
US-10-296-115-603
; Sequence 603, Application US/10296115
; Publication No. US20040053248A1
; GENERAL INFORMATION:
;   APPLICANT: Hyseq Inc
;   TITLE OF INVENTION: No. US2004005324 8Alel Nucleic Acids and Polypeptides
;   FILE REFERENCE: 784PCT
;   CURRENT APPLICATION NUMBER: US/10/296,115
;   CURRENT FILING DATE: 2002-11-18
;   PRIOR APPLICATION NUMBER: US09/488,725
;   PRIOR FILING DATE: 2000-01-21
;   PRIOR APPLICATION NUMBER: US09/552,317
;   PRIOR FILING DATE: 2000-04-25
;   NUMBER OF SEQ ID NOS: 1478
; SEQ ID NO 603
;   LENGTH: 1927
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-296-115-603

Query Match   96.1%;   Score 568.8;   DB 13;   Length 1927;
Best Local Similarity   98.8%;   Pred. No. 1.4e-168;
Matches 573;   Conservative   0;   Mismatches   7;   Indels   0;   Gaps   0;

Qy   13 GCTCTGTGCTGGGATCATGGAACTTGCACTGCTGTGTGGGCTGGTGGTGGTGATGGCTGGTGT 72
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Db   2 GCGGTGGAATTCGATCATGCACTTGCACTGCTGTGTGGGCTGGTGGTGGTGATGGCTGGTGT 61

Qy   73 GATTCCAATCCAGGGCGGATCCTCCTACTGGCCCTACGGCTGTCACTGCGGAGTGACTGGGAA 132
       |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   62 GATTCCAATCCAGGGCGGGATCCTCGAACCTGACGGCTGTCACTGCGGAGTGACTGGGAA 121

Qy   133 AATGCCATCCATCCTCTCCTACTGGCCCTACGGCCTGTCACTGCGGACTAGGTGGCAGAGGCCA 192
       |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   122 AATGCCACATCCTCTCCTACTGGCCCTACGGCCTGTCACTGCGGACTAGGTGGCAGAGGCCA 181

Qy   193 ACCCAAAGATGCCACGGACTGGTGCTGCCAGACCCATGACTGCTATGACCACCTGAA 252
       |||||||||||||||||||||||||||||||||||||||||||||||
Db   182 ACCCAAAGATGCCACGGACTGGTGCTGCCAGACCCATGACTGCTCTGCGGACTATGACCACCTGAA 241

Db   242 GACCCAGGGGTGCGGCATCTACAAGGACTATTACAGATACAACTTTTCCCAGGGGGAACAT 301
           ||||||||||||||||||||||||||||||||||||||||||||||||
Qy   253 GACCCAGGGGTGCGGCATCTACAAGGACTATTACAGATACAACTTTTCCCAGGGGAACAT 312

Qy   313 CCACTGCTCTGACAAGGAAGCTGGTGTGAGCAGCAGCAGTTGGTCGTGTGTGCCTGTGACAAGGAGT 372
           |||||||||||||||||||||||||||||||||||||||||||
Db   302 CCACTGCTCTGACAAGGAAGCTGGTGTGAGCAGCAGTTGGTCGTGTGTGCCTGTGACAAGGAGGT 361

Qy   373 GGCCTTCTGCCTGAAGCGCAACCTGACACCTACCAGAAGCGACTGCGTTTCTACTGGCG 432
           |||||||||||||||||||||||||||||||||||||||||||||||
Db   362 GGCCTTCTGCCTGAAGCGCAACCTGACACCTACCAGAAGCGACTGCGTTTCTACTGGCG 421

Qy   433 GCCCCACTGCCGCGGGGGCAGACCCCTGGGTGCTAGAAGCCCACACCCTCTACCCTGTTCCT 492
           ||||||||||||||||||||||||||||||||||||||||||||||
Db   422 GCCCCACTGCCGCGGGGGCAGACCCCTGGGTGCTAGAAGCCCACACCCTCTACCCTGTTCCT 481

Qy   493 CAGCATGGAGCTCTGGCATCCCCACCTCAGTATCTAACCTCAGTATCTAACCTCAGTAAGCCTGGCTTTTCAA 552
           |||||||||||||||||||||||||||||||||||||||||||||
Db   482 CAGCATGGAGCTCTGGCATCCCCACCTCAGTATCTAACCTCAGTAAGCCTGGCTTTTCAA 541

Qy   553 ACACTCCGGGGGAGTAGTCCCAGCCTCCCCCGGAACCC 592
           |||||||||||||||||||||||||||||||||||||
Db   542 ACACTCCGGGGGAGTAGTCCCAGCCTCCCCCGGAACCC 581

RESULT 3
US-09-835-996A-5
; Sequence 5, Application US/09835996A
; Patent No. US20020142953A1
; GENERAL INFORMATION:
;   APPLICANT: Ballinger, Dennis
;   APPLICANT: Loeb, Debra
;   APPLICANT: Montgomery, Julie
;   APPLICANT: Tang, Y. Tom
;   APPLICANT: Zhou, Ping
;   APPLICANT: Goodrich, Ryle
;   APPLICANT: Liu, Chenghua
;   APPLICANT: Asundi, Vinod
;   APPLICANT: Zhao, Qing
;   APPLICANT: Wehrman, Tom
;   APPLICANT: Drmanac, Radoje
;   APPLICANT: Ren, Feiyan
;   APPLICANT: Qian, Xiahong
;   APPLICANT: Wang, Dunrui
;   TITLE OF INVENTION: MATERIALS AND METHODS RELATING TO LIPID METABOLISM
;   FILE REFERENCE: 28110/35915A
;   CURRENT APPLICATION NUMBER: US/09/835,996A
;   CURRENT FILING DATE: 2001-04-16
;   PRIOR APPLICATION NUMBER: US 60/197,137
;   PRIOR FILING DATE: 2000-04-14
;   PRIOR APPLICATION NUMBER: US 09/714,936
;   PRIOR FILING DATE: 2000-11-17
;   PRIOR APPLICATION NUMBER: US 09/667,298
;   PRIOR FILING DATE: 2000-09-22
;   PRIOR APPLICATION NUMBER: US 09/631,451
;   PRIOR FILING DATE: 2000-08-03
;   PRIOR APPLICATION NUMBER: US 09/598,042
;   PRIOR FILING DATE: 2000-06-20
;   NUMBER OF SEQ ID NOS: 45
;   SOFTWARE: PatentIn version 3.0
; SEQ ID NO 5
;   LENGTH: 1931
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (18)..(452)
US-09-835-996A-5

Query Match   95.8%;   Score 567.4;   DB 9;   Length 1931;
Best Local Similarity   99.8%;   Pred. No. 3.8e-168;
Matches 568;   Conservative   0;   Mismatches   0;   Indels   1;   Gaps   0;

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Qy    24  GGATCATGGAACTGCACTGCTGCTGTGGTGTGGCTGGTGTGGCTGGTGTGATTCCAATCC  83
              ||||||||||||||||||||||||||||||||| |||| ||||| ||||||||||||||
Db    13  GGACCATGGAACTGCACTGCTGCTGTGGTGTGGGCTGGTGTGGATGGCTGGTGTGATTCCAATCC  72

Qy    84  AGGGCGGGATCCTGAACCTGAACAAGATGGTCAAGCAAGTGACTGGAGAAAATGCCCATCC  143
              ||||||||||||||||||||||||||||||||| |||||||||||||||||||||||||
Db    73  AGGGCGGGATCCTGAACCTGAACAAGATGGTCAAGCAAGTGACTGGGAAAATGCCCATCC  132

Qy   144  TCTCCTACTGGCCCTACGGCTGTCACTGCGGACTAGGTGGCAGAGGCCAACCCAAAGATG  203
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   133  TCTCCTACTGGCCCTACGGCTGTCACTGCGGACTAGGTGGCAGAGGCCAACCCAAAGATG  192

Qy   204  CCACGGACTGGTGCTGCCAGACCCATGACTGCTCTATGACCACCTGAAGACCCAGGGGT  263
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   193  CCACGGACTGGTGCTGCCAGACCCATGACTGCTCTATGACCACCTGAAGACCCAGGGGT  252

Qy   264  GCGGCATCTACAAGGACTATTACAGATACAACTTTTCCCAGGGGAACATCCACTGCTCTG  323
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   253  GCGGCATCTACAAGGACTATTACAGACTATTACAACTTTTCCCAGGGGAACATCCACTGCTCTG  312

Qy   324  ACAAGGGAAGCTGGTGTGAGCAGCAGCTGTGTGCCTGTGACAAGGAGTCGGCCTTCTGCC  383
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   313  ACAAGGGAAGCTGGTGTGAGCAGCAGCTGTGTGCCTGTGACAAGGAGGTGGCCTTCTGCC  372

Qy   384  TGAAGCGCAACCTGGACACCTACCAGAAGGACTGCGTTCTACTGGCCGCCCACTGCC  443
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   373  TGAAGCGCAACCTGGACACCTACCAGAAGCGACTGCGTTTCTACTGGCCGCCCACTGCC  432

Qy   444  GGGGGCAGACCCCTGGGTGCTAGAAGCCACACCCTGTTCCTACCCGTTCCTCCAGCATGGAGC  503
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   433  GGGGGCAGACCCCTGGGTGCTAGAAGCCACACCCTGTTCCTACCCGTTCCTCCAGCATGGAGC  492

Qy   504  TCTGGCATCCCCACCTCAGTATCTAACCTGAACCAGCCTGGCTTTCAAACACTCCGGGG  563
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   493  TCTGGCATCCCCACCTCAGTATCTAACCTGAACCAGCCTGGCTTTCAAACACTCCGGGG  552

Qy   564  GGAGGTAGTCCCAGCCTCCCCCGGAACCC  592
              ||||||||||||||||||||||||||||
Db   553  GGAGGTAGTCCCAGCCTCCCCCGGAACCC  581
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RESULT 4
US-09-946-374-377
; Sequence 377, Application US/09946374
; Publication No. US2003007312 9A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Smith, Victoria
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2830P1C1
; CURRENT APPLICATION NUMBER: US/09/946,374
; CURRENT FILING DATE: 2001-09-04
; PRIOR APPLICATION NUMBER: 60/098716

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;    PRIOR FILING DATE: 1998-09-01
;    PRIOR APPLICATION NUMBER: 60/098723
;    PRIOR FILING DATE: 1998-09-01
;    PRIOR APPLICATION NUMBER: 60/098749
;    PRIOR FILING DATE: 1998-09-01
;    PRIOR APPLICATION NUMBER: 60/098750
;    PRIOR FILING DATE: 1998-09-01
;    PRIOR APPLICATION NUMBER: 60/098803
;    PRIOR FILING DATE: 1998-09-02
;    PRIOR APPLICATION NUMBER: 60/098821
;    PRIOR FILING DATE: 1998-09-02
;    PRIOR APPLICATION NUMBER: 60/098843
;    PRIOR FILING DATE: 1998-09-02
;    PRIOR APPLICATION NUMBER: 60/099536
;    PRIOR FILING DATE: 1998-09-09
;    PRIOR APPLICATION NUMBER: 60/099596
;    PRIOR FILING DATE: 1998-09-09
;    PRIOR APPLICATION NUMBER: 60/099598
;    PRIOR FILING DATE: 1998-09-09
;    PRIOR APPLICATION NUMBER: 60/099602
;    PRIOR FILING DATE: 1998-09-09
;    PRIOR APPLICATION NUMBER: 60/099642
;    PRIOR FILING DATE: 1998-09-09
;    PRIOR APPLICATION NUMBER: 60/099741
;    PRIOR FILING DATE: 1998-09-10
;    PRIOR APPLICATION NUMBER: 60/099754
;    PRIOR FILING DATE: 1998-09-10
;    PRIOR APPLICATION NUMBER: 60/099763
;    PRIOR FILING DATE: 1998-09-10
;    PRIOR APPLICATION NUMBER: 60/099792
;    PRIOR FILING DATE: 1998-09-10
;    PRIOR APPLICATION NUMBER: 60/099808
;    PRIOR FILING DATE: 1998-09-10
;    PRIOR APPLICATION NUMBER: 60/099812
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;    PRIOR APPLICATION NUMBER: 60/099815
;    PRIOR FILING DATE: 1998-09-10
;    PRIOR APPLICATION NUMBER: 60/099816
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;    PRIOR APPLICATION NUMBER: 60/100385
;    PRIOR FILING DATE: 1998-09-15
;    PRIOR APPLICATION NUMBER: 60/100388
;    PRIOR FILING DATE: 1998-09-15
;    PRIOR APPLICATION NUMBER: 60/100390
;    PRIOR FILING DATE: 1998-09-15
;    PRIOR APPLICATION NUMBER: 60/100584
;    PRIOR FILING DATE: 1998-09-16
;    PRIOR APPLICATION NUMBER: 60/100627
;    PRIOR FILING DATE: 1998-09-16
;    PRIOR APPLICATION NUMBER: 60/100661
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;    PRIOR FILING DATE: 1998-09-16
;    PRIOR APPLICATION NUMBER: 60/100664
;    PRIOR FILING DATE: 1998-09-16
;    PRIOR APPLICATION NUMBER: 60/100683
;    PRIOR FILING DATE: 1998-09-17
;    PRIOR APPLICATION NUMBER: 60/100684
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;    PRIOR FILING DATE: 1998-09-17
;    PRIOR APPLICATION NUMBER: 60/100711
;    PRIOR FILING DATE: 1998-09-17
;    PRIOR APPLICATION NUMBER: 60/100848
;    PRIOR FILING DATE: 1998-09-18
;    PRIOR APPLICATION NUMBER: 60/100849
;    PRIOR FILING DATE: 1998-09-18
;    PRIOR APPLICATION NUMBER: 60/100919
;    PRIOR FILING DATE: 1998-09-17
;    PRIOR APPLICATION NUMBER: 60/100930
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;    PRIOR APPLICATION NUMBER: 60/101014
;    PRIOR FILING DATE: 1998-09-18
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; PRIOR APPLICATION NUMBER: 60/101068
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/101071
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/101279
; PRIOR FILING DATE: 1998-09-22
; PRIOR APPLICATION NUMBER: 60/101471
; PRIOR FILING DATE: 1998-09-23
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; PRIOR APPLICATION NUMBER: 60/101474
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; PRIOR FILING DATE: 1998-09-24
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; PRIOR FILING DATE: 1998-09-24
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; PRIOR FILING DATE: 1998-09-24
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; PRIOR FILING DATE: 1998-09-29
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; PRIOR FILING DATE: 1998-09-29
; PRIOR APPLICATION NUMBER: 60/102484
; PRIOR FILING DATE: 1998-09-30
; PRIOR APPLICATION NUMBER: 60/102487
; PRIOR FILING DATE: 1998-09-30
; PRIOR APPLICATION NUMBER: 60/102570
; PRIOR FILING DATE: 1998-09-30
; PRIOR APPLICATION NUMBER: 60/102571
; PRIOR FILING DATE: 1998-09-30
; PRIOR APPLICATION NUMBER: 60/102684
; PRIOR FILING DATE: 1998-10-01
; PRIOR APPLICATION NUMBER: 60/102687
; PRIOR FILING DATE: 1998-10-01
; PRIOR APPLICATION NUMBER: 60/102965
; PRIOR FILING DATE: 1998-10-02
; PRIOR APPLICATION NUMBER: 60/103258
; PRIOR FILING DATE: 1998-10-06
; PRIOR APPLICATION NUMBER: 60/103314
; PRIOR FILING DATE: 1998-10-07
; PRIOR APPLICATION NUMBER: 60/103315
; PRIOR FILING DATE: 1998-10-07
; PRIOR APPLICATION NUMBER: 60/103328
; PRIOR FILING DATE: 1998-10-07
; PRIOR APPLICATION NUMBER: 60/103395
; PRIOR FILING DATE: 1998-10-07
; PRIOR APPLICATION NUMBER: 60/103396
; PRIOR FILING DATE: 1998-10-07
; PRIOR APPLICATION NUMBER: 60/103401
; PRIOR FILING DATE: 1998-10-07
; PRIOR APPLICATION NUMBER: 60/103449
; PRIOR FILING DATE: 1998-10-06
; PRIOR APPLICATION NUMBER: 60/103633
; PRIOR FILING DATE: 1998-10-08
; PRIOR APPLICATION NUMBER: 60/103678

; PRIOR FILING DATE: 1998-10-08
; PRIOR APPLICATION NUMBER: 60/103679
; PRIOR FILING DATE: 1998-10-08
; PRIOR APPLICATION NUMBER: 60/103711
; PRIOR FILING DATE: 1998-10-08
; PRIOR APPLICATION NUMBER: 60/104257
; PRIOR FILING DATE: 1998-10-14
; PRIOR APPLICATION NUMBER: 60/104987
; PRIOR FILING DATE: 1998-10-20
; PRIOR APPLICATION NUMBER: 60/105000
; PRIOR FILING DATE: 1998-10-20
; PRIOR APPLICATION NUMBER: 60/105002
; PRIOR FILING DATE: 1998-10-20
; PRIOR APPLICATION NUMBER: 60/105104
; PRIOR FILING DATE: 1998-10-21
; PRIOR APPLICATION NUMBER: 60/105169
; PRIOR FILING DATE: 1998-10-22
; PRIOR APPLICATION NUMBER: 60/105266
; PRIOR FILING DATE: 1998-10-22
; PRIOR APPLICATION NUMBER: 60/105693
; PRIOR FILING DATE: 1998-10-26
; PRIOR APPLICATION NUMBER: 60/105694
; PRIOR FILING DATE: 1998-10-26
; PRIOR APPLICATION NUMBER: 60/105807

Query Match   48.0%; Score 284.2; DB 10; Length 496;
Best Local Similarity   97.3%; Pred. No. 4.4e-79;
Matches 289; Conservative   0; Mismatches   8; Indels   0; Gaps   0;

Qy   1 TCTGCCTCCACTGCTCTGTGCTGGGATCATGGAACTTGCACTGCTGTGTGGGCTGGTGGT   60
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 TCTGCCTCCACTGCTCTGTGCTGGGATCATGGAACTTGCACTGCTGTGTGGGCTGGTGGT   60

Qy   61 GATGGCTGGTGTGATTCCAATCCAGGGCGGATCCTGAACCTGAACAAGATGGTCAAGCA 120
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 GATGGCTGGTGTGATTCCAATCCAGGGCGGATCCTGAACCTGAACAAGATGGTCAAGCA 120

Qy   121 AGTGACTGGGAAAATGCCATCCTCCTACTGCCCTACGGCGTGTCACTGCGGACTAGG 180
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121 AGTGACTGGGAAAATGCCATCCTCCTACTGCCCTACGGCGTGTCACTGCGGACTAGG 180

Qy   181 TGGCAGAGGCCAACCCAAAGATGCCACGGACTGGTGCTGCCAGACCCATGACTGCTGCTA 240
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181 TGGCAGAGGCCAACCCAAAGATGCCACGGACTGGTGCTGCCAGACCCATGACTGCTGCTA 240

Qy   241 TGACCACCTGAAGACCCAGGGGTGCGGCATCTACAAGGACTATTACAGATACAACTT 297
         || ||| ||||||||||||||||||||||||||||||||||| ||| ||||||||||
Db   241 TGACCACCTGAAGACCCAGGGGTGCGGCATCTACAAGGACAACAACAAAAGCAGCAT 297

RESULT 5
US-10-015-395A-377
; Sequence 377, Application US/10015395A5
; Publication No. US20040073015A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan l.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2830P1C57
; CURRENT APPLICATION NUMBER: US/10/015,395A

; CURRENT FILING DATE: 2001-12-12
; Prior application removed - See file Wrapper or Palm
; NUMBER OF SEQ ID NOS: 477
; SEQ ID NO 377
; LENGTH: 496
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: unsure
; LOCATION: 396
; OTHER INFORMATION: unknown base
US-10-015-395A-377

Query Match   48.0%; Score 284.2; DB 12; Length 496;
Best Local Similarity 97.3%; Pred. No. 4.4e-79;
Matches 289; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Qy   1 TCTGCCTCCACTGCTCTGTGCTGCTGGGATCATGGAACTTGCACTGCTGTGTGGGGCTGGTGGT 60
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 TCTGCCTCCACTGCTCTGTGCTGCTGGGATCATGGAACTTGCACTGCTGTGTGGGGCTGGTGGT 60

Qy   61 GATGGCTGGTGTGATTCCAATCCAGGGCGGATCCTGAACCTGAACAAGATGGTCAAGCA 120
         ||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 GATGGCTGGTGTGATTCCAATCCAGGGCGGATCCTGAACCTGAACAAGATGGTCAAGCA 120

Qy 121 AGTGACTGGGAAAATGCCCATCCTCTCCTACTGGCCCTACGGCTGTCACTGCGGACTAGG 180
         ||||||||||||||||||||||||||||||||||||||||||||||||||
Db 121 AGTGACTGGGAAAATGCCCATCCTCTCCTACTGGCCCTACGGCTGTCACTGCGGACTAGG 180

Qy 181 TGGCAGAGGCCAACCCAAAGATGCCACGGACTGGTGCTGCCAGACCCATGACTGCTGCTA 240
         ||||||||||||||||||||||||||||||||||||||||||||||||||
Db 181 TGGCAGAGGCCAACCCAAAGATGCCACGGACTGGTGCTGCCAGACCCATGACTGCTGCTA 240

Qy 241 TGACCACCTGAAGACCCAGGGGTGCGGCATCTACAAGGACTATTACAGATACAACT 297
         |||||||||||||||||||||||||||| ||| |||
Db 241 TGACCACCTGAAGACCCAGGGGTGCGGCATCTACAAGGACAACAACAAAAGCAGCAT 297

RESULT 6
US-10-147-493-533
; Sequence 533, Application US/10147493
; Publication No. US20040029217A1
; GENERAL INFORMATION:
; APPLICANT: Baker,Kevin P.
; APPLICANT: Beresini,Maureen
; APPLICANT: DeForge,Laura
; APPLICANT: Desnoyers,Luc
; APPLICANT: Filvaroff,Ellen
; APPLICANT: Gao,Wei-Qiang
; APPLICANT: Gerritsen,Mary E.
; APPLICANT: Goddard,Audrey
; APPLICANT: Godowski,Paul J.
; APPLICANT: Gurney,Austin L.
; APPLICANT: Sherwood,Steven
; APPLICANT: Smith,Victoria
; APPLICANT: Stewart,Timothy A.
; APPLICANT: Tumas,Daniel
; APPLICANT: Watanabe,Colin K
; APPLICANT: Wood,William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3330R1C345
; CURRENT APPLICATION NUMBER: US/10/147,493
; CURRENT FILING DATE: 2002-05-17
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 533
; LENGTH: 496
; TYPE: DNA
; ORGANISM: Homo Sapien
; FEATURE:
; NAME/KEY: unsure

; LOCATION: 396
; OTHER INFORMATION: unknown base
US-10-147-493-533

Query Match   48.0%; Score 284.2; DB 13; Length 496;
Best Local Similarity 97.3%; Pred. No. 4.4e-79;
Matches 289; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Qy   1 TCTGCCTCCACTGCTCTGTGCTGCTGGGATCATGGAACTTGCACTGCTGTGTGGGGCTGGTGGT 60
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 TCTGCCTCCACTGCTCTGTGCTGCTGGGATCATGGAACTTGCACTGCTGTGTGGGGCTGGTGGT 60

Qy   61 GATGGCTGGTGTGATTCCAATCCAGGGCGGATCCTGAACCTGAACAAGATGGTCAAGCA 120
         ||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 GATGGCTGGTGTGATTCCAATCCAGGGCGGATCCTGAACCTGAACAAGATGGTCAAGCA 120

Qy 121 AGTGACTGGGAAAATGCCCATCCTCTCCTACTGGCCCTACGGCTGTCACTGCGGACTAGG 180
         ||||||||||||||||||||||||||||||||||||||||||||||||||
Db 121 AGTGACTGGGAAAATGCCCATCCTCTCCTACTGGCCCTACGGCTGTCACTGCGGACTAGG 180

Qy 181 TGGCAGAGGCCAACCCAAAGATGCCACGGACTGGTGCTGCCAGACCCATGACTGCTGCTA 240
         ||||||||||||||||||||||||||||||||||||||||||||||||||
Db 181 TGGCAGAGGCCAACCCAAAGATGCCACGGACTGGTGCTGCCAGACCCATGACTGCTGCTA 240

Qy 241 TGACCACCTGAAGACCCAGGGGTGCGGCATCTACAAGGACTATTACAGATACAACTT 297
         |||||||||||||||||||||||||||| ||| |||
Db 241 TGACCACCTGAAGACCCAGGGGTGCGGCATCTACAAGGACAACAACAAAAGCAGCAT 297

RESULT 7
US-10-145-127-533
; Sequence 533, Application US/10145127
; Publication No. US2004003358A1
; GENERAL INFORMATION:
; APPLICANT: Baker,Kevin P.
; APPLICANT: Beresini,Maureen
; APPLICANT: DeForge,Laura
; APPLICANT: Desnoyers,Luc
; APPLICANT: Filvaroff,Ellen
; APPLICANT: Gao,Wei-Qiang
; APPLICANT: Gerritsen,Mary E.
; APPLICANT: Goddard,Audrey
; APPLICANT: Godowski,Paul J.
; APPLICANT: Gurney,Austin L.
; APPLICANT: Sherwood,Steven
; APPLICANT: Smith,Victoria
; APPLICANT: Stewart,Timothy A.
; APPLICANT: Tumas,Daniel
; APPLICANT: Watanabe,Colin K
; APPLICANT: Wood,William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3330R1C252
; CURRENT APPLICATION NUMBER: US/10/145,127
; CURRENT FILING DATE: 2002-05-13
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 533
; LENGTH: 496
; TYPE: DNA
; ORGANISM: Homo Sapien
; FEATURE:
; NAME/KEY: unsure
; LOCATION: 396
; OTHER INFORMATION: unknown base
US-10-145-127-533

Query Match   48.0%; Score 284.2; DB 13; Length 496;
Best Local Similarity 97.3%; Pred. No. 4.4e-79;
Matches 289; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Qy   1 TCTGCCTCCACTGCTCTGTGCTGCTGGGATCATGGAACTTGCACTGCTGTGTGGGGCTGGTGGT 60

Left column

```
Db             |||||||||||||||||||||||||||||||||||||||||||||
Qy     1  TCTGCCTCCACTGCTCTGTGCTGGATCATGGAACTTGCACTGCTGTGTGGCTGGTGGT   60

Db    61  GATGGCTGGTGTGATTCCAATCCAGGGCGGATCATCCAGGCCGGGATCATGGAACTTGCACTGCTGAACCTGAACCTGGTCAAGCA  120
Qy    61  GATGGCTGGTGTGATTCCAATCCAGGGCGGATCATCCAGGCCGGGATCATGGAACTTGCACTGCTGAACCTGAACCTGGTCAAGCA  120

Db   121  AGTGACTGGGAAAATGCCCATCTCCTCCTACTGGCCCTACGGCTGTCACTGCGGACTAGG  180
Qy   121  AGTGACTGGGAAAATGCCCATCTCCTCCTACTGGCCCTACGGCTGTCACTGCGGACTAGG  180

Db   181  TGGCAGAGGCCAACCCAAAGATGCCACGGACTGGTGCTGCCAGACCCATGACTGCTGCTA  240
Qy   181  TGGCAGAGGCCAACCCAAAGATGCCACGGACTGGTGCTGCCAGACCCATGACTGCTGCTA  240

Db   241  TGACCACCTGAAGACCCAGGGGTGCGGCATCTACAAGGACTATTACAGATACAACTT  297
Qy   241  TGACCACCTGAAGACCCAGGGGTGCGGCATCTACAAGGACTATTACAGATACAACTT  297
```

RESULT 8

US-10-160-503-533

; Sequence 533, Application US/10160503
; Publication No. US20040033559A1
; GENERAL INFORMATION:
;   APPLICANT: Baker,Kevin P.
;   APPLICANT: Beresini,Maureen
;   APPLICANT: DeForge,Laura
;   APPLICANT: Desnoyers,Luc
;   APPLICANT: Filvaroff,Ellen
;   APPLICANT: Gao,Wei-Qiang
;   APPLICANT: Gerritsen,Mary E.
;   APPLICANT: Goddard,Audrey
;   APPLICANT: Godowski,Paul J.
;   APPLICANT: Gurney,Austin L.
;   APPLICANT: Sherwood,Steven
;   APPLICANT: Smith,Victoria
;   APPLICANT: Stewart,Timothy A.
;   APPLICANT: Tumas,Daniel
;   APPLICANT: Watanabe,Colin K
;   APPLICANT: Wood,William
;   APPLICANT: Zhang, Zemin
;   TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
;   TITLE OF INVENTION: ACIDS ENCODING THE SAME
;   FILE REFERENCE: P3330R1C446
;   CURRENT APPLICATION NUMBER: US/10/160,503
;   CURRENT FILING DATE: 2002-05-30
;   NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 533
;   LENGTH: 496
;   TYPE: DNA
;   ORGANISM: Homo Sapien
;   FEATURE:
;   NAME/KEY: unsure
;   LOCATION: 396
;   OTHER INFORMATION: unknown base

US-10-160-503-533

Query Match   48.0%;   Score 284.2;   DB 13;   Length 496;
Best Local Similarity   97.3%;   Pred. No. 4.4e-79;
Matches   289;   Conservative   0;   Mismatches   8;   Indels   0;   Gaps   0;

```
Qy     1  TCTGCCTCCACTGCTCTGTGCTGGATCATGGAACTTGCACTGCTGTGTGGCTGGTGGT   60
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1  TCTGCCTCCACTGCTCTGTGCTGGATCATGGAACTTGCACTGCTGTGTGGCTGGTGGT   60

Qy    61  GATGGCTGGTGTGATTCCAATCCAGGGCGGATCATCCAGGCCGGGATCATGGAACTTGCACTGCTGAACCTGAACCTGGTCAAGCA  120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    61  GATGGCTGGTGTGATTCCAATCCAGGGCGGATCATCCAGGCCGGGATCATGGAACAAGATGGTCAAGCA  120

Qy   121  AGTGACTGGGAAAATGCCCATCTCCTCCTACTGGCCCTACGGCTGTCACTGCGGACTAGG  180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121  AGTGACTGGGAAAATGCCCATCTCCTCCTACTGGCCCTACGGCTGTCACTGCGGACTAGG  180
```

Right column

```
Qy   181  TGGCAGAGGCCAACCCAAAGATGCCACGGACTGGTGCTGCCAGACCCATGACTGCTGCTA  240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181  TGGCAGAGGCCAACCCAAAGATGCCACGGACTGGTGCTGCCAGACCCATGACTGCTGCTA  240

Qy   241  TGACCACCTGAAGACCCAGGGGTGCGGCATCTACAAGGACTATTACAGATACAACTT  297
          ||||||||||||||||||||||||||||||||| |||  |||||||||||
Db   241  TGACCACCTGAAGACCCAGGGGTGCGGCATCTACAAGGACAACAACAAAAGCAGCAT  297
```

RESULT 9

US-10-143-118-533

; Sequence 533, Application US/10143118
; Publication No. US20040038335A1
; GENERAL INFORMATION:
;   APPLICANT: Baker,Kevin P.
;   APPLICANT: Beresini,Maureen
;   APPLICANT: DeForge,Laura
;   APPLICANT: Desnoyers,Luc
;   APPLICANT: Filvaroff,Ellen
;   APPLICANT: Gao,Wei-Qiang
;   APPLICANT: Gerritsen,Mary E.
;   APPLICANT: Goddard,Audrey
;   APPLICANT: Godowski,Paul J.
;   APPLICANT: Gurney,Austin L.
;   APPLICANT: Sherwood,Steven
;   APPLICANT: Smith,Victoria
;   APPLICANT: Stewart,Timothy A.
;   APPLICANT: Tumas,Daniel
;   APPLICANT: Watanabe,Colin K
;   APPLICANT: Wood,William
;   APPLICANT: Zhang, Zemin
;   TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
;   TITLE OF INVENTION: ACIDS ENCODING THE SAME
;   FILE REFERENCE: P3330R1C228
;   CURRENT APPLICATION NUMBER: US/10/143,118
;   CURRENT FILING DATE: 2002-05-09
;   Prior Application removed - See Palm or File Wrapper
;   NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 533
;   LENGTH: 496
;   TYPE: DNA
;   ORGANISM: Homo Sapien
;   FEATURE:
;   NAME/KEY: unsure
;   LOCATION: 396
;   OTHER INFORMATION: unknown base

US-10-143-118-533

Query Match   48.0%;   Score 284.2;   DB 13;   Length 496;
Best Local Similarity   97.3%;   Pred. No. 4.4e-79;
Matches   289;   Conservative   0;   Mismatches   8;   Indels   0;   Gaps   0;
```

```
Qy     1  TCTGCCTCCACTGCTCTGTGCTGGATCATGGAACTTGCACTGCTGTGTGGCTGGTGGT   60
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1  TCTGCCTCCACTGCTCTGTGCTGGATCATGGAACTTGCACTGCTGTGTGGCTGGTGGT   60

Qy    61  GATGGCTGGTGTGATTCCAATCCAGGGCGGATCATCCAGGCCGGGATCATGGTCAAGCA  120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    61  GATGGCTGGTGTGATTCCAATCCAGGGCGGATCATCCAGGCCGGGATCATGGAACAAGATGGTCAAGCA  120

Qy   121  AGTGACTGGGAAAATGCCCATCTCCTCCTACTGGCCGTCGTCACTGCGGACTAGG  180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121  AGTGACTGGGAAAATGCCCATCTCCTCCTACTGGCCGTCGTCACTGCGGACTAGG  180

Qy   181  TGGCAGAGGCCAACCCAAAGATGCCACGGACTGGTGCTGCCAGACCCATGACTGCTGCTA  240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181  TGGCAGAGGCCAACCCAAAGATGCCACGGACTGGTGCTGCCAGACCCATGACTGCTGCTA  240

Qy   241  TGACCACCTGAAGACCCAGGGGTGCGGCATCTACAAGGACTATTACAGATACAACTT  297
          ||||||||||||||||||||||||||||||||| |||  |||||||||||
Db   241  TGACCACCTGAAGACCCAGGGGTGCGGCATCTACAAGGACAACAACAAAAGCAGCAT  297
```

RESULT 10
US-10-144-993-533
; Sequence 533, Application US/10144993
; Publication No. US20040038336A1
; GENERAL INFORMATION:
; APPLICANT: Baker,Kevin P.
; APPLICANT: Beresini,Maureen
; APPLICANT: DeForge,Laura
; APPLICANT: Desnoyers,Luc
; APPLICANT: Filvaroff,Ellen
; APPLICANT: Gao,Wei-Qiang
; APPLICANT: Gerritsen,Mary E.
; APPLICANT: Goddard,Audrey
; APPLICANT: Godowski,Paul J.
; APPLICANT: Gurney,Austin L.
; APPLICANT: Sherwood,Steven
; APPLICANT: Smith,Victoria
; APPLICANT: Stewart,Timothy A.
; APPLICANT: Tumas,Daniel
; APPLICANT: Watanabe,Colin K
; APPLICANT: Wood,William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3330R1C261
; CURRENT APPLICATION NUMBER: US/10/144,993
; CURRENT FILING DATE: 2002-05-13
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 533
; LENGTH: 496
; TYPE: DNA
; ORGANISM: Homo Sapien
; FEATURE:
; NAME/KEY: unsure
; LOCATION: 396
; OTHER INFORMATION: unknown base
US-10-144-993-533

Query Match   48.0%; Score 284.2; DB 13; Length 496;
Best Local Similarity 97.3%; Pred. No. 4.4e-79;
Matches 289; Conservative 0; Mismatches 8; Indels 8; Gaps 0;

```
Qy       1 TCTGCCTCCACTGCTCTGTGCTGGATCATGGAACTTGCACTGCTGTGTGGGCGTGGTGGT 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 TCTGCCTCCACTGCTCTGTGCTGGATCATGGAACTTGCACTGCTGTGTGGGCGTGGTGGT 60

Qy      61 GATGGCTGGTGTGATTCAATCCAGGGCGGGATCCTGAACAAGATGGTCAAGCA 120
           |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 GATGGCTGGTGTGATTCAATCCAGGGCGGGATCCTGAACAAGATGGTCAAGCA 120

Qy     121 AGTGACTGGGAAAATGCCCATCCTCCTACTGGCCCTACGGCTGTCACTGCCGGACTAGG 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 AGTGACTGGGAAAATGCCCATCCTCCTACTGGCCCTACGGCTGTCACTGCCGGACTAGG 180

Qy     181 TGGCAGAGGCCAACCCAAAGATGCCACGGACTGGTGCTGCCAGACCCATGACTGCTGCTA 240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     181 TGGCAGAGGCCAACCCAAAGATGCCACGGACTGGTGCTGCCAGACCCATGACTGCTGCTA 240

Qy     241 TGACCACCTGAAGACCCAGGGGTGCGGCATCTACAAGGACTATTACAGATACAACTT 297
           ||||||||||||||||||||||||||||||||||||||||| |  ||   ||| ||
Db     241 TGACCACCTGAAGACCCAGGGGTGCGGCATCTACAAGGACAACAACAAAAGCAGCAT 297
```

; APPLICANT: Desnoyers,Luc
; APPLICANT: Filvaroff,Ellen
; APPLICANT: Gao,Wei-Qiang
; APPLICANT: Gerritsen,Mary E.
; APPLICANT: Goddard,Audrey
; APPLICANT: Godowski,Paul J.
; APPLICANT: Gurney,Austin L.
; APPLICANT: Sherwood,Steven
; APPLICANT: Smith,Victoria
; APPLICANT: Stewart,Timothy A.
; APPLICANT: Tumas,Daniel
; APPLICANT: Watanabe,Colin K
; APPLICANT: Wood,William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3330R1C449
; CURRENT APPLICATION NUMBER: US/10/158,787
; CURRENT FILING DATE: 2003-04-03
; PRIOR APPLICATION NUMBER: 60/049911
; PRIOR FILING DATE: 1997-06-18
; PRIOR APPLICATION NUMBER: 60/056974
; PRIOR FILING DATE: 1997-08-26
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059115
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059117
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059122
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059184
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059352
; PRIOR FILING DATE: 1997-09-19
; PRIOR APPLICATION NUMBER: 60/059588
; PRIOR FILING DATE: 1997-09-19
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 533
; LENGTH: 496
; TYPE: DNA
; ORGANISM: Homo Sapien
; FEATURE:
; NAME/KEY: unsure
; LOCATION: 396
; OTHER INFORMATION: unknown base
US-10-158-787-533

Query Match   48.0%; Score 284.2; DB 13; Length 496;
Best Local Similarity 97.3%; Pred. No. 4.4e-79;
Matches 289; Conservative 0; Mismatches 8; Indels 8; Gaps 0;

```
Qy       1 TCTGCCTCCACTGCTCTGTGCTGGATCATGGAACTTGCACTGCTGTGTGGGCGTGGTGGT 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 TCTGCCTCCACTGCTCTGTGCTGGATCATGGAACTTGCACTGCTGTGTGGGCGTGGTGGT 60

Qy      61 GATGGCTGGTGTGATTCAATCCAGGGCGGGATCCTGAACAAGATGGTCAAGCA 120
           |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 GATGGCTGGTGTGATTCAATCCAGGGCGGGATCCTGAACAAGATGGTCAAGCA 120

Qy     121 AGTGACTGGGAAAATGCCCATCCTCCTACTGGCCCTACGGCTGTCACTGCCGGACTAGG 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 AGTGACTGGGAAAATGCCCATCCTCCTACTGGCCCTACGGCTGTCACTGCCGGACTAGG 180

Qy     181 TGGCAGAGGCCAACCCAAAGATGCCACGGACTGGTGCTGCCAGACCCATGACTGCTGCTA 240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     181 TGGCAGAGGCCAACCCAAAGATGCCACGGACTGGTGCTGCCAGACCCATGACTGCTGCTA 240

Qy     241 TGACCACCTGAAGACCCAGGGGTGCGGCATCTACAAGGACTATTACAGATACAACTT 297
           ||||||||||||||||||||||||||||||||||||||||| |  ||   |||  ||
```

RESULT 11
US-10-158-787-533
; Sequence 533, Application US/10158787
; Publication No. US20040039164A1
; GENERAL INFORMATION:
; APPLICANT: Baker,Kevin P.
; APPLICANT: Beresini,Maureen
; APPLICANT: DeForge,Laura

Db   241 TGACCACCTGAAGACCCAGGGGTGCGGCATCTACAAGGACAACAACAAAGCAGCAT 297

RESULT 12
US-10-140-024-533
; Sequence 533, Application US/10140024
; Publication No. US20040058424A1
; GENERAL INFORMATION:
; APPLICANT: Baker,Kevin P.
; APPLICANT: Beresini,Maureen
; APPLICANT: DeForge,Laura
; APPLICANT: Desnoyers,Luc
; APPLICANT: Filvaroff,Ellen
; APPLICANT: Gao,Wei-Qiang
; APPLICANT: Gerritsen,Mary E.
; APPLICANT: Goddard,Audrey
; APPLICANT: Godowski,Paul J.
; APPLICANT: Gurney,Austin L.
; APPLICANT: Sherwood,Steven
; APPLICANT: Smith,Victoria
; APPLICANT: Stewart,Timothy A.
; APPLICANT: Tumas,Daniel
; APPLICANT: Watanabe,Colin K
; APPLICANT: Wood,William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3330R1C69
; CURRENT APPLICATION NUMBER: US/10/140,024
; CURRENT FILING DATE: 2002-05-06
; Prior Application removed - See Palm or File Wrapper
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 533
; LENGTH: 496
; TYPE: DNA
; ORGANISM: Homo Sapien
; FEATURE:
; NAME/KEY: unsure
; LOCATION: 396
; OTHER INFORMATION: unknown base
US-10-140-024-533

Query Match   48.0%; Score 284.2; DB 13; Length 496;
Best Local Similarity   97.3%; Pred. No. 4.4e-79;
Matches   289; Conservative   0; Mismatches   8; Indels   0; Gaps   0;

Qy   1 TCTGCCTCCACTGCTCTGTGCTGGGATCATGGAACTTGCACTGCTGTGTGGGCTGGTGGT   60
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 TCTGCCTCCACTGCTCTGTGCTGGGATCATGGAACTTGCACTGCTGTGTGGGCTGGTGGT   60

Qy   61 GATGGCTGGTGTGATTCCAATCCAGGGCGGGATCCTGAACCTGAACAAGATGGTCAAGCA 120
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 GATGGCTGGTGTGATTCCAATCCAGGGCGGGATCCTGAACCTGAACAAGATGGTCAAGCA 120

Qy   121 AGTGACTGGGAAAATGCCCATCCTCTTCCTACTGGCCGTGTCACTGCGGACTAGG   180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121 AGTGACTGGGAAAATGCCCATCCTCTTCCTACTGGCCGTGTCACTGCGGACTAGG   180

Qy   181 TGGCAGAGGCCAACCCAAAGATGCCACGGACCCATGGTGCTGCCAGACCCATGACTGCTGCTA 240
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181 TGGCAGAGGCCAACCCAAAGATGCCACGGACCCATGGTGCTGCCAGACCCATGACTGCTGCTA 240

Qy   241 TGACCACCTGAAGACCCAGGGGTGCGGCATCTACAAGGACTATTACAGATACAACTT   297
          ||||||||||||||||||||||||||||||||||| ||| || ||||||||||||||
Db   241 TGACCACCTGAAGACCCAGGGGTGCGGCATCTACAAGGACAACAACAAAGCAGCAT   297

RESULT 13
US-10-140-808-533
; Sequence 533, Application US/10140808
; Publication No. US20030017563A1
; GENERAL INFORMATION:
; APPLICANT: Baker,Kevin P.

APPLICANT: Beresini,Maureen
APPLICANT: DeForge,Laura
APPLICANT: Desnoyers,Luc
APPLICANT: Filvaroff,Ellen
APPLICANT: Gao,Wei-Qiang
APPLICANT: Gerritsen,Mary E.
APPLICANT: Goddard,Audrey
APPLICANT: Godowski,Paul J.
APPLICANT: Gurney,Austin L.
APPLICANT: Sherwood,Steven
APPLICANT: Smith,Victoria
APPLICANT: Stewart,Timothy A.
APPLICANT: Tumas,Daniel
APPLICANT: Watanabe,Colin K
APPLICANT: Wood,William
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3330R1C182
CURRENT APPLICATION NUMBER: US/10/140,808
CURRENT FILING DATE: 2002-05-07
Prior Application removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 550
SEQ ID NO 533
LENGTH: 496
TYPE: DNA
ORGANISM: Homo Sapien
FEATURE:
NAME/KEY: unsure
LOCATION: 396
OTHER INFORMATION: unknown base
US-10-140-808-533

Query Match   48.0%; Score 284.2; DB 13; Length 496;
Best Local Similarity   97.3%; Pred. No. 4.4e-79;
Matches   289; Conservative   0; Mismatches   8; Indels   0; Gaps   0;

Qy   1 TCTGCCTCCACTGCTCTGTGCTGGGATCATGGAACTTGCACTGCTGTGTGTGGGCTGGTGGT   60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 TCTGCCTCCACTGCTCTGTGCTGGGATCATGGAACTTGCACTGCTGTGTGTGGGCTGGTGGT   60

Qy   61 GATGGCTGGTGTGATTCCAATCCAGGGCGGGATCCTGAACCTGAACAAGATGGTCAAGCA 120
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 GATGGCTGGTGTGATTCCAATCCAGGGCGGGATCCTGAACCTGAACAAGATGGTCAAGCA 120

Qy   121 AGTGACTGGGAAAATGCCCATCCTCTTCCTACTGGCCGTGTCACTGCGGACTAGG   180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121 AGTGACTGGGAAAATGCCCATCCTCTTCCTACTGGCCGTGTCACTGCGGACTAGG   180

Qy   181 TGGCAGAGGCCAACCCAAAGATGCCAACCCAAAGATGCCACGGACCCATGACTGCTGCTA 240
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181 TGGCAGAGGCCAACCCAAAGATGCCAACCCAAAGATGCCACGGACCCATGACTGCTGCTA 240

Qy   241 TGACCACCTGAAGACCCAGGGGTGCGGCATCTACAAGGACTATTACAGATACAACTT   297
          ||||||||||||||||||||||||||||||||||| ||| || ||||||||||||||
Db   241 TGACCACCTGAAGACCCAGGGGTGCGGCATCTACAAGGACAACAACAAAGCAGCAT   297

RESULT 14
US-10-006-485A-377
; Sequence 377, Application US/10006485A
; Publication No. US20030064062A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan 1.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.

APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2830P1C9
CURRENT APPLICATION NUMBER: US/10/006,485A
CURRENT FILING DATE: 2001-12-06
PRIOR APPLICATION NUMBER: 60/098716
PRIOR FILING DATE: 1998-09-01
PRIOR APPLICATION NUMBER: 60/098723
PRIOR FILING DATE: 1998-09-01
PRIOR APPLICATION NUMBER: 60/098749
PRIOR FILING DATE: 1998-09-01
PRIOR APPLICATION NUMBER: 60/098750
PRIOR FILING DATE: 1998-09-01
PRIOR APPLICATION NUMBER: 60/098803
PRIOR FILING DATE: 1998-09-02
PRIOR APPLICATION NUMBER: 60/098821
PRIOR FILING DATE: 1998-09-02
PRIOR APPLICATION NUMBER: 60/098843
PRIOR FILING DATE: 1998-09-02
PRIOR APPLICATION NUMBER: 60/099536
PRIOR FILING DATE: 1998-09-09
PRIOR APPLICATION NUMBER: 60/099596
PRIOR FILING DATE: 1998-09-09
PRIOR APPLICATION NUMBER: 60/099598
PRIOR FILING DATE: 1998-09-09
PRIOR APPLICATION NUMBER: 60/099602
PRIOR FILING DATE: 1998-09-09
PRIOR APPLICATION NUMBER: 60/099642
PRIOR FILING DATE: 1998-09-09
PRIOR APPLICATION NUMBER: 60/099741
PRIOR FILING DATE: 1998-09-10
PRIOR APPLICATION NUMBER: 60/099754
PRIOR FILING DATE: 1998-09-10
PRIOR APPLICATION NUMBER: 60/099763
PRIOR FILING DATE: 1998-09-10
PRIOR APPLICATION NUMBER: 60/099792
PRIOR FILING DATE: 1998-09-10
PRIOR APPLICATION NUMBER: 60/099808
PRIOR FILING DATE: 1998-09-10
PRIOR APPLICATION NUMBER: 60/099812
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PRIOR APPLICATION NUMBER: 60/100684
PRIOR FILING DATE: 1998-09-17
PRIOR APPLICATION NUMBER: 60/100710
PRIOR FILING DATE: 1998-09-17
PRIOR APPLICATION NUMBER: 60/100711
PRIOR FILING DATE: 1998-09-17

PRIOR APPLICATION NUMBER: 60/100848
PRIOR FILING DATE: 1998-09-18
PRIOR APPLICATION NUMBER: 60/100849
PRIOR FILING DATE: 1998-09-18
PRIOR APPLICATION NUMBER: 60/100919
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PRIOR APPLICATION NUMBER: 60/100930
PRIOR FILING DATE: 1998-09-17
PRIOR APPLICATION NUMBER: 60/101014
PRIOR FILING DATE: 1998-09-18
PRIOR APPLICATION NUMBER: 60/101068
PRIOR FILING DATE: 1998-09-18
PRIOR APPLICATION NUMBER: 60/101071
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PRIOR APPLICATION NUMBER: 60/101279
PRIOR FILING DATE: 1998-09-22
PRIOR APPLICATION NUMBER: 60/101471
PRIOR FILING DATE: 1998-09-23
PRIOR APPLICATION NUMBER: 60/101472
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PRIOR APPLICATION NUMBER: 60/101474
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PRIOR APPLICATION NUMBER: 60/101475
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PRIOR APPLICATION NUMBER: 60/101477
PRIOR FILING DATE: 1998-09-23
PRIOR APPLICATION NUMBER: 60/101479
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PRIOR APPLICATION NUMBER: 60/101738
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PRIOR APPLICATION NUMBER: 60/101743
PRIOR FILING DATE: 1998-09-24
PRIOR APPLICATION NUMBER: 60/101915
PRIOR FILING DATE: 1998-09-24
PRIOR APPLICATION NUMBER: 60/101916
PRIOR FILING DATE: 1998-09-24
PRIOR APPLICATION NUMBER: 60/102207
PRIOR FILING DATE: 1998-09-24
PRIOR APPLICATION NUMBER: 60/102240
PRIOR FILING DATE: 1998-09-29
PRIOR APPLICATION NUMBER: 60/102307
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PRIOR APPLICATION NUMBER: 60/102331
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PRIOR APPLICATION NUMBER: 60/102484
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PRIOR APPLICATION NUMBER: 60/102487
PRIOR FILING DATE: 1998-09-30
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PRIOR APPLICATION NUMBER: 60/102687
PRIOR FILING DATE: 1998-10-01
PRIOR APPLICATION NUMBER: 60/102965
PRIOR FILING DATE: 1998-10-02
PRIOR APPLICATION NUMBER: 60/103258
PRIOR FILING DATE: 1998-10-06
PRIOR APPLICATION NUMBER: 60/103314
PRIOR FILING DATE: 1998-10-07
PRIOR APPLICATION NUMBER: 60/103315
PRIOR FILING DATE: 1998-10-07
PRIOR APPLICATION NUMBER: 60/103328
PRIOR FILING DATE: 1998-10-07
PRIOR APPLICATION NUMBER: 60/103395

; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan l.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2830P1C34
; CURRENT APPLICATION NUMBER: US/10/013,907A
; CURRENT FILING DATE: 2001-12-10
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 477
; SEQ ID NO 377
; LENGTH: 496
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: unsure
; LOCATION: 396
; OTHER INFORMATION: unknown base
US-10-013-907A-377

Query Match   48.0%; Score 284.2; DB 13; Length 496;
Best Local Similarity   97.3%; Pred. No. 4.4e-79;
Matches 289; Conservative   0; Mismatches   8; Indels   8; Gaps   0;

Qy   1 TCTGCCTCCACTGCTCTGTGCTGGGATCATGGAACTTGCACTGCTGTGTGGGCTGGTGGT 60
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Qy   61 GATGGCTGGTGTGATTCCAATCCAGGGCGGGATCCTGAACCTGAACAAGATGGTCAAGCA 120
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Qy 121 AGTGACTGGGAAAATGCCCATCCTCTCCTACTGGCCCTACGGCTGTCACTGCGGACTAGG 180
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 121 AGTGACTGGGAAAATGCCCATCCTCTCCTACTGGCCCTACGGCTGTCACTGCGGACTAGG 180

Qy 181 TGGCAGAGGCCAACCCAAAGATGCCACGGACTGGTGCTGCCAGACCCATGACTGCTGCTA 240
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Db 181 TGGCAGAGGCCAACCCAAAGATGCCACGGACTGGTGCTGCCAGACCCATGACTGCTGCTA 240

Qy 241 TGACCACCTGAAGACCTGAAGACCCAGGGGTGCGGCATCTACAAGGACTATTACAGATACAACTT 297
         |||||||||||||||||||||||||| |||| ||||
Db 241 TGACCACCTGAAGACCTGAAGACCCAGGGGTGCGGCATCTACAAGGACAACAACAAAAGCAGCAT 297

Search completed: October 7, 2004, 22:40:42
Job time : 307.834 secs

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              GenCore version 5.1.6
     Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on:    October 7, 2004, 11:14:15 ; Search time 937.252 Seconds
                                      (without alignments)
                                      9989.875 Million cell updates/sec

Title:          US-09-830-321A-5
Perfect score:  2204
Sequence:       1 catggtttgggcgcagaga........actcatacaaaaaaaaaaa 2204

Scoring table:  IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched:       373863 seqs, 2124099041 residues

Total number of hits satisfying chosen parameters:    6747726

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :  N_Geneseq_29Jan04:*
        1:  geneseqn1980s:*
        2:  geneseqn1990s:*
        3:  geneseqn2000s:*
        4:  geneseqn2001as:*
        5:  geneseqn2001bs:*
        6:  geneseqn2002s:*
        7:  geneseqn2003as:*
        8:  geneseqn2003bs:*
        9:  geneseqn2003cs:*
       10:  geneseqn2004s:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Length	DB	ID	Description
1	2202	99.9	2204	3	AAA53270	Aaa53270 Human pho
2	1816.8	82.4	3085	3	AAZ88757	Aaz88757 Human PLA
3	1816.8	82.4	3085	3	AAZ88758	Aaz88758 Human PLA
4	1816.8	82.4	3085	4	AAF74999	Aaf74999 Phospholi
5	1816.8	82.4	3085	4	AAF75000	Aaf75000 Phospholi
6	1816.8	82.4	3085	4	AAF90489	Aaf90489 Human pho
7	1816.8	82.4	3085	4	AAF90488	Aaf90488 Human pho
8	1806.2	82.0	2699	6	AAS17363	Aas17363 cDNA enco
9	1806.2	82.0	2699	7	ABX11884	Abx11884 Human cDN
10	1806.2	82.0	4183	6	AAS17362	Aas17362 Partial c
11	1806.2	82.0	4183	7	ABX11883	Abx11883 Human par
12	1788.8	81.2	1925	2	AAV34229	Aav34229 Human sec
13	1788.8	81.2	1925	2	ACD08100	Acd08100 cDNA enco
14	1777.8	80.7	1926	2	AAV34164	Aav34164 Human sec
15	1777.8	80.7	1926	7	ACD08035	Acd08035 cDNA enco
c 16	1676.6	76.1	1818	7	AAV34230	Aav34230 Human sec
c 17	1676.6	76.1	1818	7	ACD08101	Acd08101 cDNA enco
18	1432.2	65.0	3419	5	AAS84341	Aas84341 DNA encod
19	1408.6	63.9	8517	3	AAZ88756	Aaz88756 Human PLA
20	1408.6	63.9	8517	4	AAF74998	Aaf74998 Phospholi
21	1408.6	63.9	8517	4	AAF90487	Aaf90487 Human pho
22	1388.8	63.0	3068	5	AAS70058	Aas70058 DNA encod
23	728.8	33.1	5241	5	AAS70056	Aas70056 DNA encod
24	602	27.3	2409	6	AAD36478	Aad36478 Human pho
25	602	27.3	3138	9	ADC10173	Adc10173 Human NOV
26	602	27.3	3197	8	ABA94700	Aba94700 Human lip
27	602	27.3	3587	8	ADB61644	Adb61644 Human DNA
28	539.4	24.5	4499	5	AAS84340	Aas84340 DNA encod
29	483.8	22.0	1915	5	AAS34883	Aas34883 cDNA enco
30	483.8	22.0	1915	9	ADC46041	Adc46041 Human neo
31	451.4	20.5	567	8	AAS84337	Aas84337 DNA encod
32	439	19.9	494	8	ACH45352	Ach45352 Human foe
33	429.6	19.5	3879	6	ABV72127	Abv72127 Nucleotid
34	415.6	18.9	4049	9	ADD93423	Add93423 Human lip
35	398.2	18.1	3418	9	ADE07210	Ade07210 Novel cod
36	398.2	18.1	3460	6	ABL51334	Abl51334 Human pho
37	393.4	17.8	4803	4	AAD11574	Aad11574 Human pho
38	393.4	17.8	4820	4	AAD11388	Aad11388 Human pho
39	385.8	17.5	2547	6	ABA94697	Aba94697 Human lip
40	365	16.6	2694	6	ABL51366	Abl51366 Mouse pho
41	358.6	16.3	3112	6	ABL51352	Abl51352 Mouse pho
42	342.8	15.6	369	3	AAA44804	Aaa44804 Human sec
43	336.2	15.3	2397	6	AAD36905	Aad36905 Human pho
44	324	14.7	4875	5	AAD11386	Aad11386 Human pho
45	321.4	14.6	1317	5	AAS84338	Aas84338 DNA encod

ALIGNMENTS

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RESULT 1
AAA53270
ID   AAA53270 standard; cDNA; 2204 BP.
XX
AC   AAA53270;
XX
DT   05-OCT-2000  (first entry)
XX
DE   Human phospholipase 2 HPPL2 coding sequence.
XX
KW   Human; phospholipase 2; HPPL2; cancer; autoimmune disorder;
KW   inflammatory disorder; reproductive disorder; infection; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             95..1912
FT                   /*tag= a
FT                   /product= "HPPL2"
XX
PN   WO20024911-A2.
XX
PD   04-MAY-2000.
XX
PF   27-OCT-1999;  99WO-US025021.
XX
PR   27-OCT-1998;  98US-00181317.
PR   21-JAN-1999;  99US-00234726.
XX
PA   (INCY-) INCYTE PHARM INC.
XX
PI   Hillman JL, Bandman O, Guegler KJ, Corley NC, Baughn MR;
PI   Azimzai Y, Lal P, Lu DAM;
XX
DR   WPI; 2000-350750/30.
DR   P-PSDB; AAB03628.
XX
PT   Human phospholipase genes and proteins useful to diagnose, prevent or
PT   treat cancer, autoimmune or inflammatory or reproductive disorders.
XX
PS   Claim 9; Page 74-75; 80pp; English.
XX
CC   The present sequence is the coding sequence of human phospholipase 2
CC   (HPPL2). The protein produced from this sequence is involved in the
CC   hydrolysis of membrane phospholipids. The protein and its coding sequence
CC   can be used to diagnose and treat the following: cancers such as
```

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CC   prostate, breast and testicular cancers, autoimmune and inflammatory
CC   disorders such as AIDS, allergies, anaemia, asthma, atherosclerosis,
CC   Crohn's disease, diabetes mellitus, emphysema, Graves' disease, irritable
CC   bowel syndrome, multiple sclerosis, myasthenia gravis, psoriasis,
CC   rheumatoid arthritis and systemic lupus erythematosus, infection caused
CC   by viruses, fungi, bacteria, parasites and protozoa, and reproductive
CC   disorders including infertility, disruptions of the menstrual cycle,
CC   polycystic ovary syndrome, ectopic pregnancies, disruptions of
CC   spermatogenesis, cancers within the reproductive tract and impotence. The
CC   present sequence was obtained from clone no.1430683, which was
CC   constructed using ileum tissue
XX
SQ   Sequence 2204 BP; 429 A; 686 C; 625 G; 462 T; 0 U; 2 Other;

Query Match             99.9%;  Score 2202;  DB 3;  Length 2204;
Best Local Similarity   100.0%;  Pred. No. 0;
Matches 2204;  Conservative  0;  Mismatches  0;  Indels  0;  Gaps  0;
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Qy      1  CATGGTTTGGGGCGCAGAGAGGGCAGGNANACCAAGGAGGAGAAGAGGGGAAATTGCGCC   60
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Db      1  CATGGTTTGGGGCGCAGAGAGGGCAGGNANACCAAGGAGGAGAAGAGGGGAAATTGCGCC   60

Qy     61  CTTTTGGGGTGGAAGCTGTGTTATGGCTGACCTTAAATGATCTTCGTAGAGTTGTCGCCCAC  120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61  CTTTTGGGGTGGAAGCTGTGTTATGGCTGACCTTAAATGATCTTCGTAGAGTTGTCGCCCAC  120

Qy    121  CCTGGCCCTCTGTCTTGAGAGAGTGCTTCTCACCTCACAGACACAGGATTATTGGTCTT  180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121  CCTGGCCCTCTGTCTTGAGAGAGTGCTTCTCACCTCACAGACACAGGATTATTGGTCCT  180

Qy    181  TTTCTGCCCGCCCCCTGCCCTTTTTTTTTTTTTGAGATGAGTCTCTCTCTGTCGC  240
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Db    181  TTTCTGCCCCCCCCTGCCCTTTTTTTTTTTTTTGAGATGAGTCTCTCTCTGTCGC  240

Qy    241  CCAGGCTGGAGTGCAATGGCGTGATCTTGGCTCACTGCAACCTCCGCCTCCCGGGTTCAA  300
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Db    241  CCAGGCTGGAGTGCAATGGCGTGATCTTGGCTCACTGCAACCTCCGCCTCCCGGGTTCAA  300

Qy    301  GCGATTCTCCTGCCTCAGCCTCCCGAGTAGCTGGGATTACAGACTGAGGGAGTGGCCGT  360
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301  GCGATTCTCCTGCCTCAGCCTCCCGAGTAGCTGGGATTACAGACTGAGGGAGTGGCCGT  360

Qy    361  CCAGGCTGGTCTCGGGCCCTGTGCAGAGACGAGGCAGGCCTTCCTGAGCCAGGAGCAGGT  420
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361  CCAGGCTGGTCTCGGGCCCCTGTGCAGAGACGAGGCAGGCCTTCCTGAGCCAGGAGCAGGT  420

Qy    421  GGTGGCCGCGGCCTTGAGGGCCTGCGAGCTGACGAGGATGAGAT  480
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Db    421  GGTGGCCGCGGCCTTGAGGGCCTGCGAGCTGACGAGGATGAGAT  480

Qy    481  CCCAGTGGTAGCTATTATGGCCACTGGTGTGGCCTCTTGGATTGCTCCTACATCACCGGGGC  540
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    481  CCCAGTGGCAGGGCCCACTGAGTTGCTGAAGACCCCAGGTGCTGAAGACAAGCTGGGTGTGT  540

Qy    541  GCAGCTGGCTGGCTGGCCTGAAGGAGTGGGCCTTGGGCCTCTCCTACGGGGGC  600
           ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    541  GCAGCTGGCTGGCTGGCCTGAAGGAGTGGGCCTTGGGCCTCTCCTACGGGGGC  600

Qy    601  CTCGGGCTCCACCTGGCCTTGCGCCCAACCTTTATGAGGACCCAGAGTGTCTCAGAAGGA  660
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    601  CTCGGGCTCCACCTGGCCTTGCGCCCAACCTTTATGAGGACCCAGAGTGTCTCAGAAGGA  660

Qy    661  CCTTGGCAGGGCCCACTGAGTTGCTGAAGACCCCAGGTGCTGAAGACAAGCTGGGTGTGCT  720
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    661  CCTTGGCAGGGCCCACTGAGTTGCTGAAGACCCCAGGTGCTGAAGACAAGCTGGGTGTGCT  720

Qy    721  GGCCCCAGCCAGCTGCAGCGGGTACCGGCAGCTGGCCGAGCGTGCCCGGCTTGGGGCTA  780
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    721  GGCCCCAGCCAGCTGCAGCGGGTACCGGCAGCTGGCCGAGCGTGCCCGGCTTGGGGCTA  780

Qy    781  CCCAAGCTGCTTCACCAACCTGTGGGCCCTCATCAACGGGCCCTGCTGCTGCTGCATGATGAGCC  840
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    781  CCCAAGCTGCTTCACCAACCTGTGGGCCCTCATCAACGGGCCCTGCTGCTGCTGCATGATGAGCC  840
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Qy    841  CCATGATCACAAGCTTCTCAGATCAACGGAGCCCTGAGTCATGGCGAGAAACCCTCTGCC  900
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    841  CCATGATCACAAGCTTCTCAGATCAACGGAGCCCTGAGTCATGGCGAGAAACCCTCTGCC  900

Qy    901  CATCTACTGTGCCTCAACACCAAAGGGCAGAGCTGACCACTTTGAATTGGGGAGTG  960
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Db    901  CATCTACTGTGCCTCAACACCAAAGGGCAGAGCTGACCACTTTGAATTGGGGAGTG  960

Qy    961  GTGCGAGTTCTCTCCTACGAGTCGGCTTCCCAAGTACGGGGCCTTCATCCCTCTGA  1020
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Db    961  GTGCGAGTTCTCTCCTACGAGTCGGCTTCCCAAGTACGGGGCCTTCATCCCTCTGA  1020

Qy   1021  GCTCTTTGGCTCCGAGTTCTTTATGGGCAGCTGATGAAGAGGCTTCCTGAGTCCCGCAT  1080
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1021  GCTCTTTGGCTCCGAGTTCTTTATGGGCAGCTGATGAAGAGAGGCTTCCTGAGTCCCGCAT  1080

Qy   1081  CTGCTTCTTAGAAGTATCTGGAGCAACCTGTATGCAGCCAACCTCCAGGACAGCTATA  1140
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Db   1081  CTGCTTCTTAGAAGTATCTGGAGCAACCTGTATGCAGCCAACCTCCAGGACAGCTATA  1140

Qy   1141  CTGGGCCTCAGAGCCCAGCCAGTTCTCGGGACCGCTGGGTCAGGAACCAGGCCAACCTGA  1200
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1141  CTGGGCCTCAGAGCCCAGCCAGTTCTCGGGACCGCTGGGTCAGGAACCAGGCCAACCTGA  1200

Qy   1201  CAAGGAGCAGTGTCCCCTTCTGAAGATAGAAGAACCACCCCCAACAGCCCGGCAGAATAGC  1260
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Db   1201  CAAGGAGCAGTGTCCCCTTCTGAAGATAGAAGAACCACCCCCAACAGCCCGGCAGAATAGC  1260

Qy   1261  TGAGTTTTTCACCGATCTTCTGACGTGGCGTCCACTGGCCCAGGCCACACATAATTTCCT  1320
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Db   1261  TGAGTTTTTCACCGATCTTCTGACGTGGCGTCCACTGGCCCAGGCCACACATAATTTCCT  1320

Qy   1321  GCGTGGCCTCCATTTCCACAAAGACTACTTTCAGCATCCACATGGAAAGC  1380
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Db   1321  GCGTGGCCTCCATTTCCACAAAGACTACTTTCAGCATCCACATGGAAAGC  1380

Qy   1381  TACCACTCTGATGGGCTCCCCAACCAGCTGACACCTGTGCTCTGCT  1440
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Qy   1441  GGATGTTGGCTACCTCCATCAATACCAGGAGACTACAACTTCCGGACGT  1500
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Db   1441  GGATGTTGGCTACCTCCATCAATACCAGGAGACTACAACTTCCGGACGT  1500

Qy   1501  GGACCTCATCCTGCTCATTGGACTACAACCTCCAGGAGCCTTCAGCAGTTGCAGCTCCT  1560
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Db   1501  GGACCTCATCCTGCTCATTGGACTACAACCTCCAGGAGCCTTCAGCAGTTGCAGCTCCT  1560

Qy   1561  GGGCCGGTTCTGCCAGGAGCGGGATCCCGAGTGCCACCCATTCGCCCCAGCCCCGAAGA  1620
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Db   1561  GGGCCGGTTCTGCCAGGAGCGGGATCCCGAGTGCCACCCATTCGCCCCAGCCCCGAAGA  1620

Qy   1621  GCAGCTTCCAGCCTCGGAGCTGGGCCTCCACCTCTTCTCCGGAGCCCCGAGCCCCTGC  1680
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Db   1621  GCAGCTTCCAGCCTCGGAGCTGGGCCTCCACCTCTTCTCCGGAGCCCCGAGCCCCTGC  1680

Qy   1681  GGTGCTGCACTTTTCCTCTGCGGGGTCCTGGGGTCCGGCGACACCCGGAGGAGGGCGCAGCTGGGAGGT  1740
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1681  GGTGCTGCACTTTTCCTCTGCGGGGTCCTGGGGTCCGGCGACACCCGGAGGAGGGCGCAGCTGGGAGGT  1740

Qy   1741  GAACCTGTCTTCATCGGACTCATCGGACTCTGCAACAGTGACTCGGGTGTGCT  1800
           |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1741  GAACCTGTCTTCATCGGACTCATCGGACTCTACCACTACAGCCAGGAGAGGA  1800

Qy   1801  CGTGACAAGCTGCTGTCGCACCTGACAGCATTACAATGTCTGCAACAACTGCTGCT  1860
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1801  CGTGACAAGCTGCTGTCGCACCTGACACATTACAATGTCTGCAACAACTGCTGCT  1860

Qy   1861  GGAGGCTCTGCGCGCAGCCAGCAGTGCAGCCCCACTGATGGCCGGG  1920
           ||||||||||||||||||||||||||||||||||||||||||||||
Db   1861  GGAGGCTCTGCGCGCAGCCAGCAGTGCAGCCCCACTGATGGCCGGG  1920
```

CC   phospholipase A2. This sequence encodes the human PLA2 protein (also
CC   known as phosphatide 2-acyl hydrolase)
XX
SQ   Sequence 3085 BP; 607 A; 959 C; 907 G; 612 T; 0 U; 0 Other;

Query Match   82.4%; Score 1816.8; DB 3; Length 3085;
Best Local Similarity   98.2%; Pred. No. 0;
Matches 1861; Conservative 0; Mismatches 2; Indels 33; Gaps 1;

Qy   342 GACTGAGGGAGCTGCCGTGCGACTGGCTTCGGCGACTGCAGGAGGAGCAGGCTTCC 401
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1186 GACTGAGGGAGCTGCCGTGCGACTGGCTTCGGCGACTGCAGGAGGAGCAGGCTTCC 1245

Qy   402 TGAGCAGGAGGAAGCAGGTGGTGGCCGGCCGGCCCTGCAGCTGGATGGAG 461
          ||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1246 TGAGCAGGAGGAAGCAGGTGGTGGCCGGCCGGCCCTGCAGCTGGATGGAG 1305

Qy   462 ACCTGCAGGAGGATGAGATCCCAGTGTATTATGGCCACTGGTGGTGGGATCCGGG 521
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1306 ACCTGCAGGAGGATGAGATCCCAGTGTATTATGGCCACTGGTGGTGGGATCCGGG 1365

Qy   522 CAATGACTTCCCTGTATGGCAGCTGGCCTGGAAGGAGCTGGGCCTCTTGGATTGCG 581
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1366 CAATGACTTCCCTGTATGGCAGCTGGCCTGGAAGGAGCTGGGCCTCTTGGATTGCG 1425

Qy   582 TCTCCTACATCACCGGGCCTCGGGTCCACCTGGGCCTTGGCCAACCTTTATGAGGACC 641
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1426 TCTCCTACATCACCGGGCCTCGGGTCCACCTGGGCCTTGGCCAACCTTTATGAGGACC 1485

Qy   642 CAGAGTGGTCTCAGAAGGACCTGGCCAGGGCCCACTGAGTGCTGAAGACCCAGTGACCA 701
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1486 CAGAGTGGTCTCAGAAGGACCTGGCCAGGGCCCACTGAGTGCTGAAGACCCAGTGACCA 1545

Qy   702 AGAACAAGCTGGGTGTGCTGGCCCCAGCAGCTGCAGCGCAGCGGTACCGGCAGGAGCTGGCCG 761
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1546 AGAACAAGCTGGGTGTGCTGGCCCCAGCAGCTGCAGCGCAGCGGTACCGGCAGGAGCTGGCCG 1605

Qy   762 AGCGTGCCGCTTGGGCTACCAAGTCTGCTTCACCAAGCTGCTTCACCAAGCTGTCGGGCCCTCATCAACGAGG 821
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1606 AGCGTGCCGCTTGGGCTACCAAGTCTGCTTCACCAAGCTGCTTCACCAAGCTGTCGGGCCCTCATCAACGAGG 1665

Qy   822 CCGTGCTCATGATGAGCCCCATGATCACAAGCTCTCAGATCACAAGCTCTCAGATCACAAGGGCAGAGCCCTGAGTC 881
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1666 CGCTGCTGCATGATGAGCCCCATGATCACAAGCTCTCAGATCACAAGCTCTCAGATCACAAGGGCAGAGCCCTGAGTC 1725

Qy   882 ATGGCCAGAACCCTGCCATCTACTGTGCCCTCAACACCAAAGGGCAGAGCCTGACCA 941
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1726 ATGGCCAGAACCCTGCCATCTACTGTGCCCTCAACACCAAAGGGCAGAGCCTGACCA 1785

Qy   942 CTTTTGAATTTGGGAGTGGTGCGAGTTCTTCCCCTACGAGTTCCCCAAGTACG 1001
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1786 CTTTTGAATTTGGGAGTGGTGCGAGTTCTTCCCCTACGAGTTCCCCAAGTACG 1845

Qy   1002 GGGGCCTTCATCCCCCTCGAGTCTTTGCTCCGAGTTCTTTATGGGCAGCTGATGAGA 1061
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1846 GGGGCCTTCATCCCCCTCGAGTCTTTGCTCCGAGTTCTTTATGGGCAGCTGATGAGA 1905

Qy   1062 GGCTTCCTGAGTCCCGCATCGTCCTTCTGAGAGGTATCTGAGCAACCTGTATGCAGCA 1121
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1906 GGCTTCCTGAGTCCCGCATCGTCCTTCTGAGAGGTATCTGAGCAACCTGTATGCAGCA 1965

Qy   1122 ACCTCCAGGACAGCTTATACATGGGCCTCAGAGCCCAGCCAGTTCTCGGACCCGTGGGTCA 1181
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1966 ACCTCCAGGACAGCTTATACATGGGCCTCAGAGCCCAGCCAGTTCTCGGACCCGTGGGTCA 2025

Qy   1182 GGAACCAGGCCAACCTGGACAAGGAGCAGTCCCCCTTCTGAAGATAGAGAACCACCCT 1241
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2026 GGAACCAGGCCAACCTGACGACAAGGAGCAGTCCCCCTTCTGAAGATAGAGAACCACCCT 2085

Qy   1242 CAACAGCCCGCAGAATAGCTGAGTTTTCACCGGATCTTCTGACGTGGCGGTCCACTGGCCC 1301
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2086 CAACAGCCCGCAGAATAGCTGAGTTTTCACCGGATCTTCTGACGTGGCGGTCCACTGGCCC 2145

Qy   1921 GCCCCTGCCACCCCTAACTCTCATTCATTCCCTGGCTGGCTGCTGAGTTGCAGGTGGGAACTGT 1980
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1921 GCCCCTGCCACCCCTAACTCTCATTCATTCCCTGGCTGGCTGCTGAGTTGCAGGTGGGAACTGT 1980

Qy   1981 CATCACGGCAGTGCTTCAGAGCCTCGGGCTCAGTGGCACTGTCCCAGGGTCCAGGCTGAG 2040
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1981 CATCACGGCAGTGCTTCAGAGCCTCGGGCTCAGTGGCACTGTCCCAGGGTCCAGGCTGAG 2040

Qy   2041 GGCTGGGAGCTCCCTTGGCGTCCCTCAGCAGTTGCAGTGGGTAAGGAGGGCCAAGCCCATTT 2100
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2041 GGCTGGGAGCTCCCTTGGCGTCCCTCAGCAGTTGCAGTGGGTAAGGAGGGCCAAGCCCATTT 2100

Qy   2101 GTGTAATCACCCAAAACCCCGGCCTGCCCTGTCCTGTTTTCCCTTCTGCGCTTACCTTGAGTA 2160
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2101 GTGTAATCACCCAAAACCCCGGCCTGCCCTGTCCTGTTTTCCCTTCTGCGCTTACCTTGAGTA 2160

Qy   2161 GTTGGAGCACTTGATACATCACAGACTTCATACACAAAAAAAAAA 2204
          |||||||||||||||||||||||||||||||||||||||||||||
Db   2161 GTTGGAGCACTTGATACATCACAGACTTCATACACAAAAAAAAAAA 2204

RESULT 2
AAZ88757
ID   AAZ88757 standard; cDNA; 3085 BP.
XX
AC   AAZ88757;
XX
DT   18-MAY-2000 (first entry)
XX
DE   Human PLA2 cDNA.
XX
KW   PLA2; phospholipase A2; phosphatide 2-acyl hydrolase; human; therapy;
KW   arachidonic acid; lysophospholipid; Alzheimer's disease; ss.
XX
OS   Homo sapiens.
XX
FH   Key   Location/Qualifiers
FT   CDS   48..2789
FT   /*tag= a
FT   /product= "PLA2"
XX
PN   US6025178-A.
XX
PD   15-FEB-2000.
XX
PF   28-MAR-1997; 97US-00827208.
XX
PR   29-MAR-1996; 96US-0014608P.
XX
PA   (ELIL) LILLY & CO ELI.
XX
PI   Sharp JD, Strifler BA, Choiu XC, Kramer RM, Pickard RT;
XX
DR   WPI; 2000-181816/16.
DR   P-PSDB; AAY51557.
XX
PT   An isolated amino acid having phospholipase (PL)A2 activity is useful in
PT   assays to identify inhibitors having a therapeutic benefit, such as
PT   inhibiting the central role of PLA2 in the inflammatory component of
PT   Alzheimer's disease.
XX
PS   Example 5; Col 47-54; 32pp; English.
XX
CC   This invention describes a novel human phospholipase A2 (PLA2) protein
CC   (I) and its encoding nucleic acid. The amino acid (I) releases
CC   arachidonic acid in specific tissues characterized by unique membrane
CC   phospholipids, by generating lysophospholipid species which are
CC   deleterious to membrane integrity or by remodeling of unsaturated species
CC   of membrane phospholipids through deacylation/reacylation mechanisms. The
CC   amino acid is useful in assays to identify inhibitors having a
CC   therapeutic benefit, such as inhibiting the central role of PLA2 in the
CC   inflammatory component of Alzheimer's disease. The amino acid (I) allows
CC   sensitive and rapid screening and identification of inhibitors of

DE   Human PLA2 mRNA.
XX
KW   PLA2; phospholipase A2; phosphatide 2-acyl hydrolase; human; therapy;
KW   arachidonic acid; lysophospholipid; Alzheimer's disease; ss.
XX
OS   Homo sapiens.
XX
PN   US6025178-A.
XX
PD   15-FEB-2000.
XX
PF   28-MAR-1997;   97US-00827208.
XX
PR   29-MAR-1996;   96US-0014608P.
XX
PA   (ELIL) LILLY & CO ELI.
XX
PI   Sharp JD, Strifler BA, Choiu XC, Kramer RM, Pickard RT;
XX
DR   WPI; 2000-181816/16.
XX
PT   An isolated amino acid having phospholipase (PL)A2 activity is useful in
PT   assays to identify inhibitors having a therapeutic benefit, such as
PT   inhibiting the central role of PLA2 in the inflammatory component of
PT   Alzheimer's disease.
XX
PS   Disclosure; Col 57-62; 32pp; English.
XX
CC   This invention describes a novel human phospholipase A2 (PLA2) protein
CC   (I) and its encoding nucleic acid. The amino acid (I) releases
CC   arachidonic acid in specific tissues characterized by unique membrane
CC   phospholipids, by generating lysophospholipid species which are
CC   deleterious to membrane integrity or by remodeling of unsaturated species
CC   of membrane phospholipids through deacylation/reacylation mechanisms. The
CC   amino acid is useful in assays to identify inhibitors having a
CC   therapeutic benefit, such as inhibiting the central role of PLA2 in the
CC   inflammatory component of Alzheimer's disease. The amino acid (I) allows
CC   sensitive and rapid screening and identification of inhibitors of
CC   phospholipase A2. This sequence encodes the human PLA2 protein (also
CC   known as phosphatide 2-acyl hydrolase
XX
SQ   Sequence 3085 BP; 607 A; 959 C; 907 G; 0 T; 612 U; 0 Other;

Query Match   82.4%; Score 1816.8; DB 3; Length 3085;
Best Local Similarity   78.9%; Pred. No. 0;
Matches 1496; Conservative 365; Mismatches 2; Indels 33; Gaps 1;

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Qy    342 GACTGAGGGAGCTGCGCGTGCGACTGGGCTTCGGGCGTCGCAGAGGAGGAGGCCTTCC 401
          ||||:|||||||||||||||||||||:|||||:||||||||||||||||||||||::||
Db   1186 GACUGAGGAGCUGCGCGUGCGACUGGGCUUCGGGCGUCGCAGAGGAGGAGGCCUUCC 1245

Qy    402 TGAGCAGGAAGCAGGTGGTGCGGCAGGCCCTGCAGCTGGATGGAG 461
          |||||||||||||||:||:|||||||||||:|||||:|||:||||
Db   1246 UGAGCAGGAAGCAGGUGGUGCGGCAGGCCCUGCAGCUGGAUGGAG 1305

Qy    462 ACCTGCAGCAGGATGAGATCCCAGTGTAGCTATTATGGCCACTGGTGGTGGGATCCGGG 521
          |||:|||||||||:|||||:||||:||:||:||:||||||||:|||||||||||||:|||
Db   1306 ACCUGCAGCAGGAUGAGAUCCCAGUGUAGCUAUUAUGGCCACUGGUGGUGGGAUCCGGG 1365

Qy    522 CAATGACTTCCCTGTATGGGCAGCTGCTGGCTGGAGGAGCTGGGCCTTGGATTGCG 581
          |||:|||::|||:|:|||||||||:|||:|||:||||::|:|||||:||:|||:|||
Db   1366 CAAUGACUUCCCUGUAUGGGCAGCUGCUGGCUGGAAGAGAGCUGGGCCUUUGGAUUGCG 1425

Qy    582 TCTCCTACATCACCGGGCCTCGGGCTTCGGAGGACCTGGCAGGGCCCACTGAGTTGCTGAAGACC 641
          :|||||||:||||||||||:|||||:||||||||||:||||||||||||:||||:||||||||||
Db   1426 UCUCCUACAUCACCGGGCCUCGGGCUUCGGAGGACCUGGCAGGGCCCACUGAGUUGCUGAAGACC 1485

Qy    642 CAGAGTGGTCTCAGAAGGACCTGGCAGGGACCCCACTGAGTTGCTGAAGACCCAGGTGACCA 701
          |||||:||:|:||||||||||:|||||||||||||:||||:||||||||||||||:||||||
Db   1486 CAGAGUGGUCUCAGAAGGACCUGGCAGGGACCCCACUGAGUUGCUGAAGACCCAGGUGACCA 1545

Qy    702 AGAACAAGCTGGGTGTGCTGCTGCGCCC 761
          ||||||||||:|||:||:|||||||||||
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Qy   1302 AGGCCACACATAATTTCCTGCGTGGCCTCCATTTCCACAAAGACTACTTTCAGCATCCTC 1361
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2146 AGGCCACACATAATTTCCTGCGTGGCCTCCATTTCCACAAAGACTACTTTCAGCATCCTC 2205

Qy   1362 ACTTCTCCACATGGAAAGCTACCACTCTGGATGGGCTCCCAACCAGCTGACACCCTCGG 1421
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2206 ACTTCTCCACATGGAAAGCTACCACTCTGGATGGGCTCCCAACCAGCTGACACCCTCGG 2265

Qy   1422 AGCCCCACCTGTGCCTGCTGGATGTTGGCTACCTGCTCATCAATACCAGCTGCTCCCCTCC 1481
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2266 AGCCCCACCTGTGCCTGCTGGATGTTGGCTACCTGCTCATCAATACCAGCTGCTCCCCTCC 2325

Qy   1482 TGCAGCCCACTCGGGACGTGGACCTGACCTCATCGTCATTGGACTACAACCTCCACGGAGCCT 1541
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2326 TGCAGCCCACTCGGGACGTGGACCTGACCTCATCGTCATTGGACTACAACCTCCACGGAGCCT 2385

Qy   1542 TCCAGCAGTTGCAGCTCCTGGGCCGGTTCTGCCAGGAGCAGGGGATCCCCGTTCCCACCCCA 1601
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2386 TCCAGCAGTTGCAGCTCCTGGGCCGGTTCTGCCAGGAGCAGGGGATCCCCGTTCCCACCCCA 2445

Qy   1602 TCTCGCCAGCCCGGAAGAGCAGCTCCAGCTGCCACACCTTCTCCGACCCCA 1661
          |||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2446 TCTCGCCAGCCCGGAAGAGCAGCTCCAGCTGCCACACCTTCTCCGACCCCA 2505

Qy   1662 CCTGCCCCGGAGCCCCTGCCGGTGCTGCTCGACTTT------------- 1693
          |||||||||||||||||||||||||||||||||||||
Db   2506 CCTGCCCCGGAGCCCCTGCCGGTGCTGCTCGACTTTCCCTCTGTCAGCGACTCCTTCCGGGAGT 2565

Qy   1694 -----TCCTCTGGGGTCCGGCGGACACCCGGGGCACGCGGCAGCTGGGGAGGTGAAACTGT 1748
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2566 ACTCGGCCCCCTGGGGTCCGGCGGACACCCGGGGCACGCGGCAGCTGGGGAGGTGAAACTGT 2625

Qy   1749 CTTCATCGGACTCTCCCTACCACTACAGAGCTGATGAAGCTGACTGACTACAGCCAGGAGGACGTGACA 1808
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2626 CTTCATCGGACTCTCCCTACCACTACAGAGCTGATGAAGCTGACTGACTACAGCCAGGAGGACGTGACA 2685

Qy   1809 AGCTGCTGCACCTGACACATTACAATGTCTGCAACAACCAGGAGCAGCTGCTGGAGGCTC 1868
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2686 AGCTGCTGCACCTGACACATTACAATGTCTGCAACAACCAGGAGCAGCTGCTGGAGGCTC 2745

Qy   1869 TGCGCCAGGCAGTGCAGTGCAGCGGAGGCGGAGGCGGCAGCCCCACTGATGGCCCGGGGGCCCCTGC 1928
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2746 TGCGCCAGGCAGTGCAGTGCAGCGGAGGCGGAGGCGGCAGCCCCACTGATGGCCCGGGGGCCCCTGC 2805

Qy   1929 CACCCCTAACTCTCATTCATTCCCTGGCTGCTGAGTTGCAGGTTGCAGGTGGAACTGTCATCACGC 1988
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2806 CACCCCTAACTCTCATTCATTCCCTGGCTGCTGAGTTGCAGGTTGCAGGTGGAACTGTCATCACGC 2865

Qy   1989 AGTTGCTTCAGAGCCTCGGGCTCAGCAGTTTGCAGTGGGGTAAGGAGAGGCCCATTTGTGTAATC 2048
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2866 AGTTGCTTCAGAGCCTCGGGCTCAGCAGTTTGCAGTGGGGTAAGGAGAGGCCCATTTGTGTAATC 2925

Qy   2049 GCTCCCTTGCGCCTCAGCAGTTTGCAGTGGGGTAAGGAGAGGCCAAGCCCATTTGTGTAATC 2108
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2926 GCTCCCTTGCGCCTCAGCAGTTTGCAGTGGGGTAAGGAGAGGCCAAGCCCATTTGTGTAATC 2985

Qy   2109 ACCCAAAACCCCCCGGCCTGTGCCTGTGTTTCCCTTCTGCGTCTTGAGTAGTTGGAGC 2168
          ||||||||||||||||||||||||||||||||||||||||||:||||||||||||||
Db   2986 ACCCAAAACCCCCCGGCCTGTGCCTGTGTTTCCCTTCTGCGCTACCTTGAGTAGTTGGAGC 3045

Qy   2169 ACTTGATCATCACAGACTCATACAAAAAAAAAAA 2204
          ||||||||||||||||||||||||||||||||||
Db   3046 ACTTGATCATCACAGACTCATACAAAAAAAAAAA 3081
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RESULT 3
AA288758
ID   AA288758 standard; DNA; 3085 BP.
XX
AC   AA288758;
XX
DT   18-MAY-2000 (first entry)
XX

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Db   1546 AGAACAAGCUGGUGGUGUCUGGCCCCCAGCUGCAGGCGGGUACCGGCAGGAGCUGGCCG 1605

Qy    762 AGCGUGCCGCUGGGCUGCUACCCAAGCUGCUUCAACAAGCUGUGGCCCUCAUCAACGAGG 821
          | |::|||||  ::||:|||||||||||:|||:| | |||:|||||||:||||||||||
Db   1606 AGCGUGGCCGCCUGGGCCUUCCAAGCUGCUUCAACAACCUGUGGCCCUCAUCAACGAGG 1665

Qy    822 CGCUGCUGCAUGAUGAGCCCAUGACAAAGCUUCAGAUGACAAAGCUGCCCUGAGUC 881
          | |:|||: ||||||||||||:|:||||||||:|:|||:|||:||||:|||:|||
Db   1666 CGCUGCUGCAUGAUGAGCCCCAUGACAAGCUUCUAGAUCAACGGGAGCGGCCCUGAGUC 1725

Qy    882 AUGGCCAGAACCCUCUGCCCAUCUACUGUGCCCUCAACACCAAAGGGCAGAGCCUGACCA 941
          |:||||||||||:|:|||| ||:|:|:| ||||::|:||||:|||||||||:|||||||
Db   1726 AUGGCCAGAACCCUCGAUCUCUGUGCCCUCAACACCAAAGGGCAGAGCCUGACCA 1785

Qy    942 CUUUUGAAUUUGGGAGUGGUGCGAGUUCUCUCCCUAGAGGUCGGCUUCCCCAAGUACG 1001
          |:::::||||::||||||||||  |:| ||:|||||||||:||||||:|||||||||
Db   1786 CUUUUGAAUUUGGGGAGUGGUGGGGAGUUCGUUCCCUAGAGGUCGGCUUCCCCAAGUACG 1845

Qy   1002 GGGCCUUCAUCCCCUCUGAGCUCUUUGGCUGCCGUCUUUAUGGGCAGCUGAUGAAGA 1061
          |||||||||:|:|||||||||:|:||||:||:|||:||:|||||||||:|||||||
Db   1846 GGGCCUUCAUCCCCUCUGAGCUCUUCAGUCAGUUGCAGUGGGGGUAAGGAGGCUGAUGAAGA 1905

Qy   1062 GGCUUCCUGAGUCCCGCAUCUGCUUCUUAGAAGGUAUCUGGAGCAACCUGUAUGCAGCCA 1121
          ||||||:|:||||| :||| |:|::||| ||||||:|:||||||||||:|||||||||||
Db   1906 GGCUUCCUGAGUCCCGCAUCUGCUUCUUUAGAAGGUAUCUGGAGCAACCUGUAUGCAGCCA 1965

Qy   1122 ACCUCCAGGACAGCUUAUAUCUGGGCCUCAGAGCCUGGGACCGCUGGGUCA 1181
          |||::::|||||||||||||| |:|:|||||:|:||||||||:||||||||
Db   1966 ACCUCCAGGACAGCUUAUAUACUGGGCCUCAGAGCCUGGGACCGCUGGGUCA 2025

Qy   1182 GGAACCAGGCCAACCUGGACAAGGAGGACAGGAGCAGUUCCCCUUCUGAAGAUAGAAGAACACCCU 1241
          ||||||||||||||||||||||||||||||||||||::|| ||:||||||||||:||||||||||
Db   2026 GGAACCAGGCCAACCUGGACAAGGAGGACAGGAGCAGUCCCCUUCUGAAGAUGAUAGAAGAACACCCU 2085

Qy   1242 CAACAGCGCGGCAGAAUAGCUGAGUUUUUCACCGAUCUUCUGACGUGGCUCCACUGCCCC 1301
          |||||||||||||||||||| :| ||||:||:|||:||||||:|||||||:||||||||
Db   2086 CAACAGCGCGGCAGAUAGCUGAGUUUUCACCGAUCUUCUGACGUGGCUCCACUGCCCC 2145

Qy   1302 AGGCCACACAUAAUUUCCUGCGCUGCCUCCAUUUCCACAAAGACUACUUUCCACCAUCCUC 1361
          ||||||::|||||||::||:|||||||||||||  | ::|:|||||||:|:|||||||||
Db   2146 AGGCCACACAUAAUUUCCUGCGGCAGGUCCCAUUUCCACAUCCUGAGUCCCCACCAUCCUC 2205

Qy   1362 ACUUCUCCCAAUGGAAAGCUACCACUCUGGAUGGCUCCCCAACCAGCUGACACCCUUCGG 1421
          ||:|| |:||||||:||||||||:|||||||||||||:|:|:|:|||:|||::|||:|||
Db   2206 ACUUCUCCACAUGGAAAGCUACCACUCUGGAUGGGCUCCCAGCAGCUGACUGACCCCUCGG 2265

Qy   1422 AGCCCCACCUGUGCCUCUGGAUGUUGGCUACCUACCAGCUGCCCUGCCCUCC 1481
          |||||||||||||||:|:|||||||||:||:|||:|:||||||:|||||||:
Db   2266 AGCCCCACCUGUGCCCCUCCAGGAGGCUACCUACCAGCUGCCCUGCCCUCCC 2325

Qy   1482 TGCAGCCCACUCGGGACGUGACCUGACCUCAUCCUGUCAUUGGACUACAACCUCCACGGACCU 1541
          :|||||||||:||||||:|:||| |:|:|||:|:|:||||:|||||||||||||:||||||:
Db   2326 UGCAGCCCACUCGGGACGUGACCUGACCUCAUCCUGUCAUUGGACUACAACCUCCACGAGCCU 2385

Qy   1542 TCCAGCAGUUGCAGCUCCUGGCCGGUUCUGCCAGGAGCAGGGGAUCCCGUUCCACCCA 1601
          :||||||||||||||:|||||||||:||||||:|||||||||||||:|||:|||||||
Db   2386 UCCAGCAGUUGCAGCUCCUGGCCGGUUCUGCCAGGAGCAGGGGAUCCCGUUCCACCCA 2445

Qy   1602 TCTCGCCCAGCCGGAAGAGCAGCUCCAGCCUCGGGAGUGCCACACCUUCUCCGACCCCA 1661
          :|:||||||||||||||||||||||||||||:|||||||:||||||||:|:|||||||
Db   2446 UCUCGCCCAGCCGGAAGAGCAGCUCCAGCAGCUCCGGGAGUGCCACACCUUCUCCGACCCCA 2505

Qy   1662 CCTGCCCCGGAGCCCCCUGCGGUGCUGCACUUU------------------ 1693
          :||||||||||||||||||||||:|:|||||||::|||
Db   2506 CCUGCAGCCCCGGAGCCCCCUGCGGUGCUGCACUUUCCUGCACUUUCCUGGUCAGUCCCUCCUGGAGU 2565

Qy   1694 ----TCCTCTGGGGUCCGGCGGACACCCGGACACCCGGACACCCGGACCUGU 1748
              :||||||||||| ||||||:||||||:||||||:||:||||:|||||
Db   2566 ACUUCGCGCCCCUGGGGUCCGGCGGUCGGCGCGACACCCGGACACCCGGAACCUGU 2625

Qy   1749 CTTCATCGGACTCCCTACCACTACACGAAGGTGACCTAGCCAGCAGAGACGTGGACA 1808
          |:::||:||||||:||:||||||||||:|||||:|||:||||||||||||:||||||
Db   2626 CUUCAUCGGACUCCCUACCACUACACGAAGGUGACCUAGCCAGCAGGAGACGCGUGGACA 2685
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Qy   1809 AGCGTGCTGCACCTGACACATTACAATGTCTGCAACAACCAGGAGCAGCAGCTGCTGGAGGCTC 1868
          ||:|||||||:|||||||||||:||||||||||||||:|||||||||||||||||:||||||:
Db   2686 AGCUGCUGCACCUGACACAUUACAAUGUCUGCAACAACCAGGAGCAGCAGCUGCUGGAGGCUC 2745

Qy   1869 TGCGCCAGCAGTGCAGCGAGGCGGCAGGCGGCGCAGGCCCCACTGATGGCCCGGGCCCCTGC 1928
          |||||||||||:|||||:||||:||||||:||:||||||||||:|||||||||:||||||||
Db   2746 UGCGCCAGCAGUGCAGCGAGGCGGCAGGCGGCGCAGGCCCCACUGAUGGCCCGGGCCCCUGC 2805

Qy   1929 CACCCCTAACTCTCATTCCTCGGCTGCTGAGTTGCAGGTGGGAACTGTCATCACGC 1988
          |||||||||:|:|:||||:|:||||||||||||:||:|||||||||||:|:|||||
Db   2806 CACCCCUAACUCUCAUUCCCUGGCUGCUGAGUUGCAGGUGGGAACUGUCAUCACGC 2865

Qy   1989 AGTGCTTCAGAGCCTCGGGCTGCCACTGTCCCAGGGTCCAGGCTGCAGGGCTGGGA 2048
          |:|||||||||||||:||||||||:||||:|||||||:||||||||:||||||||
Db   2866 AGUGCUUCAGAGCCUCGGGCUGCCACUGUCCCAGGGUCCAGGCUGCAGGGCUGGGA 2925

Qy   2049 GCTCCCTGCGCCTCAGCAGTTGCAGTGGGTGAAGGAGGCCAAGCCCATTGTGTAATC 2108
          |||||:|||||:|||||||:||||||:||||:|||||||||||||||:|:||:||||
Db   2926 GCUCCCUGCGCCUCAGCAGUUGCAGUGGGGUAAGGAGGCCAAGCCCAUUGUGUAAUC 2985

Qy   2109 ACCCAAAACCCCCGGCCTGTGCCTCTGTTTTCCCTTCTGCTACCTTGAGTAGTTGGAGC 2168
          |||||||||||||||||:|:||:|:|||::|||| ||||:||||||:|||:||:||||||
Db   2986 ACCCAAAACCCCCGGCCUGUGCCUCUGUUUUCCCUUCUGCUACCUUGAGUAGUUGGAGC 3045

Qy   2169 ACTTGATACATCACAGACTCATACAAAAAAAAAAAAA 2204
          ||:|||||||||||||||||:||||:||||||||||||
Db   3046 ACUUGAUACAUCACAGACUCAUCAUACAAAAAAAAAAAAA 3081
```

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RESULT 4
AAF74999
ID   AAF74999  standard; cDNA; 3085 BP.
XX
AC   AAF74999;
XX
DT   23-MAY-2001  (first entry)
XX
DE   Phospholipase A2 (PLA2) encoding cDNA SEQ ID NO:2.
XX
KW   Phospholipase A2; PLA2; antiinflammatory; inflammatory condition;
KW   rheumatoid arthritis; psoriasis; asthma; cytosolic PLA2; cPLA2; ss.
XX
OS   Homo sapiens.
XX
PN   US6197569-B1;
PD   06-MAR-2001.
XX
PF   07-FEB-2000; 2000US-00500358.
XX
PR   29-MAR-1996;  96US-0014608P.
PR   19-MAR-1997;  97US-0041264P.
PR   28-MAR-1997;  97US-00827208.
XX
PA   (ELIL ) LILLY & CO ELI.
XX
PI   Choiu XC, Kramer RM, Pickard RT, Sharp JD, Strifler BA;
XX
DR   WPI; 2001-256372/26.
DR   P-PSDB; AAB74635.
XX
PT   Novel nucleic acid molecules encoding phospholipase A2 enzyme, useful in
PT   screening assays for identifying compounds that inhibit or block
PT   phospholipase A2 enzyme activity.
XX
PS   Claim 1; Col 47-54; 32pp; English.
XX
CC   The present invention describes an isolated polynucleotide (I),
CC   comprising a 3085 base pair phospholipase A2 (PLA2) sequence (given in
CC   AAF74999), encoding a 913 residue phospholipase A2 protein sequence
CC   (given in AAB74635), or a nucleotide sequence which hybridises under
CC   stringent conditions to the above mentioned nucleotide sequence. Also
```

22.0/0

US6197569-B1

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CC  described are: (1) an isolated polynucleotide (II) comprising an 8517
CC  base pair sequence, given in AAF74998; (2) an expression vector (III)
CC  comprising (I) and an expression control sequence; (3) a host cell
CC  transformed with (III); (4) an expression vector (IV) comprising (II)
CC  operably linked to an expression control sequence; and (5) a host cell
CC  transformed with (IV). (I) is useful for screening compounds which
CC  inhibit or block cytosolic PLA2 (cPLA2) enzyme activity. The host cells
CC  transformed or transfected with cPLA2 enzymes in large
CC  quantities which are useful in screening assays for discovering agents
CC  that inhibit PLA2. The inhibitors identified are useful for treating
CC  inflammatory conditions such as rheumatoid arthritis, psoriasis, or
CC  asthma. (I) is also useful in the detection of mutant genomic DNA which
CC  has been digested with restriction enzymes and run on an electrophoretic
CC  gel by hybridising to the genomic DNA
XX
SQ  Sequence 3085 BP; 607 A; 959 C; 907 G; 612 T; 0 U; 0 Other;

Query Match      82.4%;  Score 1816.8;  DB 4;  Length 3085;
Best Local Similarity   98.2%;  Pred. No. 0;
Matches 1861;  Conservative 0;  Mismatches 2;  Indels 33;  Gaps 1;
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Qy    342 GACTGAGGGAGTGGCCCGTGCGACTGGCTTCGGCCCTGTCGAGAGGAGGAGCAGGCCTTCC 401
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1186 GACTGAGGGAGTGGCCCGTGCGACTGGCTTCGGCCCTGTCGAGAGGAGGAGCAGGCCTTCC 1245

Qy    402 TGAGCAGGAGGAAGCAGGTGGTGCCGCGGCCTTGAGGCAGGCCCTGCAGCTGGATGGAG 461
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1246 TGAGCAGGAGGAAGCAGGTGGTGCCGCGGCCTTGAGGCAGGCCCTGCAGCTGGATGGAG 1305

Qy    462 ACCTGCAGGAGGATGAGATCCCAGTGGTAGCATTATTGGCCACTGGTGGTGGAATCCGGG 521
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1306 ACCTGCAGGAGGATGAGATCCCAGTGGTAGCATTATTGGCCACTGGTGGTGGAATCCGGG 1365

Qy    522 CAATGACTTCCCTGTATGGGCAGCTGGCTGGCCTGAAGGAGCTGGGGCCTCTTTGGATTGCG 581
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1366 CAATGACTTCCCTGTATGGGCAGCTGGCTGGCCTGAAGGAGCTGGGGCCTCTTTGGATTGCG 1425

Qy    582 TCTCCTACATCACCGGGGCCTCGGGCTTGGGGCCAACCTTTATGAGGACC 641
          ||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1426 TCTCCTACATCACCGGGGCCTCGGGCTTGGGGCCAACCTTTATGAGGACC 1485

Qy    642 CAGAGTGGTCTCAGAAGGACCTGCAGGGCCCACTGAGTTGCTGAAGACCCAGTGACCA 701
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1486 CAGAGTGGTCTCAGAAGGACCTGCAGGGCCCACTGAGTTGCTGAAGACCCAGTGACCA 1545

Qy    702 AGAACAAGCTGGGTGGTCTGGCCCCAGCAGCTGCAGCGGTACCGGCAGGAGAGCTGGCCG 761
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1546 AGAACAAGCTGGGTGGTCTGGCCCCAGCAGCTGCAGCGGTACCGGCAGGAGAGCTGGCCG 1605

Qy    762 AGCGGTGCCCGCTACCCAAGCTGCTTCACCAACCTGTGGGCCCTCATCAACGAGG 821
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1606 AGCGGTGCCCGCTACCCAAGCTGCTTCACCAACCTGTGGGCCCTCATCAACGAGG 1665

Qy    822 CGCTGCTGCATGATGAGCCCATGATGAGCCCTCGACATCACAAGCTCTCAGATCACAAGCTCTCAAGAGGGCCCTGAGTC 881
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1666 CGCTGCTGCATGATGAGCCCATGATGAGCCCTCGACATCACAAGCTCTCAGATCACAAGCTCTCAAGAGGGCCCTGAGTC 1725

Qy    882 ATGGCCAGGAACCCTCGCCCATCTACTGTGCCCTCAACACCAAAGGGCAGAGCCTGACCA 941
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1726 ATGGCCAGGAACCCTCGCCCATCTACTGTGCCCTCAACACCAAAGGGCAGAGCCTGACCA 1785

Qy    942 CTTTTGAATTGGGGAGTGGTGCAGTTCTTCTCCCTTACGGAGGTCGGCTTCCCCAAGTACG 1001
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1786 CTTTTGAATTGGGGAGTGGTGCAGTTCTTCTCCCTTGGCTACGGAGGTCGGCTTCCCCAAGTACG 1845

Qy   1002 GGGCCTTCATCCCCTGAGCTCTTTGGCTCCGAGTTCTTTATGGGGCAGTCGATGAAGA 1061
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1846 GGGCCTTCATCCCCTGAGCTCTTTGGCTCCGAGTTCTTTATGGGGCAGTCGATGAAGA 1905

Qy   1062 GGCTTCCTGAGTCCCGCATCCGCTTCTGCTTCTTAGAAGGTATCTGGAGCAACCTGTATGCAGCCA 1121
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1906 GGCTTCCTGAGTCCCGCATCCGCTTCTGCTTCTTAGAAGGTATCTGGAGCAACCTGTATGCAGCCA 1965
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Qy   1122 ACCTTCCAGGACAGCTTATATACTGGGCCTCAGAGCCCAGCCAGTTCTGGGACCGCTGGGTCA 1181
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1966 ACCTTCCAGGACAGCTTATATACTGGGCCTCAGAGCCCAGCCAGTTCTGGGACCGCTGGGTCA 2025

Qy   1182 GGAACCAGGCCAACCTGGACAACAGGAGCAGGTCCCCCTTCTGAAGATAGAAGAACCACCCT 1241
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2026 GGAACCAGGCCAACCTGGACAACAGGAGCAGGTCCCCCTTCTGAAGATAGAAGAACCACCCT 2085

Qy   1242 CAACAGCCGGCAGAATAGCTGAGTTTTCACCGATCTTCTGACTGGCGTCCACTGGCCC 1301
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2086 CAACAGCCGGCAGAATAGCTGAGTTTTCACCGATCTTCTGACTGGCGTCCACTGGCCC 2145

Qy   1302 AGGCCACACATAATTTCCTGCGTGGCCTCCATTTCCACAAAGACTACTTTCAGCATCCTC 1361
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2146 AGGCCACACATAATTTCCTGCGTGGCCTCCATTTCCACAAAGACTACTTTCAGCATCCTC 2205

Qy   1362 ACTTTCTCCACATGGAAAGCTACCACTCTGGATGGCTCTCCCACCCAGCTGACACCCTCGG 1421
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2206 ACTTTCTCCACATGGAAAGCTACCACTCTGGATGGCTCTCCCACCCAGCTGACACCCTCGG 2265

Qy   1422 AGCCCCACCTGTGCCGTGCTGGATGTTGGCTACCTCATCAATACCAGCTGCCTGCCCCTCC 1481
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2266 AGCCCCACCTGTGCCGTGCTGGATGTTGGCTACCTCATCAATACCAGCTGCCTGCCCCTCC 2325

Qy   1482 TGCAGCGCCACTCGGGACGTGGACCTCATCCTGTCATTGGACTACAACCTCCACGGAGCCT 1541
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2326 TGCAGCCCACTCGGGACGTGGACCTCATCCTGTCATTGGACTACAACCTCCACGGAGCCT 2385

Qy   1542 TCCAGCAGTTGCAGCTCCTGGGCCCGGTTCTGCCAGGAGCAGGGGATCCGTTCCCACCCA 1601
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2386 TCCAGCAGTTGCAGCTCCTGGGCCCGGTTCTGCCAGGAGCAGGGGATCCGTTCCCACCCA 2445

Qy   1602 TCTGCCCAGCCCGAAGAGCAGCTCCAGCCTCGGGAGTGCCACACCTTCTCCGACCCA 1661
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2446 TCTGCCCAGCCCGAAGAGCAGCTCCAGCCTCGGGAGTGCCACACCTTCTCCGACCCA 2505

Qy   1662 CCTGCCCCGGAGCCCTGCGGGTGTCCACTTT------------------------ 1693
          |||||||||||||||||||||||||||||
Db   2506 CCTGCCCCGGAGCCCTGCGGGTGTCCACTTTCCTCTGCGTCAGCGACTCCTTCCGGGAGT 2565

Qy   1694 -----TCCTCTGGGGTCCGGCGGACACCGGAGGCGGCAGCTGGGGAGGTGAACCTGT 1748
               ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2566 ACTCGGCCCCTGGGGTCCGGCGGACACCGGAGGCGGCAGCTGGGGAGGTGAACCTGT 2625

Qy   1749 CTTCATCGGACTCTCCCTACCGGAGCTGTCAGCAGGACGTGACACTACAGCCAGGACGTGACA 1808
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2626 CTTCATCGGACTCTCCCTACCGGAGCTGTCAGCAGGACGTGACACTACAGCCAGGACGTGACA 2685

Qy   1809 AGCTGCTGCACCTGACACATTACAATGTCTGCAACAACCAGGAGCAGCTGCTGGAGCTC 1868
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2686 AGCTGCTGCACCTGACACATTACAATGTCTGCAACAACCAGGAGCAGCTGCTGGAGCTC 2745

Qy   1869 TGGCCAGGCAGTGAGCGAGGCGGCAGCGGCGGCCCACTGATGCCCGGGGCCCCTGC 1928
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2746 TGGCCAGGCAGTGAGCGAGGCGGCAGCGGCGGCCCACTGATGCCCGGGGCCCCTGC 2805

Qy   1929 CACCCCTAACTCTCATTCCTGGCTGCAGGTGCAGGTGGGAACTGTCATCACGC 1988
          |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2806 CACCCCTAACTCTCATTCCTGGCTGCAGGTGCAGGTGGGAACTGTCATCACGC 2865

Qy   1989 AGTGCTTCAGAGCCTCAGCGTCCAGGCTGGCACTGTCCAGGGCTGGGA 2048
          ||||||||||||||||||||||||||||||||||||||||||||||||
Db   2866 AGTGCTTCAGAGCCTCAGCGTCCAGGCTGGCACTGTCCAGGGCTGGGA 2925

Qy   2049 GCTCCCTTGCGCCTGTGCCGGTAAGGAGGCCAAGCCCATTTGTGTAATC 2108
          |||||||||||||||||||||||||||||||||||||||||||||||||
Db   2926 GCTCCCTTGCGCCTGTGCCGGTAAGGAGGCCAAGCCCATTTGTGTAATC 2985

Qy   2109 ACCCAAACCCCCGGCCTGTCCGTGCTGTTTCCCTTGCCTGTTTCCCTTCCTGCGCTACCTTGAGTAGTTGGAGC 2168
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2986 ACCCAAACCCCCGGCCTGTCCGTGCTGTTTCCCTTGCCTGTTTCCCTTCCTGCGCTACCTTGAGTAGTTGGAGC 3045

Qy   2169 ACTTGATCACATCACAGACTCATACAAAAAAAAAAA 2204
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Db     3046 ACTTGATACATCACAGACTCATACAGAAAAAAAAAAA 3081
            |||||||||||||||||||||||||||||||||||||
```

RESULT 5
AAF75000
ID   AAF75000 standard; mRNA; 3085 BP.
XX
AC   AAF75000;
XX
DT   23-MAY-2001 (first entry)
XX
DE   Phospholipase A2 (PLA2) mRNA sequence SEQ ID NO:4.
XX
KW   Phospholipase A2; PLA2; antiinflammatory; inflammatory condition;
KW   rheumatoid arthritis; psoriasis; asthma; cytosolic PLA2; cPLA2; ss.
XX
OS   Homo sapiens.
XX
PN   US6197569-B1.
XX
PD   06-MAR-2001.
XX
PF   07-FEB-2000; 2000US-00500358.
XX
PR   29-MAR-1996; 96US-0014608P.
PR   19-MAR-1997; 97US-0041264P.
PR   28-MAR-1997; 97US-0827208.
XX
PA   (ELIL) LILLY & CO ELI.
XX
PI   Choiu XC, Kramer RM, Pickard RT, Sharp JD, Strifler BA;
XX
DR   WPI; 2001-256372/26.
XX
PT   Novel nucleic acid molecules encoding phospholipase A2 enzyme, useful in
PT   screening assays for identifying compounds that inhibit or block
PT   phospholipase A2 enzyme activity.
XX
PS   Disclosure; Col 57-62; 32pp; English.
XX
CC   The present invention describes an isolated polynucleotide (I),
CC   comprising a 3085 base pair phospholipase A2 (PLA2) sequence (given in
CC   AAF74999), encoding a 913 residue phospholipase A2 protein sequence
CC   (given in AAB74635), or a nucleotide sequence which hybridises under
CC   stringent conditions to the above mentioned nucleotide sequence. Also
CC   described are: (1) an isolated polynucleotide (II) comprising an 8517
CC   base pair sequence, given in AAF74998; (2) an expression vector (III)
CC   comprising (I) and an expression control sequence; (3) a host cell
CC   transformed with (III); (4) an expression control sequence (IV) comprising (II)
CC   operably linked to an expression control sequence; and (5) a host cell
CC   transformed with (IV). (I) is useful for screening compounds which
CC   inhibit or block cytosolic PLA2 (cPLA2) enzyme activity. The host cells
CC   transformed or transfected with cPLA2 enzymes in large
CC   quantities which are useful in screening assays for discovering agents
CC   that inhibit PLA2. The inhibitors identified are useful for treating
CC   inflammatory conditions such as rheumatoid arthritis, psoriasis, or
CC   asthma. (I) is also useful in the detection of mutant genomic DNA which
CC   has been digested with restriction enzymes and run on an electrophoretic
CC   gel by hybridising to the genomic DNA. The present sequence represents a
CC   PLA2 mRNA sequence, which is given in the exemplification of the present
CC   invention
XX
SQ   Sequence 3085 BP; 607 A; 959 C; 907 G; 0 T; 612 U; 0 Other;

Query Match 82.4%; Score 1816.8; DB 4; Length 3085;
Best Local Similarity 78.9%; Pred. No. 0;
Matches 1496; Conservative 365; Mismatches 2; Indels 33; Gaps 1;

```
Qy    342 GACTGAGGGAGCTGGCCGTGCGACTGGGCTTCGGGCCCTGTGCAGAGAGGAGGAGGCCTTCC 401
          ||:||||||||||||||||||||||||||||:|:||||||||||:|:|||||||||:|||
Db   1186 GACUGAGGGAGCAGGAGGAGCUGGCCGGACUGGGGCUCUUCGGGCCCCUGUGCAGAGAGGAGGAGGCAGGCCUUCC 1245
```

PD   05-JUN-2001.
XX
PF   07-FEB-2000; 2000US-00498809.
XX
PR   29-MAR-1996; 96US-0014608P.
PR   19-MAR-1997; 97US-0041264P.
PR   28-MAR-1997; 97US-00827208.
XX
PA   (ELIL) LILLY & CO ELI.
XX
PI   Choiu XC, Kramer RM, Pickard RT, Sharp JD, Strifler BA;
XX
DR   WPI; 2001-366537/38.
DR   P-PSDB; AAB82415.
XX
PT   Assays to evaluate the effectiveness of inhibitors of phospholipase A2,
PT   used to screen candidate compounds, comprise recombinant expression of a
PT   novel phospholipase A2.
XX
PS   Disclosure; Col 58-62; 32pp; English.
XX
CC   The present sequence is that of human mRNA encoding a novel phospholipase
CC   A2 (PLA2, also referred to bPLA2 or PLA2-beta). PLA2 liberates
CC   arachidonic acid from phospholipids, leading to the production of
CC   eicosanoids involved in inflammatory reaction. A claimed assay for
CC   evaluating the effectiveness of a compound as an inhibitor of
CC   phospholipase A2 (PLA2) involves culturing a cell transformed with an
CC   expression vector comprising PLA2 genomic DNA or cDNA, isolating the
CC   PLA2, contacting it with a candidate compound, and determining whether
CC   the PLA2 activity has been inhibited. The assay provides rapid and
CC   efficient screening for new antiinflammatory drugs that inhibit the
CC   arachidonic acid cascade. These may be especially useful in the treatment
CC   of the inflammatory component of Alzheimer's disease
XX
SQ   Sequence 3085 BP; 607 A; 959 C; 907 G; 0 T; 612 U; 0 Other;

Query Match   82.4%; Score 1816.8; DB 4; Length 3085;
Best Local Similarity   78.9%; Pred. No. 0;
Matches 1496; Conservative 365; Mismatches 365; Indels 33; Gaps 1;

```
Qy    342  GACTGAGGAGCTGGCGCCGTGCGACTGGCTTCGGGCTCGGAGGAGGAGCAGGCCTTCC  401
           |||||:::|:||||:|:|||||||||||:||||||||||||||||||||||||::::|
Db   1186  GACUGAGGAGGAGCUGGCGCCGUCGCGACUGGCUUCGGGCUCGGAGGAGGAGCAGGCCUUCC  1245

Qy    402  TGAGCAGGAGGAAGCAGGTGGTGCGCCGCCTTGAGCAGGCCTTGAGCTCGATGGAG  461
           :|||||||||||||||||||||||||||||:|:||||:|||||||:||:|:||||||
Db   1246  UGAGCAGGAGGAAGCAGGUGGUGCGCCGCCGCCUGAGCAGGCCCUGAGCUCAGCUGAUGGAGACCA  1305

Qy    462  ACCTGCAGAGGATGAGATCCCAGTGTAGCTATTATGGCGGATCCGGG  521
           |||||||||||||||||||:|:||||||:|||||:||||||:|||||
Db   1306  ACCUGCAGAGGAUGAGAUCCCAGUGUGGUGGGAUCCGG  1365

Qy    522  CAATGACTTCCCTGTATGGCGCAGCTGGCTGGCCTGAAGGAGCTGGGCTTCTTGGATTGCG  581
           ||||||||:|||:::|:||||:|||||||||||::|:||||||||:|||||:||:||||||
Db   1366  CAAUGACUUCCCCGUAUGGCGGCAGCUGGCUGGCCUCCACCUGGCCUGAAGGAGCUGGGCCUUGCCCUCUUGGAUUGCG  1425

Qy    582  TCTCCTACATCACCGGGCCTCGGGCTCTGGGTTAGGAGGGCCAAGCCCATTTGTAATC  641
           :|:|::|||:||||||||||||||:|:|||:|||:|||||||||:|||||||||||||
Db   1426  UCUCCUACAUCACCGGGCCUCGGGCUCUGGGGUUAGGAGGGCCAAGCCCACUUUAUGAGAGACC  1485

Qy    642  CAGAGTGGTCTCAGAAGGACCTGGCAGGGCCCCAGCCAGTTGCTAGAACCCAGGTGACCA  701
           ||||||||||||||||||||||||||||||||||||||:||||||||:||||||||||||
Db   1486  CAGAGUGGUCUCAGAAGGACCUGGCAGGGCCCCAGCCAGCUGCUAGAACCCAGGUGACCA  1545

Qy    702  AGAACAAGCTGGGTGTGCTGGCCCCAGCCAGCTGCGCGGTACCGGCGGTCGGCCG  761
           ||||||||||||:|||||||||||||||||||||||||:||:||||||||||||:
Db   1546  AGAACAAGCUGGGUGUGCUUGGCCUACCCAAGCUGCUUGAGCAGCUGCUGGUGUACGGAGCUGGCCG  1605

Qy    762  AGCGTGCCCGCTTGGCTACCCAAGCTGCTTCACCAACTGTGGGCCCTCATCAACGAGAGG  821
           |||:|||||||::|||||:||||||||||||||||||:|::||:|||||||||||:||||
Db   1606  AGCGUGCCCGCUUGGCUACCCAAGCUGCUUCACCAACUGUGGGCCCUCAUCAACGAGAGG  1665

Qy    822  CGCTGCTGCATGATGAGCCCATGATCGATCAACAAGCTCTCAGATCAACGGAGCCCTGAGTC  881
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Db   2326  UGCAGCCCACUCGGGACGUGGACCUCAUCCUGUCAUUGGACUACAACCUCCACGGAGCCU  2385
           :|||||||||||||||||||:|:||:::||:||||:|:||||:::|||||:|||||||||
Qy   1542  TCCAGCAGTTGCAGTCCATCCGGGGCGTTCTGCCAGGAGCAGCAGGGATCCCGTTCCACCCA  1601

Db   2386  UCCAGCAGUUGCAGUCCAUCCGGGGCCGGUUCUGCGCCAGGAGCAGGGAUCCCGUUCCACCCA  2445
           :|:|||||||||||||||||||||||||:||||:||:::|||||||||||||||||||||||
Qy   1602  TCTCGCCCAGCCCCAGAAGACAGCTCCAGCCTCGGGAGTTGCCACACCTTCTCCGACCCCA  1661

Db   2446  UCUCGCCCAGCCCCAGAAGAGAGCUCCAGCCUGGGAGUGCCACACCUUCUCCGACCCCA  2505
           :|:|||||||||:|||||||:|:|||||||||:||||||:|||||::||||||||||||
Qy   1662  CCTGCCCCGGAGCCCCTGCCGGCGTGCACTTT------------------  1693

Db   2506  CCCUGCCCCGGAGCCCCUGCCGGCGUGCUGGCCGCCUCUUCCUCGGACUCUCGGGAGU  2565
           :::|||||||||||||||||||:|:|||:::::::
Qy   1694  --------TCCTCTGGGTCCGGCGGACACCCGGGAGGAGGCGGCAGCTGCGGAGGTGAACCTGT  1748

Db   2566  ACUCGGCCUUGGGGGCACCCGGCGAGGCGGCAGCGGCGGAGGUGAACCUGU  2625
           ||:||||:||||||||||:||||:|||||||||||||||||||||||||||
Qy   1749  CTTCATCGGACTCTCCCTACCACTACGAAGGTGACCTACAGCCAGGACGTGGACA  1808

Db   2626  CUUCAUCGGACUCUCCCUACCACUACAAGGUGACCUACAGCCAGGACGUGGACA  2685
           :||||||||||||||||||||||||||:|||||||||||||||||||||||||
Qy   1809  AGTGCTGCACCTGACACATTACAATGTCTGCAACAACCAGCAGCTGCTGGAGGTC  1868

Db   2686  AGUGCUGCACCUGACACAUUACAAUAUACAAUGUCUGCAACAACCAGCAGCUGCUGGAGCUC  2745
           ||||||||||||||||||||||||:::|||||||||||||||||||||||||||||||:||
Qy   1869  TGGCGCAGGTGCAGCGCGGAGGCGGCAGCGCGCAGGCCCCACTGATGGCCGGGGCCCCTGC  1928

Db   2746  UGGCGCAGGUGCAGCGCGGAGGCGGCAGCGCGCAGGCCCCACUGAUGGCCGGGGCCCCUGC  2805
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   1929  CACCCCTAACTTCATTCATTCCTGCTGCTGAGTTGCAGTGGGAACTGTCATCACGC  1988

Db   2806  CACCCCUAACUUCAUUCCUCCUGCCUGGCCAUUCAUUCCCGCUGCAGGUGGGGAACUGUCAUCACGC  2865
           :||||:||||||||||:|::|:|||::|||::::|:|:::|:|||||||||:||||||||||||||
Qy   1989  AGTGCTTCAGAGCCTCGGGCTCAGGTGCCACTGTCCAGGGTCCCAGCTGAGGGCTGGGA  2048

Db   2866  AGUGCCUUCAGAGCCUCGGGCUCAGGUGGCACUGGCUGGCAGGGCUGAGGGCUGGGA  2925
           ||||||:|||||||||||||||||||||:|||||:||::||||:|:||||||||||
Qy   2049  GTCCCCTGCGCCTCAGCGTTTGCAGTTGCAGTGGGGTAAGGAGGGCCAATGCCCATTTGTAATC  2108

Db   2926  GUCCCCUGCGCCUCAGCAGUUGCGCUCAGCUGGGGGGUAAGGAGGGCCAAGCCCAUUGUGUAAUC  2985
           :|||||||||||||||||:|||||:::||||||||||:|||||||||||:|||||||::|||||
Qy   2109  ACCCAAAAACCCCCGGCTCCTGCCTGTCCTGTTTTCCCTTCTGCGCTACCTTGAGTAGTTGGAGC  2168

Db   2986  ACCCAAAAAACCCCCGGCUCCUGCCUGGCCUGUUUCCCUCUCGGCUACCUUGGCUCUUGAGUAGUGGGAC  3045
           |||||||||:||||||||||||||||:||:|||||:|||:|::::|:|:||||||||||:||||||
Qy   2169  ACTTGATACATCACAGACTCATACAAAAAAAAAAAAAAA  2204

Db   3046  ACUUGAUACAUCACAGACUCAUCAUCAAAAAAAAAAAAAAAAAAAA  3081
           |||||||||||||||||||||:||:||||||||||||||||||||
```

RESULT 6

AAF90489
ID   AAF90489 standard; mRNA; 3085 BP.
XX
AC   AAF90489;
XX
DT   06-AUG-2001 (first entry)
XX
DE   Human phospholipase A2 RNA.
XX
KW   Phospholipase A2; PLA2; bPLA2; PLA2-beta; inhibitor; screening;
KW   antiinflammatory; human; Alzheimer's disease; therapy; ss.
XX
OS   Homo sapiens.
XX
FH   Key   Location/Qualifiers
FT   CDS   48..2789
FT   /*tag= a
XX
PN   US6242206-B1.
XX

Db   1666 |||:||:|||:||||:|::|||||||||||||||||||||||||:|:|||||::|
          CGCUGCUGCAGCCAUGAUGAGCCCAUGAGAUCACAGAGCUCUGAGACUGGGAGCUCCUGAGUC 1725

Qy   882 ATGGCCAGAACCCCUCUGCCCAUCUACUGUGCCCCUCAACACCAAAGGGCAGAGCCUGACCA 941
          :||||||||||||:|||||||||||||||||:|||||||||||||||:|||||:||||||
Db   1726 AUGGCCAGAACCCCUGCCCAUCUAAUGUGCCCCUCAACACCAAAGGGCAGAGCACUGUCAUCACGC 1785

Qy   942 CTTTTGAATTTGGGAGGGAGUGGUGCGAGTTCTCTCCCUACGAGAGUGCCGGCTTCCCCAAGTACG 1001
          |::||:||:||||||||||||||||||||||||||:|:|||||||||||||:|||||||
Db   1786 CUUUGAAUUUGGGAGGGAGUGGUGCAGAGUUCUCCUGAGAGUGGGCACUGUCCCCAAGUACG 1845

Qy   1002 GGGCCUUCAUCCCCUCUGAGCUCUUUGGCUCCGAGUUCUUUAUGGGCAGCUGAUGAAGA 1061
          |||||||||||||||:|:||:||||||||||:||||||||||||||||||||||||
Db   1846 GGGCCUUCAUCCCCUCUGAGCUCUCUGAGUUCCGAGUUCCGAGUUCCGAGUUCUGAUGAGA 1905

Qy   1062 GGCUUCCUGAGUCCCGCAUCUGCUUCUCUUAGAAGGTACUGGAGCAACCUGUAUGCAGCCA 1121
          ||||||||||||:|||||||:|:|||||||||||||||||||||:||||:|||||||
Db   1906 GGCUUCCUGAGUCCCGCAUCUGCUUCUCUUAGAAGGUACUGGAGCAACCUGUAUGCAGCCA 1965

Qy   1122 ACCUCCAGACAGCAGCUUAUACUGGGCCUCAGAGCCCAGCCAGUUCUGGGACCGCUGGGUCA 1181
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1966 ACCUCCAGACAGCAGCUUAUACUGGGCCUCAGAGCCCAGCCAGUUCUGGGACCGCUGGGUCA 2025

Qy   1182 GGAACCAGGCCAACCUGGACAAGGAGCAGGAGUGUCCCCUUCUGAAGAUAGAAGAACCACCU 1241
          ||||||||||||||||||||||||||||||||||||||||:|::||||||||||||||
Db   2026 GGAACCAGGCCAACCUGGACAAGGAGCAGGAGUGUCCCCUUCUGAAGAUAGAAGAACCACCU 2085

Qy   1242 CAACAGCGCGGCAGAAUAGCUGAGUTTTTCACCGAUCUUCUGACGUGGCGUCCACUGGCCC 1301
          :||||||||||||||||||||:|::||:|||||||:|||:|||||||||||||||
Db   2086 CAACAGCGCGGCAGAAUGCUGAGUUUUCACCGAUCUUCUGACGUGGCGUCCACUGGCCC 2145

Qy   1302 AGGCCACACAUAAUUUCCGGCGCUCCAUUUCCACAAAGACUACUUUCAGCAUCCUC 1361
          |||||||||||||||||||||:|||||||||||||||||||||||||||||||
Db   2146 AGGCCACACAUAUUCCGGCGCUCCAUUUCCACAAAGACUACUUUCAGCAUCCUC 2205

Qy   1362 ACTTCTCCACAUGGAAAGCUACCACUCUGGAUGGCUCCCCAACCAGCUGACACCCUCGG 1421
          |::||:|||||||||||||||||||||||||||||||||||||||||||||||||
Db   2206 ACUUCUCCACAUGGAAAGCUACCACUCUGGAUGGGCUCCCCAACCAGCUGACACCCUCGG 2265

Qy   1422 AGCCCCACCUGUCGUCCUGCUGCGAUGUUGGCUACCUCAUCAAUACCAGCUGCCUGCCCCUCC 1481
          ||||||||||||||:|||||||||:|||||:|||:|||||||||||||||||:||||||
Db   2266 AGCCCCACCUGUGCCUGGACUGGCCUGGAUGUGGCUACCUCAUCUCAUCCAGCUGCCCGCCCUCC 2325

Qy   1482 TGCAGCCACUCGGGAGACGUGGACCUGUCCAUCUCGUGUCAUUGGACUACAACCUCCACGGAGCCU 1541
          :||||:||||||||||||||||:|||||||:||||||||||||:|||||||||||||||||
Db   2326 UGCAGCCCACUCGGGAGACGUGGAACCUGUCCAUCUCGUGUCAUUGGACUACAACCUCCACGGAGCCU 2385

Qy   1542 TCCAGCAGTTGCAGCTCTTCCTGGCCCGGTTCTGCAGAGCAGGAGGAUCCCGUUCCCACCCA 1601
          :|||||||||||||||:||||||||||||||||||||||||||||||:||||||||||
Db   2386 UCCAGCAGUUGCAGCUCUUCCUGGCCCGGUUCUGCAGAGCAGGAGGAUCCCGUUCCCACCCA 2445

Qy   1602 TCTCGCCCAGCCCAGCGUCCGAAGAGACGCAGCTCCAGCCTCGGGAGUUGCCACACCUUCUCCGACCCCA 1661
          |:||||:||||||:|||||||||||||:|||||||||||||:|:||:||||||||||||||
Db   2446 UCUCGCCCAGCCCAGCUCCGAAGAGACUCAGCCUCGGGAGUUGCCUCGGGAGUUGCCACACCUUCUCCGACCCCA 2505

Qy   1662 CCTCCCCCGGAGCCCCUGGGUGCUGCACUUU------------- 1693
          ::|:|||:|||||||||||||||:||||||:::
Db   2506 CCUGCCCCGGAGCCCCGGAGCCCCGGUGCUGCACUUUCCUCUGGCGUCAGCGGCGACUCCUUCCUGGGGGAGU 2565

Qy   1694 -----TCCUCUGGGGTCCGGGCGGUCCGGCGGACACCCGAGGAGGCGGCAGCGAGUGGGGAGGGUGAACCUGU 1748
          :::||:|||||:|||||||:|||||||:||||||||||||||:|||:|:
Db   2566 ACUCGGCGCCCCGGGGGUCCGGGUCCGGACACCCGGACACCCGGGGAGCAGGUGGGGAGGGGUGAACCUGU 2625

Qy   1749 CTTCATCGGACTCTCCCTACCACUACAGAAGUGACCUUACAGCCCAGGAGGACCUGACA 1808
          :||||:||||||||||:||||||||||||||||:|:|||||||||||||||||||
Db   2626 CUUCAUCGGACUCUCCCUACCACUACAGGAGGUGGCCAGGAGGACCAGGAGGACGUGACA 2685

Qy   1809 AGCTGCTGCACCTGACCATTACAAUGUCUGCAACAACCAGACAGCTGCUGGAGGCTC 1868
          ||:||:|||||||||:|:|||||||:||||||||||||||||||||||||||
Db   2686 AGCUGCUGCACCUGACCAUUACAAUGUCUGCAACAACCAGACAGCAGCGCUGGAGGCUC 2745

Qy   1869 TGCGCCAGGCAGTGCAGCCGAGCGGCGCAGGCCCCACUGAUGCCGCGGGGCCCCUGC 1928
          |||||||||||||||||||:||||||||||||||||||:||||||||||||:||
Db   2746 UGCGCCAGGCAGUGCAGCCGAGCGGCGCAGGCCGGCAGCCCCACUGAUGCCGCGGGGCCCCUGC 2805

Qy   1929 CACCCCUAACUCUCAUUCCCUGCCUGCUGAGUUGCAGUGCGAGGAACUGUCAUCACGC 1988
          ||||||||||||||||||||||||||:|||||||||||||||||||||||||
Db   2806 CACCCCUUAACUCAUUCCUCCAUUCCCUGAGUGCUGGUUGCAGUGGGGAACUGUCAUCACGC 2865

Qy   1989 AGTGCTTCAGAGCCTCCGGGCTCCGGGCTCCAGTGGCACTGCCCCAGGGCTCGAGGGCTCGGA 2048
          |||:||::|||||||:||||||||||||||||||||||||:|||||||||||||||||
Db   2866 AGUGCUUCAGAGCCUCGGGGCACUGGGGCACGUGGGGCACGUGGGGCACGUCCCAGGGUCCGGGCCUGGGA 2925

Qy   2049 GCTCCCTTGCGCCTCAGCAGTTGCAGTGGGTAAGGAGGCCAAGCCAUUUGTGTAATC 2108
          |||||||||||:|:||||||||||||||:|||:|||||||||||||||||||||:|||:|||
Db   2926 GCUCCCUGCGCCUCAGCAGUUGCAGUGGUGGGGUAAGGAGGCCAAGCCCAUUUGUGUAAUC 2985

Qy   2109 ACCCAAAACCCCCCGCCTGTGCCTGTTTTCCCTTCTGCCGUACCUUGAGUAGUUGGAGC 2168
          ||||||||||||||||||||||||||||:::|||||||:||||||||||:::|||||
Db   2986 ACCCAAAACCCCCCGCCCUGUGCCUGUUUCCCUUCUGCCGUACCUUGAGUAGUUGGAGC 3045

Qy   2169 ACTTGATACATCACAGACTCATACAAAAAAAAAAAA 2204
          ||:|:||:|:|||:|||||||||||||||||||||||||||
Db   3046 ACUUGAUACAUCACAGACUCAUACAAAAAAAAAAAAAAA 3081

RESULT 7
AAF90488
ID   AAF90488   standard; cDNA; 3085 BP.
XX
AC   AAF90488;
XX
DT   06-AUG-2001 (first entry)
XX
DE   Human phospholipase A2 cDNA.
XX
KW   Phospholipase A2; PLA2; bPLA2; PLA2-beta; inhibitor; screening;
KW   antiinflammatory; human; Alzheimer's disease; therapy; ss.
XX
OS   Homo sapiens.
XX
FH   Key   Location/Qualifiers
FT   CDS   48..2789
FT   /*tag= a
FT   /EC_number= "3.1.1.4"
XX
PN   US6242206-B1.
XX
PD   05-JUN-2001.
XX
PF   07-FEB-2000; 2000US-00498809.
XX
PR   29-MAR-1996; 96US-0014608P.
PR   19-MAR-1997; 97US-041264P.
PR   28-MAR-1997; 97US-0827208.
XX
PA   (ELIL) LILLY & CO ELI.
XX
PI   Chaiu XC, Kramer RM, Pickard RT, Sharp JD, Strifler BA;
XX
DR   WPI; 2001-366537/38.
DR   P-PSDB; AAB82415.
XX
PT   Assays to evaluate the effectiveness of inhibitors of phospholipase A2,
PT   used to screen candidate compounds, comprise recombinant expression of a
PT   novel phospholipase A2.
XX
PS   Claim 1(a); Col 47-54; 32pp; English.
XX
CC   The present sequence is that of human cDNA encoding a novel phospholipase
CC   A2 (PLA2, also referred to bPLA2 or PLA2-beta). PLA2 liberates
CC   arachidonic acid from phospholipids, leading to the production of
CC   eicosanoids involved in inflammatory reaction. A claimed assay for
CC   evaluating the effectiveness of a compound as an inhibitor of
CC   phospholipase A2 (PLA2) involves culturing a cell transformed with an
CC   expression vector comprising PLA2 genomic DNA or cDNA, isolating the

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CC   PLA2, contacting it with a candidate compound, and determining whether
CC   the PLA2 activity has been inhibited. The assay provides rapid and
CC   efficient screening for new antiinflammatory drugs that inhibit the
CC   arachidonic acid cascade. These may be especially useful in the treatment
CC   of the inflammatory component of Alzheimer's disease
XX
SQ   Sequence 3085 BP; 607 A; 959 C; 907 G; 612 T; 0 U; 0 Other;

Query Match   82.4%;  Score 1816.8;  DB 4;  Length 3085;
Best local Similarity   98.2%;  Pred. No. 0;
Matches 1861;  Conservative  0;  Mismatches  2;  Indels  33;  Gaps  1;

Qy    342 GACTGAGGAGGAGCTGGCCGTCGCCGTGCCGATCGGGTCGGGCTTCGGGCTCCACCTGCCCTGTGCAGAGGAGCAGGCCTTCC 401
          ||||||||||||||||||||| ||||||||||||||| |||||||||||| |||||||||||||||||||||||||||||||||
Db   1186 GACTGAGGAGGAGCTGGCCGTGCCGTGCCGATCGGGCTTCGGGCTTCCACCTGCCCTGTGCAGAGGAGCAGGCCTTCC 1245

Qy    402 TGAGCAGGAAGCAGTGTGGCCGCGGCCCTTGAGGCAGGCCCTTGAGCAGCTGGATGGAG 461
          ||||||||||||| |||||||||||||||||||||||||||||||||||||||||||||
Db   1246 TGAGCAGGAAGCAGGTGTGGCCGCGGCCCTTGAGGCAGGCCCTTGAGCAGCTGGATGGAG 1305

Qy    462 ACCTGCAGGAGGATGAGATCCCAGTGGTAGTAGTATTATGGCCACTGGTGGTGGGATCCGGG 521
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||| |||||
Db   1306 ACCTGCAGGAGGATGAGATCCCAGTGGTAGTAGTATTATGGCCACTGGTGGTGGGATCCGGG 1365

Qy    522 CAATGACTTCCCTGTATGGCCAGCTGGCTGGCTGGCTGAAGGAGTGGGCCTCTTGGATTGCG 581
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1366 CAATGACTTCCCTGTATGGCCAGCTGGCTGGCTGGCTGAAGGAGTGGGCCTCTTGGATTGCG 1425

Qy    582 TCTCCTACATCACCGGGCCTCGGGCTTCCACCTGGGCCTTGCCCAACCTTTATGAGGACC 641
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1426 TCTCCTACATCACCGGGCCTCGGGCTTCCACCTGGGCCTTGCCCAACCTTTATGAGGACC 1485

Qy    642 CAGAGTGGTTCTCAGAAGGACCTCGGCAGGGCCCACTGAGTTGCTGAAGACCCAGGTGACCA 701
          |||||||| |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1486 CAGAGTGTGCTCAGAAGGACCTCGGCAGGGCCCACTGAGTTGCTGAAGACCCAGGTGACCA 1545

Qy    702 AGAACAAGCTGGGTGTGCTGGCCCCAGCCAGCTGCAGCGGTACCGGCAGGAGCTGGCCG 761
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1546 AGAACAAGCTGGGTGTGCTGGCCCCAGCCAGCTGCAGCGGTACCGGCAGGAGCTGGCCG 1605

Qy    762 AGGGTGCCCGCGTTGGGCGTACCCAAGCTGCTTCACCAACCTGTGGGCCCTCATCAACGAGG 821
          |||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||||||
Db   1606 AGGGTGCCCGCGTTGGGCGTACCCAAGCTGCTTCACCAACCTGTGGGCCCTCATCAACGAGG 1665

Qy    822 CGCTGCTGTCATGATGAGCCCCATGATCACAAGCTCTCAGATCAACAAGGGCAGAGCCCTGAGTC 881
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1666 CGCTGCTGTCATGATGAGCCCCATGATCACAAGCTCTCAGATCAACAAGGGCAGAGCCCTGAGTC 1725

Qy    882 ATGGCCAGAACCCCTGCCCATCTACTGTGCCCTCAACACCAAGGGCAGAGCCCTGACCA 941
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1726 ATGGCCAGAACCCCTGCCCATCTACTGTGCCCTCAACACCAAGGGCAGAGCCCTGACCA 1785

Qy    942 CTTTTGAATTTGGGAGTGTGCCGAGTTGTCCGAGTTCTCCCCTACCAGAGGTCGGCTTC 1001
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1786 CTTTTGAATTTGGGAGTGTGCCGAGTTGTCCGAGTTCTCCCCTACCAGAGGTCGGCTTC 1845

Qy   1002 GGGGCTTCATCCCTCTGAGCTCTTTGGCTCTTTGGCTCCGAGTTCTTTATGGGCAGTTGATGAAGA 1061
          |||||||||||||||||||||||||||| |||||||||||||||||||||||||||||||||||||
Db   1846 GGGGCTTCATCCCTCTGAGCTCTTTGGCTCTTTGGCTCCGAGTTCTTTATGGGCAGCTGATGAAGA 1905

Qy   1062 GGCTTCCTGAGTCCCGCATCCGCATCGTCTTGAGAGGTATCTGGAGCAACCGTGTATGCAGCCA 1121
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1906 GGCTTCCTGAGTCCCGCATCCGCATCGTCTTGAGAGGTATCTGGAGCAACCGTGTATGCAGCCA 1965

Qy   1122 ACCTCCAGGACAGCAGCTTATACTGGGCTTGCAGCCCAGAGCCCAGTTCTGGCACCGCTGGGGTCA 1181
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||||||
Db   1966 ACCTCCAGGACAGCAGCTTATACTGGGCTTGCAGCCCAGAGCCCAGTTCTGGCACCGGGGTCA 2025

Qy   1242 CAACAGCCGGCAGAATAGCTGAGTTTTTCACCGATCTTCTGACGTGGCGGTCCACTGGCCC 1301
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Db   2086 CAACAGCCGGCAGAATAGCTGAGTTTTTCACCGATCTTCTGACGTGGCGGTCCACTGGCCC 2145
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   1302 AGGGCACACATAATTCCTGGGTGGCCTCCATTTCCACAAAGACTACTTTCAGCATCCTC 1361
          ||||| ||||||||||||| ||||||||||||||||||||||||||||||||||||||||
Db   2146 AGGGCCACATAATTCCTGCGTGGCCTCCATTTCCACAAAGACTACTTTCAGCATCCTC 2205

Qy   1362 ACTTCTCCACATGGAAAGCTACCACTCTGGATGGCCTCCCAACCAGTGACACCCTCGG 1421
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2206 ACTTCTCCACATGGAAAGCTACCACTCTGGATGGGCTCCCAACCAGCTGACACCCTCGG 2265

Qy   1422 AGCCCCACCTGTGCCTGTTGCTACCTCATCAATACCAGCTGCCTGCCCCTCC 1481
          |||||||||||| ||||||| |||||||||||||||||||||||| |||||||
Db   2266 AGCCCCACCTGTCGCCTGTTGCTACCTCATCAATACCAGCTGCCTGCCCCTCC 2325

Qy   1482 TGCAGCCACTCGGGACGTGACCTGACCTGTCGTCATTGGACTACAACCTCCACGACGCCT 1541
          |||||||||||||| |||||||||||||||||||||||||||||||||||||||||||||
Db   2326 TGCAGCCCACTCGGGACGTGGACCTGACTCGTCATTGGACTACAACCTCCACGACGCCT 2385

Qy   1542 TCCAGCAGTTGCAGCTCTCGGGGCCGGTTCTGCCGCAGGAGCAGGGATCCCCGTTCCCACCCA 1601
          ||||||||||||||||||||||||||||||||||||||||||||| |||||||||||||||||
Db   2386 TCCAGCAGTTGCAGCTCTCGGGGCCGGTTCTGCCGCAGGAGCAGGGATCCCCTTCCCACCCA 2445

Qy   1602 TCTCGCGCCAGCCCGAAGAGCAGCTCCAGCCTCGGGAGTGCCACACCTTCTCCGACCCCA 1661
          |||||||||||||||||||||||||||||||| |||||||||||||||||||||||||||
Db   2446 TCTCGCGCCAGCCCGAAGAGCAGCTCCAGCCTCGGGAGTGCCACACCTTCTCCGACCCCA 2505

Qy   1662 CCTGCCCCGGAGCCCCTGCGGTCTGCACTTT------------------- 1693
          ||||| |||||||||||||||||||||||||
Db   2506 CCTGCCCCGGAGCCCCTGCGGTCTGCACTTTCCTCGTGCAGCCGACTCCTTCCGGGAGT 2565

Qy   1694 -----TCCTGGGGTCCGGGGTCCGGCGACACCCGAGAGGGACGTGACA 1748
               ||||||| |||| |||||||||||||||||||||||||||||||
Db   2566 ACTCGGCGGCCCTGGGGTCCGGCGACACTACAGCCGCAGGAGGACGTGACA 2625

Qy   1749 CTTCATCGGACTCTCCCTACCACTACACGAAGTGAACAACAAGGAGGCAGCAGCAGTCTG 1808
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2626 CTTCATCGGACTCTCCCTACCACTACACGAAGTGAACAACAAGGAGGCAGCAGCAGTCTG 2685

Qy   1809 AGTGCTGCACCTGACACATTACAATGTCTGCAACAACCAAGGAGCAGCTGCTGAGGCTC 1868
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2686 AGTGCTGCACCTGACACATTACAATGTCTGCACACAACCAAGGAGCAGCTGCTGAGGCTC 2745

Qy   1869 TGCGCCAGCAGTGACCTCGCAGGTGGCACTGTGGGGTCCGCGGGCCCCTGC 1928
          ||||||||||||||| ||||||||||||||||||||||||||||||||||||
Db   2746 TGCGCCAGCAGTGACGTCGCAGGTGGCACTGTGGGGTCCGCGGGCCCCTGC 2805

Qy   1929 CACCCCTAACTCTCATTCCTTGGCACTGTCAGTGGCACTGTGGGAACTGTCATCACGC 1988
          ||||||||||||||||| |||||||||||||||||||||||||||||||||||||||||
Db   2806 CACCCCTAACTCTCATTCCTTGGCACTGTCAGTGGCACTGTGGGAACTGTCATCACGC 2865

Qy   1989 AGTGCTTCAGAGCCTCAGGTGGCACTCCCAGGTCCAGGGCTGGGA 2048
          |||||||||||||||||||||||||||||||||||||||||||||
Db   2866 AGTGCTTCAGAGCCTCAGGTGGCACTCCCAGGTCCAGGGCTGGGA 2925

Qy   2049 GCTGCTTCCCTTGCCCTACACGGCCAGTTTGCAGTTTGCGCTACCTTGTGTAATC 2108
          |||||||||||||||||||||||||||||||||||||| |||||||||||||||||
Db   2926 GCTGCTTCCCTTGCCCTACACGGCCAGTTTGCAGTTTGCGCTACCTTGTGTAATC 2985

Qy   2109 ACCCAAAACCCCCGGCCTTGTCCTTCTCCTTGTTTCCCTTGTTTCCCTTGAGTAGTTGGAGC 2168
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2986 ACCCAAAACCCCCGGCCTTGTCCTTCTCCTTGTTTCCCTTGTTTCCCTTGAGTAGTTGGAGC 3045

Qy   2169 ACTTGATACATCACAGACTCATCAGAAGAACAACCACCCT 2204
          ||||||||||||||||||||||||||| |||||||||||||
Db   3046 ACTTGATACATCACAGACTCATCAGAAGAACAACCACCCT 3081
```

RESULT 8
AAS17363
ID   AAS17363 standard; cDNA; 2699 BP.
XX
AC   AAS17363;

```
XX
DT   25-FEB-2002 (first entry)
XX
DE   cDNA encoding cPLA2 N-terminal peptide-cPLA2-beta fusion protein.
XX
KW   Calcium-independent cytosolic phospholipase A2-beta; cPLA2-beta; mutant;
KW   U937 cell; membrane phospholipid turnover; intracellular signalling;
KW   arachidonic acid cascade; inflammatory disorder; rheumatoid arthritis;
KW   psoriasis; asthma; inflammatory bowel disease; antiinflammatory; ss.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
FH   Key            Location/Qualifiers
FT   CDS            19..2412
FT                  /tag= a
FT                  /product= "cPLA2 N-terminal peptide-cPLA2-beta fusion
FT                  protein"
XX
PN   US6287838-B1.
XX
PD   11-SEP-2001.
XX
PF   13-DEC-1999;  99US-00460145.
XX
PR   24-JAN-1997;  97US-00788975.
XX
PA   (GEMY ) GENETICS INST INC.
XX
PI   Kriz R,  Song C;
XX
DR   WPI; 2002-054342/07.
DR   P-PSDB; AAU10697.
XX
PT   Novel cytosolic phospholipase A2-beta enzyme encoding polynucleotide,
PT   useful for producing the enzyme for use in assays to discover enzyme
PT   antagonists.
XX
PS   Claim 1; Col 19-22; 19pp; English.
XX
CC   The present invention relates to a novel calcium-independent cytosolic
CC   phospholipase A2 (cPLA2)-beta enzyme and the cDNA sequence encoding it.
CC   The cDNA clone is isolated from U937 cells. The cPLA2 enzyme is active in
CC   membrane phospholipid turnover and in regulation of intracellular
CC   signalling mediated by the arachidonic acid cascade. The invention
CC   describes a method for producing phospholipase enzymes which can be used
CC   to identify inhibitors of their function. The inhibitors can be used to
CC   treat inflammatory disorders such as rheumatoid arthritis, psoriasis,
CC   asthma, and inflammatory bowel disease. The present sequence represents a
CC   chimeric cDNA sequence which encodes for cPLA2 N-terminal peptide-cPLA2-
CC   beta fusion protein
XX
SQ   Sequence 2699 BP; 532 A; 841 C; 784 G; 542 T; 0 U; 0 Other;

Query Match           82.0%;  Score 1806.2;  DB 6;  Length 2699;
Best Local Similarity 98.1%;  Pred. No. 0;
Matches 1851;  Conservative   0;  Mismatches   3;  Indels  33;  Gaps  1;
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Qy    582  TCTCCTACATCACCGGGGCCTCGGCGCTTGGCCAACCTTTATGAGACC  641
           ||||||||||||||||||||||||||||||||||||||||||||||||
Db   1049  TCTCCTACATCACCGGGGCCTCGGCGCTTGGCCAACCTTTATGAGACC 1108

Qy    642  CAGAGTGGTCTCAGAAGGACCTGGCGAGGGCCACTGAGTTGCTGAAGACCCAGGTGACCA  701
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1109  CAGAGTGGTCTCAGAAGGACCTGGCGAGGGCCACTGAGTTGCTGAAGACCCAGGTGACCA 1168

Qy    702  AGAACAAGCTGGGTGTGCTGGCCCCCAGCCAGCTGCAGCGGTACCGCAGGAGTGGCGCCG  761
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1169  AGAACAAGCTGGGTGTGCTGGCCCCCAGCCAGCTGCAGCGGTACCGCAGGAGTGGCGCCG 1228

Qy    762  AGGCTGCCCCCTTGGGCTACCAAGTGCTTCACCAAGTGCTTCACCAAGTGCTTCATCAACGAGG  821
           ||||||||||||||||||||||||||||||||||||||||||||||
Db   1229  AGGCTGCCCCCTTGGGCTACCAAGTGCTTCACCAAGTGCTTCATCAACGAGG 1288

Qy    822  CGCTGCTGCATGATGAGCCCCATGATCACAAGTCTCAGATCACAAGGAGGCCCTGAGTC  881
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1289  CGCTGCTGCATGATGAGCCCCATGATCACAAGTCTCAGATCACAAGGAGGCCCTGAGTC 1348

Qy    882  ATGGCCAGAACCCTCGCCATCTACTGTGCCCTCAAACACCAAAGGGCAGAGCCTGACCA  941
           |||||||||||||||||||||||||||||||||||||||||||||||||
Db   1349  ATGGCCAGAACCCTCGCCATCTACTGTGCCCTCAAACACCAAACCAGAGCCTGACCA 1408

Qy    942  CTTTTGAATTTGGGAGTGGTGCCAGTTCTCTCCCCTACGAGGTCGGCTTCCCCAAGTACG 1001
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1409  CTTTTGAATTTGGGAGTGGTGCCAGTTCTCTCCCCTACGAGGTCGGCTTCCCCAAGTACG 1468

Qy   1002  GGGCCTTCATCCCCTCGAGCTCTTTGGCTCCGAGTTCTTTATGGGGCAGCTGATGAGA   1061
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1469  GGGCCTTCATCCCCTCGAGCTCTTTGGCTCCGAGTTCTTTATGGGGCAGCTGATGAGA  1528

Qy   1062  GGCTTCCTGAGTCCCGCATCCGCATCTGCTTCTTAGAAGGTATCGGAGCAACCTGTATGCAGCCA 1121
           |||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1529  GGCTTCCTGAGTCCCGCATCCGCATCTGCTTCTTAGAAGGTATCGGAGCAACCTGTATGCAGCCA 1588

Qy   1122  ACCTCCAGGACAGCTTATACTGGGCCTCAGAGCCCAGTTCGGGACCGGTCA         1181
           ||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1589  ACCTCCAGGACAGCTTATACTGGGCCTCAGAGCCCAGTTCGGGACCGGGGTCA        1648

Qy   1182  GGAACCAGGCCAACCTGACAAGGAGCAGGTCCCCCTTCTGAAGATAGAAGAACCACCCT  1241
           ||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1649  GGAACCAGGCCAACCTGACAAGGAGCAGGTCCCCCTTCTGAAGATAGAAGAACCACCCT 1708

Qy   1242  CAACACGCGGAGAAATAGCTGAGTTTTCACCGATCTTCTGACGTGGCGCTCCACTGGCCC 1301
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1709  CAACACGCGGAGAAATAGCTGAGTTTTCACCGATCTTCTGACGTGGCGCTCCACTGGCCC 1768

Qy   1302  AGGCCACACATAATTTCCTGCGTGGCCTCCATTTCACAAAGACTACTTTCAGCATCCTC   1361
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1769  AGGCCACACATAATTTCCTGCGTGGCCTCCATTTCACAAAGACTACTTTCAGCATCCTC  1828

Qy   1362  ACTTCTCCACATGGAAAGCTACCACTCTGGATGGGCTCCCAACCAGCTGACACCCTCGG  1421
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1829  ACTTCTCCACATGGAAAGCTACCACTCTGGATGGGCTCCCAACCAGCTGACACCCTCGG  1888

Qy   1422  AGCCCCACCTGCTGCGACTGGCTTCGGGCCGCTGCTTCGGGCCGCTGCTGCCCACTGCTGCCCTCC 1481
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1889  AGCCCCACCTGCTGCGACTGGCTTCGGGCCGCTGCTACCTGCTGCCCACTGCTGCCCTCC 1948

Qy   1482  TGCAGCCACTCGACGTGGACCTGTCATTGACCTACAACCTCGTGTTCCACGGAGCCT     1541
           |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1949  TGCAGCCACTCGGACGTGGACCTGTCATTGACGACTACAACCTCGTGTTCCACGGAGCCT  2008

Qy   1542  TCCAGAGTTGCAGCTCCTCGGCCGGTTCTGCCAGGAGCCACTGGTGGTGGAATCCGGG   1601
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2009  TCCAGAGTTGCAGCTCCTCGGCCGGTTCTGCCAGGAGCCACTGGTGGTGGAATCCGGG  2068

Qy   1602  TCTCGCCCAGCCCGAAGAGCAGCTCGGCGGAGTGCCACACCTTCTCGGATTGCG      1661
           |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2069  TCTCGCCCAGCCCGAAGAGCAGCTCGGCGGAGTGCCACACCTTCTCGGATTGCG     2128
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Qy    342  GACTGAGGGAGCTGCGCCGTGCGACTGGCTTCGGGCCGCTTCGGTCTGTGCAGAGGAGCAGGCCTTCC  401
           ||||||||||||||||||||||||||||||||||
Db    809  GACTGAGGGAGCTGCGCCGTGCGACTGGCTTCGGGCCGCTTCGGGCCGCTTCGGTCTGTGCAGAGGAGCAGGCCTTCC 868

Qy    402  TGAGCAGGAGGAAGCAGGTGGTGCGCCGCGCCCTTGAGGCAGGCCGCGTCGAGCTCGATGGAG  461
           ||||||||||||||||||||||||||||||||||||||||||||||||||
Db    869  TGAGCAGGAGGAAGCAGGTGGTGCGCCGCGCCCTTGAGGCAGGCCGCGTCGAGCTCGATGGAG 928

Qy    462  ACCTGCAGGAGGATGAGATCCCAGTGGTAGCTAATATGGCCACTGGCCTATTATGCCATTATGGCCACTGGCCTATTATGCCATTATGGCCACTGGCCTATTATGCCGGG 521
           ||||||||||||||||||||||||||||||||||||||||||||
Db    929  ACCTGCAGGAGGATGAGATCCCAGTGGTAGCTAATATGGCCACTGGCCTATTATGGCCACTGGCCTATTATGCCGGG 988

Qy    522  CAATGACTTCCCTGTATGGGCAGCTGGCTGGCCTGGCCTGGCGGCGCTTGATTGCG    581
           |||||||||||||||||||||||||||||||||||||||||||||||||
Db    989  CAATGACTTCCCTGTATGGGCAGCTGGCTGGCCTGGCGGCGCTTGGCGGCGCTTGGCTTTCTTGATTGCG 1048
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PT   Novel purified calcium-independent cytosolic phospholipase A2-beta
PT   enzyme, useful for screening compounds having antiinflammatory activity
PT   mediated by the arachidonic acid cascade.
XX
PS   Disclosure; Col 17-22; 19pp; English.
XX
CC   The invention relates to a purified phospholipase enzyme (calcium-
CC   independent cytosolic phospholipase A_2-beta enzyme) peptide appearing as
CC   ABG76482 encoded by a polynucleotide appearing as ABX11883. The protein
CC   has an enzymatic activity in a mixed micelle assay (MMA) with 1-palmitoyl
CC   -2-(1^4C)-arachidonyl- phosphatidylcholine. cPLA2-beta is useful for
CC   assaying chemical agents for antiinflammatory activity mediated by the
CC   various components of the arachidonic acid cascade. cPLA2-beta is also
CC   useful in the development of polyclonal and monoclonal antibodies which
CC   are useful as research or diagnostic tools, and to study phospholipase
CC   A_2 activity and inflammatory conditions. The present sequence encodes
CC   the cPLA2-beta protein
XX
SQ   Sequence 2699 BP; 532 A; 841 C; 784 G; 542 T; 0 U; 0 Other;

Query Match        82.0%;   Score 1806.2;   DB 7;   Length 2699;
Best Local Similarity   98.1%;   Pred. No. 0;
Matches 1851;   Conservative    0;   Mismatches    0;   Indels   33;   Gaps    1;

Qy    342 GACTGAGGGAGGCTGGCGTGCGACTGGCTTCGGCGCCCTGTGCAGGAGCAGGCCTTCC 401
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    809 GACTGAGGGAGGCTGGCCCGTGCGACTGGCTTCGGCCCCGTGTGCAGGAGCAGGCCTTCC 868

Qy    402 TGAGCAGGAGAAGCAGGTGGTGGCGGGGTCCAGTGGTAGCTATTATGGGCTGCGATGGAG 461
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    869 TGAGCAGGAGAAGCAGGTGGTGGCGGGGTCCAGTGGTAGCTATTATGGGCTGCGATGGAG 928

Qy    462 ACCTGCAGGAGGATGAGATCCCAGTGGTAGCTATTATGGCCACTGGTGGTGGGATCCGGG 521
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    929 ACCTGCAGGAGGATGAGATCCCAGTGGTAGCTATTATGGCCACTGGTGGTGGGATCCGGG 988

Qy    522 CAATGACTTCCCTGTATGGGCAGCTGGCTGGCTGGAAGGAGCTGGGCCTTCTTGGATTGCG 581
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    989 CAATGACTTCCCTGTATGGGCAGCTGGCTGGCTGGAAGGAGCTGGGCCTTCTTGGATTGCG 1048

Qy    582 TCTCCTACATCACCGGGGCCTCGGGCTCCACCTGGGCCTTGGCCAACCTTTATGAGGACC 641
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1049 TCTCCTACATCACCGGGGCCTCGGGCTCCACCTGGGCCTTGGCCAACCTTTATGAGGACC 1108

Qy    642 CAGAGTGGTCTCAGAAGGACTGGCAGGGCCCACTGAGTTGCTGAAGACCCAGGTGACCA 701
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1109 CAGAGTGGTCTCAGAAGGACTGGCAGGGCCCACTGAGTTGCTGAAGACCCAGGTGACCA 1168

Qy    702 AGAACAAGCTGGGTGTGCTGGCCGTACCGGCAGGAGTGGCCG 761
          |||||||||||||||||||||||||||||||||||||||||
Db   1169 AGAACAAGCTGGGTGTGCTGGCCGTACCGGCAGGAGTGGCCG 1228

Qy    762 AGCGTGCCCGCCTTGGGCTACCAGCTGCTTCACCAACCTGTGGGCCCTCATCACGAGG 821
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1229 AGCGTGCCCGCCTTGGGCTACCAGCTGCTTCACCAACCTGTGGGCCCTCATCACGAGG 1288

Qy    822 CGCTGCTGCATGATGAGCCCCATGAGCTCTCAGATCACAAGCTCTCAGATCACACGGAGGCCCTGAGTC 881
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1289 CGCTGCTGCATGATGAGCCCCATGAGCTCTCAGATCACAAGCTCTCAGATCACACGGAGGCCCTGAGTC 1348

Qy    882 ATGGCCAGAACCCTCTGCCCATCTACTGTGCCCTCACACCAAAGGGCAGAGCCTGACCA 941
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1349 ATGGCCAGAACCCTCTGCCCATCTACTGTGCCCTCACACCAAAGGGCAGAGCCTGACCA 1408

Qy    942 CTTTTGAATTTGGGAGTGGTGGAGTTCTTCTCCCTAGGAGTTCCCCAAGTACG 1001
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1409 CTTTTGAATTTGGGAGTGGTGGAGTTCTTCTCCCTAGGAGTTCCCCAAGTACG 1468

Qy   1002 GGGCCTTCATCCCCTGGACTCTTTGGCTCCGAGTTCTTTATGGGCAGTCGATGAAGA 1061
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1469 GGGCCTTCATCCCCTGGACTCTTTGGCTCCGAGTTCTTTATGGGCAGTCGATGAAGA 1528

Qy   1062 GGGCTTCCTGAGTCCCGCCATTCGTCTTCTTAGGAAGGTATCTGGAGCAACCTGATCGCAGCCA 1121
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Qy   1662 CCTGCCCCGGAGCCCTGCGGTGCTGCACTTT---------------------- 1693
          |||||||||||||||||||||||
Db   2129 CCTGCCCCGGAGCCCTGCGGTGCGTGCACTTTCCTCGGTCAGCGACTCCTTCCGGGAGT 2188

Qy   1694 ----TCCTCTGGGGTCCGGCGGACACCCGAGAGGCGGACACCGGTGGGGAGGTGAACCTGT 1748
          ||||||||||||||||||||||||||||||||||||||
Db   2189 ACTCGGCCCCTGGGGTCCGGCGGACACCCGAGAGGCGGACACCGGTGGGGAGGTGAACCTGT 2248

Qy   1749 CTTCATCGGACTCTCCCTACCACTACACGAAGTGACCTACAGCCAGGAGGACGTGGACA 1808
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2249 CTTCATCGGACTCTCCCTACCACTACACGAAGTGACCTACAGCCAGGAGGACGTGGACA 2308

Qy   1809 AGCTGCTGCACCTGACACATTACAATGTCTGCAACAACCAGGAGCAGCTGCTGGAGGCTC 1868
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2309 AGCTGCTGCACCTGACACATTACAATGTCTGCAACAACCAGGAGCAGCTGCTGGAGGCTC 2368

Qy   1869 TGCGGCCAGGCAGTGCAGCGGAGCGGCGGCAGGCCAGGCCCACTGATGGCCGGGGCCCCTGC 1928
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2369 TGCGGCCAGGCAGTGCAGCGGAGCGGCGGCAGGCCAGGCCCACTGATGGCCGGGGCCCCTGC 2428

Qy   1929 CACCCCTAACTCTCATTCATTCCCTGGCTGCTGAGTTGCAGTGGGAACTGTCATCACGCGC 1988
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2429 CACCCCTAACTCTCATTCATTCCCTGGCTGCTGAGTTGCAGTGGGAACTGTCATCACGCGC 2488

Qy   1989 AGTGCTTCAGAGCCTGGGCTCAGGTGCACTGTCCCAGGGTCAGGGCTGAGGGCTGGGA 2048
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2489 AGTGCTTCAGAGCCTGGGCTCAGGTGCACTGTCCCAGGGTCAGGGCTGAGGGCTGGGA 2548

Qy   2049 GCTCCCTTGCGCCTTCAGCAGTTTGCAGTGGGGTAAGGAGGCCAAGCCCATTGTGTAATC 2108
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2549 GCTCCCTTGCGCCTCAGCAGTTTGCAGTGGGGTAAGGAGGCCAAGCCCATTGTGTAATC 2608

Qy   2109 ACCCAAAACCCCCGGCCTGTGCCTGTTTCCCTTCGCGTACCTTGAGTAGTTGGAGC 2168
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2609 ACCCAAAACCCCCGGCCTGTGCCTGTTTCCCTTCGCGTACCTTGAGTAGTTGGAGC 2668

Qy   2169 ACTTGATACATCACAGACTCATACAAA 2195
          |||||||||||||||||||||||||
Db   2669 ACTTGATACATCACAGACTCATACAAA 2695

RESULT 9
ABX11884
ID   ABX11884 standard; cDNA; 2699 BP.
XX
AC   ABX11884;
XX
DT   10-MAY-2003  (first entry)
XX
DE   Human cDNA for cytosolic phospholipase A2-beta, cPLA2-beta.
XX
KW   Human; ss; calcium independent cytosolic phospholipase A2-beta;
KW   cPLA2-beta; antiinflammatory; arachidonic acid cascade; gene;
KW   inflammatory condition.
XX
OS   Homo sapiens.
XX
PN   US6482625-B1.
XX
PD   19-NOV-2002.
XX
PF   29-JUN-2001; 2001US-00895547.
XX
PR   24-JAN-1997;  97US-007B8975.
PR   13-DEC-1999;  99US-00460145.
XX
PA   (GEMY ) GENETICS INST LLC.
XX
PI   Kriz R,  Song C;
XX
DR   WPI; 2003-287361/28.
DR   P-PSDB; ABG76483.
XX
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Db    2609 ACCCAAAACCCCCGCCGCCTGCGCCTGTTTTCCCTTCGCGCTACCTTGAGTAGTTGGAGC 2668

Qy    2169 ACTTGATACATCACAGACTCATACAAA 2195

Db    2669 ACTTGATACATCACAGACTCATACAAA 2695
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RESULT 10
AAS17362
ID   AAS17362 standard; cDNA; 4183 BP.
XX
AC   AAS17362;
XX
DT   25-FEB-2002 (first entry)
XX
DE   Partial cDNA encoding human cPLA2-beta enzyme.
XX
KW   Calcium-independent cytosolic phospholipase A2-beta; cPLA2-beta;
KW   U937 cell; membrane phospholipid turnover; intracellular signalling;
KW   arachidonic acid cascade; inflammatory disorder; rheumatoid arthritis;
KW   psoriasis; asthma; inflammatory bowel disease; antiinflammatory; ss.
XX
OS   Homo sapiens.
XX
FH   Key   Location/Qualifiers
FT   CDS   1560..3896
FT   /*tag= a
FT   /partial
FT   /product= "cPLA2-beta enzyme"
FT   /note= "This sequence lacks a start codon"
XX
PN   US6287838-B1.
XX
PD   11-SEP-2001.
XX
PF   13-DEC-1999;   99US-00460145.
XX
PR   24-JAN-1997;   97US-00788975.
XX
PA   (GEMY) GENETICS INST INC.
XX
PI   Kriz R, Song C;
XX
DR   WPI; 2002-054342/07.
DR   P-PSDB; AAU10696.
XX
PT   Novel cytosolic phospholipase A2-beta enzyme encoding polynucleotide,
PT   useful for producing the enzyme for use in assays to discover enzyme
PT   antagonists.
XX
PS   Claim 1; Col 11-15; 19pp; English.
XX
CC   The present invention relates to a novel calcium-independent cytosolic
CC   phospholipase A2 (cPLA2)-beta enzyme and the cDNA sequence encoding it.
CC   The cDNA clone is isolated from U937 cells. The cPLA2 enzyme is active in
CC   membrane phospholipid turnover and in regulation of intracellular
CC   signalling mediated by the arachidonic acid cascade. The invention
CC   describes a method for producing phospholipase enzymes which can be used
CC   to identify inhibitors of their function. The inhibitors can used to
CC   treat inflammatory disorders such as rheumatoid arthritis, psoriasis,
CC   asthma, and inflammatory bowel disease. The present sequence represents a
CC   partial cDNA sequence which encodes for human cPLA2-beta enzyme
XX
SQ   Sequence 4183 BP; 983 A; 1177 C; 1168 G; 850 T; 0 U; 5 Other;

Query Match   82.0%;   Score 1806.2;   DB 6;   Length 4183;
Best Local Similarity   98.1%;   Pred. No. 0;
Matches 1851;   Conservative 0;   Mismatches 3;   Indels 33;   Gaps 1;

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Qy    342 GACTGAGGGAGCTGGCCGTGCGACTGGCGTTCGGGCCCCTGTGCAGAGGAGCAGGGCCTTCC 401
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2293 GACTGAGGGAGCTGGCCGTGCGACTGGCGTTCGGGCCCCTGTGCAGAGGAGCAGGGCCTTCC 2352
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Db   1529 GGCTTCCTGAGTCCGCATCGCTTCTTAGAAGGTATCTGGAGCAACCTGTATGCAGCCA 1588

Qy   1122 ACCTTCCAGGACAGCTTATACTGGGCCTCAGAGCCCAGCCAGTTCTGGGACCGCTGGGTCA 1181
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1589 ACCTTCCAGGACAGCTTATACTGGGCCTCAGAGCCCAGCCAGTTCTGGGACCGCTGGGTCA 1648

Qy   1182 GGAACCAGGCCAACCTGACAACCTGACAAGGACGAGCAGTCCCCTTCTGAAGATAGAAGAACCACCCT 1241
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1649 GGAACCAGGCCAACCTGACAACCTGACAAGGACGAGTCCCCTTCTGAAGATAGAAGAACCACCCT 1708

Qy   1242 CAACAGACCGGCAGAATAGCTGAGTTTTCACCGATCTTCTGACGTGGCGTCCACTGGGCCC 1301
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1709 CAACAGACCGGCAGGATAGCTGAGTTTTCACCGATCTTCTGACGTGGCGTCCACTGGGCCC 1768

Qy   1302 AGGCCACACATATTTCCTGCGTGGCCTCCATTTCCACAAAGACTACTTCAGCATCCTC 1361
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1769 AGGCCACACATATTTCCTGCGTGGCCTCCATTTCCACAAAGACTACTTCAGCATCCTC 1828

Qy   1362 ACTTCTCCACATGGAAAGTACCACTCTGGATGGCTCCCAACCAGTGACACCCTCGG 1421
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1829 ACTTCTCCACATGGAAAGTACCACTCTGGATGGCTCCCAACCAGTGACACCCTCGG 1888

Qy   1422 AGCCCCACCTGTGCCTGCTGGATGTTGGCTACCTCATCAATACCAGCTGCTGCTCCCCTCC 1481
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1889 AGCCCCACCTGTGCCTGCTGGATGTTGGCTACCTCATCAATACCAGCTGCTGCTCCCCTCC 1948

Qy   1482 TGCAGCCCACTCGGGACGTGACCTCATCCTGTCATTGGACTACAACCTCCACGGAGCCT 1541
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1949 TGCAGCCCACTCGGGACGTGACCTCATCCTGTCATTGGACTACAACCTCCACGGAGCCT 2008

Qy   1542 TCCAGCAGTTGCAGCTCCTGGGCCCGTTCTGCCAGGAGCAGGGGATCCCGTTCCCACCCA 1601
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2009 TCCAGCAGTTGCAGCTCCTGGGCCCGTTCTGCCAGGAGCAGGGGATCCCGTTCCCACCCA 2068

Qy   1602 TCTCGCCCAGCCTCCGGAGTGCCACACTTCTCCGACCCCA 1661
          ||||||||||||||||||||||||||||||||||||||||
Db   2069 TCTCGCCCAGCCTCCGGAGTGCCACACTTCTCCGACCCCA 2128

Qy   1662 CCTGCCCCGGAGCCCCGCGGCCCCCGCGGTGCTCACTTT----------------------- 1693
          |||||||||||||||||||||||||||||||||||||||
Db   2129 CCTGCCCCGGAGCCCCGCGGCCCCCGCGGTGCTCACTTTCCTCTGGTCAGCGACTCCTTCCGGGAGT 2188

Qy   1694 -----TCCTCTGGGGTCCGGCGGCGACACCCGGCAGCGGCGGCTGGGGAGTGAACCTGT 1748
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2189 ACTCGGCCCCCTGGGGTCCGGCGGCGACACCCGGCAGCGGCGGCTGGGGAGTGAACCTGT 2248

Qy   1749 CTTCATCGGACTCTCCCTACCTACGAAGTGACCTACAGCCCAGGAGGAGCAGTGGACA 1808
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2249 CTTCATCGGACTCTCCCTACCTACGAAGTGACCTACAGCCCAGGAGGAGGACGTGGACA 2308

Qy   1809 AGTGCTTCAGAGCCTGCACCTGACACATTACAATGTCTGCAACAACCAGGAGCAGCTGCTGAGGGCTC 1868
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2309 AGTGCTTCAGAGCCTGCACCTGACACATTACAATGTCTGCAACAACCAGGAGCAGCTGCTGAGGGCTC 2368

Qy   1869 TGCGCCAGGCAGTGCAGCGGAGGCGGAGGCGGCAGCGCAGCGCCACTGATGGCCCGGGCCCCTGC 1928
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2369 TGCGCCAGGCAGTGCAGCGGAGGCGGAGGCGGCAGCGCAGCGCCACTGATGGCCCGGGGCCCCTGC 2428

Qy   1929 CACCCTAACTCTCATTCATTCCCCGGCTGCTGAGTTGGGAACTGTCATCACGG 1988
          |||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2429 CACCCCTAACTCTCATTCATTCCCCGGCTGCTGAGTTGGGAACTGTCATCACGG 2488

Qy   1989 AGTGCTTCAGAGCCTCGGGCTCAGGGTCCCAGGGTCCCAGGGCTGAGGGCTGGGA 2048
          |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2489 AGTGCTTCAGAGCCTCGGGCTCAGGGTCCCAGGGTCCCAGGGCTGAGGGCTGGGA 2548

Qy   2049 GCTCCCTTGCGCGTCCCAGCAGTTTGCGCAGTTGCAGTGGGGTAAGGAGGCCAAGCCCATTGTGTAATC 2108
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2549 GCTCCCTTGCGCGTCCCAGCAGTTTGCGCAGTTGCAGTGGGGTAAGGAGGCCAAGCCCATTGTGTAATC 2608

Qy   2109 ACCCAAAACCCCCGCCGCCTGCGCCTGTTTTCCCTTCGCGCTACCTTGAGTAGTTGGAGC 2168
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy    402  TGAGCAGGAGGAGCAGGTGGTGGCCGCGCCTTGAGGCAGGCCCTGCGAGCTGCGATGGAG  461
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2353  TGAGCAGGAGGAGCAGGTGGTGGCCGCGCCTTGAGGCAGGCCCTGCGAGCTGCGATGGAG  2412

Qy    462  ACCTGCAGGAGGATCGAGATCCCAGTGGTAGCTATTATGGCCACTGGTGCTGGGATCCGGG  521
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2413  ACCTGCAGGAGGATGAGATCCCAGTGGTAGCTATTATGGCCACTGGTGCTGGGATCCGGG  2472

Qy    522  CAATGACTTCCCTGTATGGCAGCTGGCTGGCCTGGCCTGAAGGAGCTGGGCCTCTTGGATTGCG  581
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2473  CAATGACTTCCCTGTATGGCAGCTGGCTGGCCTGGCCTGAAGGAGCTGGGCCTCTTGGATTGCG  2532

Qy    582  TCTCCTACATCACCGGGCGGCCTTGGCCAACCTTTATGAGGACC  641
           ||||||||||||||||||||||||||||||||||||||||||||
Db   2533  TCTCCTACATCACCGGGCGGCCTCGGGCCTTGGCCAACCTTTATGAGGACC  2592

Qy    642  CAGAGTGGTCTCAGAAGGACCTGGCAGAGGGGCCACTGAGTTGCTGAAGACCCAGTGACCA  701
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2593  CAGAGTGGTGTCTCAGAAGGACCTGGCAGAGGGGCCCACTGAGTTGCTGAAGACCCAGTGACCA  2652

Qy    702  AGAACAAGCTGGGTGTGCTGGCCGTTGGGGCCCCCAGCCAGCTGCGCAGCCGGTACCCGGCCG  761
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Db   2653  AGAACAAGCTGGGTGTGCTGGCTGGCCGTTGGGGCCCCCAGCCAGCTGCGCAGCCGGTACCCGGCCG  2712

Qy    762  AGCGGTGCCCCGCTTGGGCTTCACCAACCTGCTTCACCAACCTGTGGGCCCTCATCAACGAGG  821
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Db   2713  AGCGGTGCCCCGCTTGGGCTTCACCAACCTGCTTCACCAACCTGTGGGCCCTCATCAACGAGG  2772

Qy    822  CGCTTGCTGCATGATGAGCCCATGATCAACAGCTCTCAGATCAACGGGAGGCCCTGAGTC  881
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Db   2773  CGCTTGCTGCATGATGAGCCCATGATCAACAGCTCTCAGATCAACGGGAGGCCCTGAGTC  2832

Qy    882  ATGGCCAGAACCCTCTGCCCATCTACTGCCCATCTGCCCTCAACACAGGCAGAGCCTGACCA  941
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Db   2833  ATGGCCAGAACCCTCTGCCCATCTGCCCATCTGCCCTCAACACAGGCAGAGCCTGACCA  2892

Qy    942  CTTTTTGAATTGGGGAGTTGGTGCGAGTTCTCTCCCTACGAGTACG  1001
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Db   2893  CTTTTTGAATTGGGGAGTTGGTGCGAGTTCTCTCCCTACGAGTACG  2952

Qy   1002  GGGCCTTCATCCCCTGAGCTCTTTGGCTCCGAGTTCTTTATGGGCAGCTGATGAAGA  1061
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Db   2953  GGGCCTTCATCCCCTGAGCTCTTTGGCTCCGAGTTCTTTATGGGCAGCTGATGAAGA  3012

Qy   1062  GGCTTCCTGAGTCCGCATCCGCATCGCTTCTTAGAAGGTATCTGGAGCAACGTATGCAGCCA  1121
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Db   3013  GGCTTCCTGAGTCCGCATCCGCATCGCTTCTTAGAAGGTATCTGGAGCAACGTATGCAGCCA  3072

Qy   1122  ACCTTCCAGACAGCAGCTTATACTGGGCCTCAGAGCCCAGTTCTGGGACCGCTGGGTCA  1181
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Db   3073  ACCTTCCAGACAGCAGCTTATACTGGGCCTCAGAGCCCAGTTCTGGGACCGCTGGGTCA  3132

Qy   1182  GGAACCAGGCCAACCTGACAAGGAGCAGTCCCCCTTCTGAAGATAGAAGACCACCCT  1241
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Db   3133  GGAACCAGGCCAACCTGACAAGGAGCAGTCCCCCTTCTGAAGATAGAAGAACCACCCCT  3192

Qy   1242  CAACAGCGCGGCAGAATAGCTGAGTTTTCACCGATCTTCGACGTGGCCTCCACTGGCCC  1301
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Db   3193  CAACAGCGCGGCAGGATAGCTGAGTTTTCACCGATCTTCGACGTGGCCTCCACTGGCCC  3252

Qy   1302  AGGCCACACATAATTTCCTGCGTGCCTCATTTCCACAAAGACTACTTTCAGCATCCTC  1361
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Db   3253  AGGCCACACATAATTTCCTGCGTGCCTCCTCATTTCCACAAAGACTACTTTCAGCATCCTC  3312

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Qy   1482  TGCAGCCCACTCGGGACGTGGACCTGCTCATCCTGTCATTGGACTACAACCTCACAACCTCCACGGGAGCCT  1541
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Db   3433  TGCAGCCCACTCGGGACGTGGACCTGCTCATCCTGTCATTGGACTACAACCTCGTCATTGGACTACAACCTCACAACCTCCACGGGAGCCT  3492

Qy   1542  TCCAGCAGTTGCAGTCTGCAGTTGCAGTCCGTTCTGCCAGGAGCAGGGGATCCCGTTCCCACCCA  1601
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Db   3673  ACTCGGCCCCTGGGTCCGGGCGACACCCGGAGGAGGCGGCAGCTGGGCAGCTGT  3732

Qy   1749  CTTCATCGGACTCTCCCTACCACTACAGCACCATTACAATGTCTGCAACAACACCAGGAGACGTGACA  1808
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Db   3733  CTTCATCGGACTCTCCCTACCACTACAGCACCATTACAATGTCTGCAACAACACCAGGAGACGTGACA  3792

Qy   1809  AGTGCTGCACCTGACACATTACAATGTCTGCAGCGAGAGCAGCAGCTGCTCTGAGGGCTC  1868
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Db   3793  AGTGCTGCACCTGACACATTACAATGTCTGCAGCGAGAGCAGCAGCTGCTCTGAGGGCTC  3852

Qy   1869  TGCGCCAGGCAGTGCAGCGGAGGCGGAGGCCCCACTGAGTTGCAGGTGGAGGCCCCCTGC  1928
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Qy   1929  CACCCCTAACTCTCATTCATTCCTGGCTCGGGCTGGACTGTCCCAGGGTCCAGGGTGGGA  1988
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Db   3913  CACCCCTAACTCTCATTCATTCCTGGCTCGGGCTGGACTGTCCCAGGGTCCAGGGTGGGA  3972

Qy   1989  AGTTGCTTCAGAGCCTTCAGAGCCTCGGGGCTGGGTAAGGAGCCAAGGCCAAGTTGTGTAATC  2048
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Qy   2049  GCTCCCTTGCGCTCAGAGTTTGCAGTGGGTAAGGAGCCAAGGCCAAGTTGTGAGTAGTTGGAGC  2108
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Qy   2109  ACCCAAAACCCCCGGCCTTGCCCTGTTTTCCCTTCTGCGCTACTTGTTTCCCTTTCGCGCCTGTGTTTCGCGCTACTTGTTTCCCTTTCGCGCC  2168
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4093  ACCCAAAACCCCCGGCCTTGCCCTGTTTTCCCTTCTGCGCTACTTGTTTCCCTTTCGCGCCTGTGTTTCGCGCTACTTGTTTCCCTTTCGCGAGC  4152

Qy   2169  ACTTGATACATTCACAGACTCATACAAA  2195
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Db   4153  ACTTGATACATTCACAGACTCATACAAA  4179
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RESULT 11
ABXI1883
ID   ABXI1883   standard; cDNA; 4183 BP.
XX
AC   ABXI1883;
XX
DT   10-MAY-2003 (first entry)
XX
DE   Human partial cDNA for cytosolic phospholipase A2-beta, cPLA2-beta.
XX
KW   Human; ss; calcium independent cytosolic phospholipase A2-beta;
KW   cPLA2-beta; antiinflammatory; arachidonic acid cascade;
KW   inflammatory condition.
XX
OS   Homo sapiens.
XX
FH   Location/Qualifiers
FT   CDS   1560..3896
FT   /*tag= a
FT   /product= "Partial cPLA2-beta"
FT   /partial

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FT
XX              /note= "No start codon shown"
XX
PN   US6482625-B1.
XX
PD   19-NOV-2002.
XX
PF   29-JUN-2001; 2001US-0895547.
XX
PR   24-JAN-1997;  97US-00788975.
PR   13-DEC-1999;  99US-00460145.
XX
PA   (GEMY ) GENETICS INST LLC.
XX
PI   Kriz R, Song C;
XX
DR   WPI; 2003-287361/28.
DR   P-PSDB; ABG76482.
XX
PT   Novel purified calcium-independent cytosolic phospholipase A2-beta
PT   enzyme, useful for screening compounds having antiinflammatory activity
PT   mediated by the arachidonic acid cascade.
XX
PS   Claim 1; Col 11-14; 19pp; English.
XX
CC   The invention relates to a purified phospholipase enzyme (calcium-
CC   independent cytosolic phospholipase A_2-beta enzyme) peptide appearing as
CC   ABG76482 encoded by a polynucleotide appearing as ABX118883. The protein
CC   has an enzymatic activity in a mixed micelle assay (MMA) with 1-palmitoyl
CC   -2-(1^4C)-arachidonyl- phosphatidylcholine. cPLA2-beta is useful for
CC   assaying chemical agents for antiinflammatory activity mediated by the
CC   various components of the arachidonic acid cascade. cPLA2-beta is also
CC   useful in the development of polyclonal and monoclonal antibodies which
CC   are useful as research or diagnostic tools, and to study phospholipase
CC   A_2 activity and inflammatory conditions. The present sequence encodes a
CC   partial cPLA2-beta protein
XX
SQ   Sequence 4183 BP; 983 A; 1177 C; 1168 G; 850 T; 0 U; 5 Other;

Query Match            82.0%;  Score 1806.2;  DB 7;  Length 4183;
Best Local Similarity  98.1%;  Pred. No. 0;
Matches 1851;  Conservative    0;  Mismatches    3;  Indels   33;  Gaps    1;
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Qy    342  GACTGAGGGAGGGAGGAGGAAGCAGGTGGTGGCCGGCGCGGCTTGGGCTGCGACTGGCA  401
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Db   2293  GACTGAGGGAGGGAGGAGGAAGCAGGTGGTGGCCGGCGCGGCTGGGCTGCGACTGGCA   2352

Qy    402  TGAGCAGGAGGAAGCAGGTGGTGGCGGCCGGCCTTGAGGCAGGCCCCTGCAGTGGATGGAG  461
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2353  TGAGCAGGAGGAAGCAGGTGGTGGCGGCCGGCCTTGAGGCAGGCCCCTGCAGTGGATGGAG  2412

Qy    462  ACCTGCAGGAGGATGAGATCCCAGTGGTAGCTATTATGGCCACTGTGGTGGGGATCCGGG   521
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Db   2413  ACCTGCAGGAGGATGAGATCCCAGTGGTAGCTATTATGGCCACTGTGGTGGGGATCCGGG   2472

Qy    522  CAATGACTTCCCTGTATGGGCAGCTGGCCTGAAGGAGCTGGGCCTTCTGGATTGCG     581
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Db   2473  CAATGACTTCCCTGTATGGGCAGCTGGCCTGCTGCCTGAAGGAGCTGGGCCTTCTGGATTGCG  2532

Qy    582  TCTCCTACATCACCGGGGCGGGGCTTCGGGCTTGGCCACCTCCAACCTTTATGAGGACC   641
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Db   2533  TCTCCTACATCACCGGGGCGGGGCTTCGGGCTTGGCCACCTCCAACCTTTATGAGGACC   2592

Qy    642  CAGAGTGGTTCTCAGAAGGACCTGGGCGCCCAGCAGGGCCCACTGAGTTGCTGAAGACCCCAGGTGACCA  701
           |||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2593  CAGAGTGGTTCTCAGAAGGACCTGGGCGCCCAGCAGGGCCCACTGAGTTGCTGAAGACCCAGGTGACCA   2652

Qy    702  AGAACAAGCTGGGTGTGCTGCCCCCAGCCAGCTGCAGCGGTACCGGCAGGAGCTGGGCCG  761
           |||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2653  AGAACAAGCTGGGTGTGCTGCCCCCAGCCAGCTGCAGCGGTACCGGCAGGAGCTGGGCCG   2712

Qy    762  AGCGTGCGCCCGCTTGGGCTACCCAAGCTGCTTCACCAACTGTCGGCCCTCATCAACGAGG  821
           |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2713  AGCGTGCGCCCGCTTGGGCTACCCAAGCTGCTTCACCAACTGTCGGCCCTCATCAACGAGG  2772
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Qy    822  CGCTGCTGCTGCATGATGAGCCCATGATCAATCACAAGCTCTCAGATCAACGGAGCCCTGAGTC   881
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Db   2773  CGCTGCTGCTGCATGATGAGCCCATGATCAATCACAAGCTCTCAGATCAACGGAGCCCTGAGTC   2832

Qy    882  ATGGCCAGAACCCCTGCCCATCTACTGTGCCCTCAACACCAAAGGCAGAGCTTGACCA   941
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Db   2833  ATGGCCAGAACCCCTGCCCATCTACTGTGCCCTCAACACCAAAGGCAGAGCCTGACCA   2892

Qy    942  CTTTTGAATTGGGAGTGGTGGCGAGTTCTCTCCCTACGAGGTCGCTTCCCCAAGTACG   1001
           |||||||||||||||||||||||||||||||||||||||||||||||
Db   2893  CTTTTGAATTGGGAGTGGTGGCGAGTTCTCTCCCTACGAGGTCGGCTTCCCCAAGTACG   2952

Qy   1002  GGGCCTTCATCCCCTCTGAGCTCTTTGGCTCGGAGTTCTTTATGGGGCAGCTGATGAAGA  1061
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Db   2953  GGGCCTTCATCCCCTCTGAGCTCTTTGGCTCTGGGCCCAGTTCTTTATGGGGCAGCTGATGAAGA   3012

Qy   1062  GGCTTCCTGAGTCCCGCATCTGCTTCTAGAAGGTATCTGGAGCAACCTGTATCAGCCA  1121
           |||||||||||||||||||||||||||||||||||||||||||||||||
Db   3013  GGCTTCCTGAGTCCCGCATCTGCTTCTAGAAGGTATCTGGAGCAACCTGTATCAGCCA   3072

Qy   1122  ACCTCCAGACAGCTTATACTGGGCCTCAGAGACCCAGCCAGTTCTCGGACCGCTGGGTCA  1181
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Db   3073  ACCTCCAGACAGCTTATACTGGGCCTCAGAGCCCAGCCAGTTCTCGGACCGCTGGGTCA   3132

Qy   1182  GGAACCAGGCCAACCTGACAACGGAGCAGGTCCCCTTCGAAGATAGAAGAACCACCCT   1241
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Db   3133  GGAACCAGGCCAACCTGACAACGGAGCAGGTCCCCTTCGAAGATAGAAGAACCACCCCT   3192

Qy   1242  CAACAGCCGGCCAGAATAGCTGAGTTTTCACCGATCTTCTGACGTGGCGTCCACTGGCCC  1301
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Db   3193  CAACAGCCGGCCAGGATAGCTGAGTTTTTCACCGATCTTCTGACGTGGCGTCCACTGGCCC   3252

Qy   1302  AGGCCACACATAATTTCCTGCGTGGCCTCCATTTCCATTTCCACAAAGACTACTTTCAGCATCCTC  1361
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Db   3253  AGCCACACATAATTTCCTGCGTGGCCTCCATTTCCATTTCCACAAAGACTACTTTCAGCATCCTC   3312

Qy   1362  ACTTCTCCACAATGGAAAGCTACCACTCTGGATGGCTCTCCCAACCAGCTGACACCCTCGG  1421
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Db   3313  ACTTCTCCACAATGGAAAGCTACCACTCTGGATGGCTCTCCCAACCAGCTGACACCCTCGG   3372

Qy   1422  AGCCCCACCTGTTGCCTGCTGGATGTTGCTACCTCATCAATACCAGCTGCCTGCCCCTCC   1481
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Db   3373  AGCCCCACCTGTTGCCTGCTGGATGTTGCTACCTCATCAATACCAGCTGCCTGCCCCTCC   3432

Qy   1482  TGCAGCCCCACTGGGACGTGGACCTCATCGTGCATTGGAGCTGGTCAGCTGGATGGAG   1541
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Qy   1542  TCCAGCAGTTGCAGCTCCTGGGCCGGTTCTGCGCCAGCTTGCGCCAGGAGCAGCGGGGATCCCGTTCCACCA  1601
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Qy   1662  CCTGCCCCGGAGCCCCTGCGCGTCTT--------------           1693
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Db   3613  CCTGCCCCGGAGCCCCTGCGCGTCTGCCACTTTCCTGTCAGCGCTCCTTCCGGGAGT   3672

Qy   1694  ----TCCTGGGGTCCGGCGGACACCCGAGGAGCGGCAGCTGGGAGGTGAACCTGT   1748
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Qy   1749  CTTCATCGGACTCTCCCTACCACTACAGGAGAAGTGACCTACCAGGAGCACGTGACA   1808
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Db   3733  CTTCATCGGACTCTCCCTACCACTACAGGGAGCTACAGCGAAGGTGACCTACCAGGAGCACGTGACA   3792

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Qy   1869 TGCGCCAGGCAGTGCAGCGCGAGGCGGCAGCGCAGGCCCCACTGATGGCCGGGGCCCCTGC 1928
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Db   3973 AGTGCTTCAGAGCCTCGGGCTTCAGGTGGCACTGTCCCAGGGTCCAGGGCTGAGGGCTGGGA 4032

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Qy   2109 ACCCAAAACCCCCCGGCCTGTGCCTGTTTTCCCTTCTGCGCTACCTTGAGTAGTTGGAGC 2168
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RESULT 12
AAV34229
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AC   AAV34229;
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DT   25-MAR-2003 (revised)
DT   28-JAN-1999 (first entry)
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DE   Human secreted protein gene 11 clone HCENJ40.
XX
KW   Human; secreted protein; fusion protein; gene therapy; protein therapy;
KW   diagnosis; tissue; cancer; tumour; neurodegenerative disorder; leukaemia;
KW   developmental abnormality; foetal deficiency; blood; allergy; renal; ds;
KW   immune system; asthma; lymphocyic disease; brain; hepatic; lymphoma;
KW   inflammation; ischaemic shock; Alzheimer's disease; restenosis; AIDS;
KW   cognitive disorder; schizophrenia; prostate; obesity; osteoclast; thymus;
KW   osteoporosis; arthritis; testis; lung; thyroiditis; thyroid; digestion;
KW   endocrine; metabolism; regulation; malabsorption; gastritis; neoplasm.
XX
OS   Homo sapiens.
XX
PN   WO9839446-A2.
XX
PD   11-SEP-1998.
XX
PF   06-MAR-1998;   98WO-US004482.
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PR   07-MAR-1997;   97US-0038621P.
PR   07-MAR-1997;   97US-0040161P.
PR   07-MAR-1997;   97US-0040162P.
PR   07-MAR-1997;   97US-0040163P.
PR   07-MAR-1997;   97US-0040333P.
PR   07-MAR-1997;   97US-0040334P.
PR   07-MAR-1997;   97US-0040336P.
PR   07-MAR-1997;   97US-0040626P.
PR   11-APR-1997;   97US-0043311P.
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PR   11-APR-1997;   97US-0043672P.
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PR   23-MAY-1997;   97US-0047583P.
PR   23-MAY-1997;   97US-0047584P.
PR   23-MAY-1997;   97US-0047585P.
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PR   23-MAY-1997;   97US-0047592P.
PR   23-MAY-1997;   97US-0047593P.
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PR   23-MAY-1997;   97US-0047612P.
PR   23-MAY-1997;   97US-0047613P.
PR   23-MAY-1997;   97US-0047614P.
PR   23-MAY-1997;   97US-0047615P.
PR   23-MAY-1997;   97US-0047617P.
PR   23-MAY-1997;   97US-0047618P.
PR   23-MAY-1997;   97US-0047632P.
PR   23-MAY-1997;   97US-0047633P.
PR   06-JUN-1997;   97US-0048964P.
PR   06-JUN-1997;   97US-0048974P.
PR   22-AUG-1997;   97US-0056630P.
PR   22-AUG-1997;   97US-0056631P.
PR   22-AUG-1997;   97US-0056632P.
PR   22-AUG-1997;   97US-0056636P.
PR   22-AUG-1997;   97US-0056637P.
PR   22-AUG-1997;   97US-0056662P.
PR   22-AUG-1997;   97US-0056664P.
PR   22-AUG-1997;   97US-0056845P.
PR   22-AUG-1997;   97US-0056862P.
PR   22-AUG-1997;   97US-0056864P.
PR   22-AUG-1997;   97US-0056872P.
PR   22-AUG-1997;   97US-0056874P.
PR   22-AUG-1997;   97US-0056875P.
PR   22-AUG-1997;   97US-0056876P.
PR   22-AUG-1997;   97US-0056877P.
PR   22-AUG-1997;   97US-0056878P.
PR   22-AUG-1997;   97US-0056879P.
PR   22-AUG-1997;   97US-0056880P.
PR   22-AUG-1997;   97US-0056881P.
PR   22-AUG-1997;   97US-0056882P.
PR   22-AUG-1997;   97US-0056884P.
PR   22-AUG-1997;   97US-0056886P.
PR   22-AUG-1997;   97US-0056887P.
PR   22-AUG-1997;   97US-0056888P.
PR   22-AUG-1997;   97US-0056889P.
PR   22-AUG-1997;   97US-0056892P.
PR   22-AUG-1997;   97US-0056893P.
PR   22-AUG-1997;   97US-0056894P.
PR   22-AUG-1997;   97US-0056903P.
PR   22-AUG-1997;   97US-0056908P.
PR   22-AUG-1997;   97US-0056909P.
PR   22-AUG-1997;   97US-0056910P.
PR   22-AUG-1997;   97US-0056911P.
PR   05-SEP-1997;   97US-0057650P.
PR   05-SEP-1997;   97US-0057761P.

XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Ruben SM, Rosen CA, Fischer CL, Soppet DR, Carter KC;
PI Bednarik DP, Endress GA, Yu G, Ni J, Feng P, Young PE, Greene JM;
PI Ferrie AM, Duan R, Hu J, Florence KA, Olsen HS, Ebner R, Brewer LA;
PI Moore PA, Shi Y, Lafleur DW, Li Y, Zeng Z, Kyaw H;
XX
DR WPI; 1998-609887/51.
DR P-PSDB; AAW75132.
XX
PT New isolated human genes and the secreted polypeptides they encode -
PT useful for diagnosis and treatment of e.g. cancers, neurological
PT disorders, immune diseases, inflammation or blood disorders.
XX
PS Claim 1; Page 229-230; 447pp; English.
XX
CC This sequence represents a nucleic acid molecule which encodes a secreted
CC human protein. The gene number, and the clone it is derived from, are
CC detailed in the descriptor line. The gene can be used to generate fusion
CC proteins by linking to the gene to a human immunoglobulin Fc portion
CC (e.g. AAV34145) for increasing the stability of the fused protein as
CC compared to the human protein only. The invention relates to 70 novel
CC genes and their fragments (nucleic acid sequences: AAV34154-v34276; amino
CC acid sequences AAW75057-W75179) which are useful for preventing, treating
CC or ameliorating medical conditions e.g. by protein or gene therapy. Also,
CC pathological conditions can be diagnosed by determining the amount of the
CC new polypeptides in a sample or by determining the presence of mutations
CC in the new polynucleotides. Specific uses are described for each of the
CC 70 polynucleotides, based on which tissues they are most highly expressed
CC in (see AAV34154 for described uses). (Updated on 25-MAR-2003 to correct
CC PF field.) (Updated on 25-MAR-2003 to correct PI field.)
XX
SQ Sequence 1925 BP; 388 A; 613 C; 545 G; 377 T; 0 U; 2 Other;

Query Match   81.2%;   Score 1788.8;   DB 2;   Length 1925;
Best Local Similarity   97.9%;   Pred. No. 0;
Matches 1844;   Conservative   1;   Mismatches   4;   Indels 34;   Gaps   2;

Qy   347 AGGGAGGAGAAGCAGTGGTGTGGCCGCGGCTTCGGGCCTGTG-CAGAGGAGCAGGAGGACCT 405
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Db   6 AGGGAGGAGAAGCAGTGGTGTGGCCGCGGCTTCGGGCCTGTGCCAGAGGAGCAGNGCCTGAG 65

Qy   406 CAGGAGGAGAAGCAGTGGTGTGGCCGCGGCTTGAGGCTATTATGGCCACTGGTGGTGGCAAT 465
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Db   66 CAGGAGGAGGATGAGATCCCAGTGGTAGCTATTATGGCCACTGGTGGTGGCAAT 125

Qy   466 GCAGGAGGATGAGATCCCAGTGGTAGCTATTATGGCCACTGGTGGTGGGCCTCTTCGGGTCTC 525
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   126 GCAGGAGGATGAGATCCCAGTGGTAGCTATTATGGCCACTGGTGGTGGGATTGCGTCTC 185

Qy   526 GACTTCCCTGTATGGGCAGTGGCTGGCTGGGCCTCGAAGAGCTGGGCTTCTTGGATTGCGTCTC 585
         ||||||||||||||||||||||||||||||:||||:|||||||||||||||:||:||||||||
Db   186 GACTTCCCTGTATGGGCAGTGGCTGGCTGGGCCTCGAAGAGCTGGGCCTCTTGGATTGCKTCTC 245

Qy   586 CTACATCACCGGGGCCTCGGGCTCCACCTGGGCCTCCACCTGGGCCTCCAACCTTTATGGAGACCCAGA 645
         |||||||||||||||||||||||||||||||||||||||:||||||||||||||||||||||||
Db   246 CTACATCACCGGGGCCTCGGGCTCCACCTGGGCCTCCACCTGGGCCTCCAACCTTTATAAGGACCCAGA 305

Qy   646 GTGGTCTCAGAAGGACCTGCAGGGCCCACTGAGTTGCTGAAGACCCAGTGACCAAGAA 705
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   306 GTGGTCTCAGAAGGACCTGCAGGGCCCACTGAGTTGCTGAAGACCCAGTGACCAAGAA 365

Qy   706 CAAGCTGGGTGTGCTGGCCCCCAGCCAGTGCCAGCGGTACCGGCAGGAGCTGGCCGAGCG 765
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Db   366 CAAGCTGGGTGTGCTGGCCCCCAGCCAGTGCCAGCGGTACCGGCAGGAGCTGGCCGAGCG 425

Qy   766 TGCCCGGCTTGGGCTACCCAAGCTGCTTCACCAAGCTGCTTCACCAAGCTGTGCCCTCATCAACGAGGCGCT 825
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Db   426 TGCCCGGCTTGGGCTACCCAAGCTGCTTCACCAAGCTGTGGGCCCTCATCAACGAGGCGCT 485

Qy   826 GCTGCATGATGAGCCCATGATCACAAGCTCTCAGATCACAAGCCCTGAGTCATGG 885
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Db   486 GCTGCATGATGAGCCCATGATCACAAGCTCTCAGATCACAAGCGGAGGCCCTGAGTCATGG 545

Qy   886 CCAGAACCCTGCCCATTCACTCTGCCCTCAACACCAAAGGGCAGAGCCTGACCACTTT 945
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Db   546 CCAGAACCCTGCCCATCACTCTGCCCTCAACACCAAAGGGCAGAGCCTGACCACTTT 605

Qy   946 TGAATTTGGGGAGTTGGTGCGAGTTCTCTCCCTAGAGGTCGGCTTCCCCAAGTACGGGGC 1005
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Db   606 TGAATTTGGGGAGTTGGTGCGAGTTCTCTCCCTAGAGGTCGGCTTCCCCAAGTACGGGGC 665

Qy 1006 CTTCATCCCCTGAGCTCTTTGGCTCCGAGTTCTTTATGGGGCAGCTGATGAAGAGGCT 1065
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Db   666 CTTCATCCCCTGAGCTCTTTGGCTCCGAGTTCTTTATGGGGCAGCTGATGAAGAGGCT 725

Qy 1066 TCCTGAGTCCCGCATCTGCTTCTTAGAAGTATCTGGAGCAACCTGTATGCAGCCAACCT 1125
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Db   726 TCCTGAGTCCCGCATCTGCTTCTTAGAAGTATCTGGAGCAACCTGTATGCAGCCAACCT 785

Qy 1126 CCAGGACAGCTTATACTGGGCCTCAGAGCCCAGCCAGTTCTCGGGACCGCTGGGTCAGGAA 1185
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Db   786 CCAGGACAGCTTATACTGGGCCTCAGAGCCCAGCCAGTTCTGGGACCGCTGGGTCAGGAA 845

Qy 1186 CCAGGCCAACCTGGACAAGGAGCAGGTCCCCCTTCTGAAGATAGAAGAACCACCCTCAAC 1245
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Qy 1246 AGCCGGCCAGAATAGCTGAGTTTTCACCGATCTTCTGACGTGGCGTCCACTGGCCCAGGC 1305
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Db   906 AGCCGGCAGAATAGCTGAGTTTTCACCGATCTTCTGACGTGGCGTCCACTGGCCCAGGC 965

Qy 1306 CACACATAATTTCCTGCGTGGCCTCCATTTCCACAAAGACTACTTTCAGCATCCTCACTT 1365
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Db   966 CACACATAATTTCCTGCGTGGCCTCCATTTCCACAAAGACTACTTTCAGCATCCTCACTT 1025

Qy 1366 CTCCACATGGAAAGCTACCACTCTGGATGGGCTCCCCAACCAGCTGACACCCTCGGAGCC 1425
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1026 CTCCACATGGAAAGCTACCACTCTGGATGGGCTCCCCAACCAGCTGACACCCTCGGAGCC 1085

Qy 1426 CCACCTGTGCCTGCTGGATGTTGGCTACCTCAATACCAGTCGCTGCCCTCCTGCA 1485
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Qy 1486 GCCCACTCGGGACGTGACCTGACCTCATCTGTCAGCTGATGAGGACCT 1545
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Qy 1546 GCAGTTGCAGCTCCTGGGCCCGTTCTGCCAGGAGCAGGGGATCCCGTTCCCACCATCTC 1605
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Db 1206 GCAGTTGCAGCTCCTGGGCCCGTTCTGCCAGGAGCAGGGGATCCCGTTCCCACCATCTC 1265

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Db 1266 GCCCAGCCCCGAAGAGCAGCTCCAGCCTCGGGAGTGCCACACCTTCTCCGACCCCACCTG 1325

Qy 1666 CCCCGGAGCCCCGCGCCCTCGGCTGCACTT----------------------- 1693
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Db 1326 CCCCGGAGCCCCGCGCCCTCGGCTGCACTTTCCTCTGGTCAGCGACTCCTTCCGGGAGTACTC 1385

Qy 1694 -TCCTCTGGGGTCCGGCGGACACCCGGACACCCCGGAGAGGCGGCAGCGTGGGAGGTGAACCTGTCTTC 1752
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Db 1386 GGCCCCTCTGGGGTCCGGCGGACACCCGGACACCCCGGAGAGGCGGCAGCGTGGGAGGTGAACCTGTCTTC 1445

Qy 1753 ATCGGACTCTCCTACCACTACACGAAGGTGACCTACAGCCAGGAGGACGTGGACAAGCT 1812
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Db 1446 ATCGGACTCTCCTACCACTACACGAAGGTGACCTACAGCCAGGAGGACGTGGACAAGCT 1505

Qy 1813 GCTGCACCTGACACATTACACAATGTGTCCAACCTGTGGCCCTCATCAACGAGGCGCT 1872
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1506 GCTGCACCTGACACATTACACAATGTGTCCAACCTGTGCAACCAGGACAGCAGTGCTGAGGCGCTGCG 1565

Qy 1873 CCAGGCAGTGCAGCCGGAGCGGGCGCCCAGCGCCAGCGCCCCACTGATGGCCGGGCCACC 1932
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1566 CCAGGCAGTGCAGCCGGAGCGGGCGCCCAGCGCCAGCGCCCCACTGATGGCCGGGCCACC 1625

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Qy   1933  CCTAACTCTCATTCATTCCCTGGCTGCTGAGTTGCAGGTGGGAACTGTCATCACGCAGTG  1992
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Db   1626  CCTAACTCTCATTCATTCCCTGGCTGCTGAGTTGCAGGTGGGAACTGTCATCACGCAGTG  1685

Qy   1993  CTTCAGAGCCTCGGGCTCAGGTGGCACTGTCCCAGGGTCAGGTTGAGGGCTGGGAGCTC  2052
                |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1686  CTTCAGAGCCTCGGGCTCAGGTGCACTGTCCCAGGGTCAGGTTGAGGGCTGGGAGCTC  1745

Qy   2053  CCTTGCGCCTCAGCAGTTTGCAGTGGGGTAAGGAGGCCAAGCCCATTTGTGTAATCACCC  2112
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Db   1746  CCTTGCGCCTCAGCAGTTTGCAGTGGGGTAAGGAGGCCAAGCCCATTTGTGTAATCACCC  1805

Qy   2113  AAAACCCCCGGCCCTGTGCCTGTTTTCCCTTCTGCGCTACCTTGAGTAGTTGGAGCACTT  2172
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Db   1806  AAAACCCCCGGCCCTGTGCCCTGTTTTCCCTTCTGCGCTACCTTGAGTAGTTGGAGCACTT  1865

Qy   2173  GATACATCACAGACTCATACAAA  2195
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Db   1866  GATACATCACAGACTCATACAAA  1888
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RESULT 13
ACD08100
ID   ACD08100 standard; cDNA; 1925 BP.
XX
AC   ACD08100;
XX
DT   12-AUG-2003   (first entry)
XX
DE   cDNA encoding novel human secreted protein #76.
XX
KW   Human; immunoglobulin G; IgG; fragment of crystallisation; Fc;
KW   immune system disorder; haematopoietic cell disorder;
KW   immunologic deficiency disorder; ataxia telangiectasia; HIV infection;
KW   Wiskott-Aldrich disorder; thrombocytopenia; haemoglobinuria;
KW   blood coagulation disorder; blood platelet disorder; autoimmune disorder;
KW   Addison's disease; haemolytic anaemia; rheumatoid arthritis; dermatitis;
KW   glomerulonephritis; Grave's disease; allergic reaction; neoplasm;
KW   graft-versus-host disease; hyperproliferative disorder; neoplasm;
KW   infectious disease; nervous system disease; spinal cord disorder;
KW   head trauma; stroke; tissue regeneration; congenital defect; trauma;
KW   wound; burn; incision; ulcer; age disease; osteoporosis;
KW   periodontal disease; liver failure; catabolism; anabolism; metabolism;
KW   food additive; preservative; secreted protein; gene; ss.
XX
OS   Homo sapiens.
XX
PN   US2003027132-A1.
XX
PD   06-FEB-2003.
XX
PF   04-SEP-1998;   98US-00148545.
XX
PR   07-MAR-1997;   97US-0038621P;
PR   07-MAR-1997;   97US-0040161P;
PR   07-MAR-1997;   97US-0040162P;
PR   07-MAR-1997;   97US-0040163P;
PR   07-MAR-1997;   97US-0040333P;
PR   07-MAR-1997;   97US-0040334P;
PR   07-MAR-1997;   97US-0040336P;
PR   07-MAR-1997;   97US-0040626P;
PR   11-APR-1997;   97US-0043311P;
PR   11-APR-1997;   97US-0043312P;
PR   11-APR-1997;   97US-0043313P;
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PR   11-APR-1997;   97US-0043580P;
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PR   23-MAY-1997;   97US-0047500P;
PR   23-MAY-1997;   97US-0047501P;
PR   23-MAY-1997;   97US-0047502P;
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PR   23-MAY-1997;   97US-0047613P;
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PR   23-MAY-1997;   97US-0047633P;
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PR   22-AUG-1997;   97US-0056877P;
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PR   22-AUG-1997;   97US-0056879P;
PR   22-AUG-1997;   97US-0056880P;
PR   22-AUG-1997;   97US-0056881P;
PR   22-AUG-1997;   97US-0056882P;
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PR   22-AUG-1997;   97US-0056911P;
PR   05-SEP-1997;   97US-0057650P;
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PR 05-SEP-1997; 97US-0057761P.
PR 06-MAR-1998; 98WO-US004482.
XX
PA (RUBE/) RUBEN S M.
PA (ROSE/) ROSEN C A.
PA (FISC/) FISCHER C L.
PA (SOPP/) SOPPET D R.
PA (CART/) CARTER K C.
PA (BEDN/) BEDNARIK D R.
PA (ENDR/) ENDRESS G A.
PA (YUGG/) YU G.
PA (NIJJ/) NI J.
PA (FENG/) FENG P.
PA (YOUN/) YOUNG P E.
PA (GREE/) GREENE J M.
PA (FERR/) FERRIE A M.
PA (DUAN/) DUAN R.
PA (HUJJ/) HU J.
PA (FLOR/) FLORENCE K A.
PA (OLSE/) OLSEN H S.
PA (EBNE/) EBNER R.
PA (BREW/) BREWER L A.
PA (SHIY/) SHI Y.
XX
PI Ruben SM, Rosen CA, Fischer CL, Soppet DR, Carter KC;
PI Bednarik DR, Endress GA, Yu G, Ni J, Feng P, Young PE, Greene JM;
PI Ferrie AM, Duan R, Hu J, Florence KA, Olsen HS, Ebner R, Brewer LA;
PI Shi Y;
XX
DR WPI; 2003-466138/44.
DR P-PSDB; AB002008.
XX
PT Novel isolated human secreted HODAZ50 polypeptide useful for diagnosing
PT or treating deficiencies or disorders of the immune system, autoimmune
PT disorders, hyperproliferative disorders, and infectious diseases.
XX
PS Claim 4; Page 130-131; 243pp; English.
XX
CC The invention describes an isolated human secreted HODAZ50 polypeptide
CC (I) comprising a sequence at least 95% identical to a sequence selected
CC from polypeptide fragment of any one of the 123 polypeptide sequences
CC (PS) fully defined in the specification and having biological activity,
CC polypeptide domain or epitope of PS, secreted form of PS, full-length
CC protein of PS, or variant, allelic variant or species homologue of PS.
CC (I) or a polynucleotide (II) encoding (I) is useful for preventing,
CC treating, or ameliorating a medical condition in a mammalian subject. (I)
CC or (II) is also useful for diagnosing a pathological condition or a
CC susceptibility to a pathological condition in a subject. (I) is useful
CC for identifying a binding partner which involves contacting the
CC polypeptide with the binding partner and determining whether the binding
CC partner affects the activity of the polypeptide. (I) or (II) is useful
CC for diagnosing or treating deficiencies or disorders of the immune
CC system, deficiencies or disorders of haematopoietic cells, to treat
CC immunologic deficiency disorders, ataxia telangiectasia, HIV infection,
CC Wiskott-Aldrich disorders, thrombocytopenia or haemoglobinuria, blood
CC coagulation disorders, blood platelet disorders, autoimmune disorders
CC (e.g., Addison's disease, haemolytic anaemia, rheumatoid arthritis,
CC dermatitis, glomerulonephritis, Grave's disease), allergic reactions,
CC graft-versus-host disease, hyperproliferative disorders (e.g., neoplasms
CC located in the abdomen, bone, breast, digestive system, liver, pancreas,
CC peritoneum, endocrine glands), infectious diseases (e.g., viral,
CC bacterial, fungal or parasitic infection), central and peripheral nervous
CC system diseases (e.g., spinal cord disorders, head trauma or stroke), to
CC differentiate, proliferate and attract cells leading to the regeneration
CC of tissues to repair, replace or protect tissue damaged by congenital
CC defects, trauma (wounds, burns, incisions, or ulcers) age disease (e.g.,
CC osteoporosis, periodontal disease, liver failure) or surgery. (I) or (IV)
CC is useful to modulate mammalian characteristics, to modulate mammalian
CC metabolism affecting catabolism, anabolism, processing, utilisation, and
CC storage of energy, to change a mammal's mental state or physical state,
CC or as a food additive or preservative, such as to increase or decrease
CC storage capabilities, fat content, lipid, protein, carbohydrate,
CC vitamins, minerals, cofactors or other nutritional components. This

CC sequence encodes a novel human secreted protein
XX
SQ Sequence 1925 BP; 388 A; 613 C; 545 G; 377 T; 0 U; 2 Other;

Query Match   81.2%; Score 1788.8; DB 7; Length 1925;
Best Local Similarity   97.9%; Pred. No. 0;
Matches 1844; Conservative 1; Mismatches 4; Indels 34; Gaps 2;

Qy   347 AGGGAGCTGGCCGTGCGACTGGGCTTCGGCGCCCTGTG-CAGAGAGGAGCAGGCCTTCCTGAG 405
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Db   6 AGGGAGCTGGCCGTGCGACTGGGCTTCGGCGCCCTGTGCCAGAGAGGAGCANGCCTTCCTGAG 65

Qy   406 CAGGAGGAGCAGGTGGTGCCGCGGCCTGAGGCAGGCCCTGCAGCTGGATGAGAGACCT 465
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Db   66 CAGGAGGAGCAGGTGGTGCCGCGGCCTGAGGCAGGCCCTGCAGCTGGATGAGAGACCT 125

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Qy   586 CTACATCACCGGGGCCTCGGGGCTTCCACCTGGGCCTTGGCCAACCTTTATGAGGACCCAGA 645
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Db   306 GTGGTCTCAGAAGGACCTGGCAGGGCCCACTGAGTTGCTGAAGACCCAGGTGACCAAGAA 365

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Db   366 CAAGAACCCCTGGTGTGCTGGCCCCAGCCAGCTGCAGCGGTACCGGCAGGAGCTGGCCGAGCG 425

Qy   766 TGCCCGCTTGGGCTACCCCAAGCTGCTTCACCAACCTGTGGGCCCTCATCAACGAGGGGCT 825
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DE   Human secreted protein gene 11 clone HCENJ40.
XX
KW   Human; secreted protein; fusion protein; gene therapy; protein therapy;
KW   diagnosis; tissue; cancer; tumour; neurodegenerative disorder; leukaemia;
KW   developmental abnormality; foetal deficiency; blood; allergy; renal; ds;
KW   immune system; asthma; lymphocytic disease; brain; hepatic; lymphoma;
KW   inflammation; ischaemic shock; Alzheimer's disease; restenosis; AIDS;
KW   cognitive disorder; schizophrenia; prostate; obesity; osteoclast; thymus;
KW   osteoporosis; arthritis; testis; lung; thyroiditis; thyroid; digestion;
KW   endocrine; metabolism; regulation; malabsorption; gastritis; neoplasm.
XX
OS   Homo sapiens.
XX
PN   WO9839446-A2.
XX
PD   11-SEP-1998.
XX
PF   06-MAR-1998;    98WO-US004482.
XX
PR   07-MAR-1997;    97US-0038621P.
PR   07-MAR-1997;    97US-0040161P.
PR   07-MAR-1997;    97US-0040162P.
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PR   07-MAR-1997;    97US-0040333P.
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PR   11-APR-1997;    97US-0043311P.
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PR   23-MAY-1997;    97US-0047614P.
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PR   23-MAY-1997;    97US-0047617P.
PR   23-MAY-1997;    97US-0047618P.
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Db   966 CACACATAATTCCTGCGTGCCTCCATTTCCACAAAGACTACTTTCAGCATCCTCACTT 1025
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Qy  1366 CTCCACATGGAAAGTACCACCTGGATGGGCTCCCACCAGCTGACACCCTCGGAGCC 1425
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Qy  1426 CCACCTGTGCCTGCTGGAGTGTTGGCTACCTCATCAATACCAGGTGCCTGCCCCCTCCTGCA 1485
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Qy  1694 -TCCTCTGGGGTCCGGCGGACACCCGAGGAGCCGGCAGCTGGGGAGTGAACCTGTCTTC 1752
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Qy  1933 CCTAACTTCATTCATTCCCTGCGTCTGAGTTGCAGTGGGAACTGTCATCACGCAGTG 1992
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RESULT 14
AAV34164
ID   AAV34164 standard; DNA; 1926 BP.
XX
AC   AAV34164;
XX
DT   25-MAR-2003 (revised)
DT   28-JAN-1999 (first entry)
XX
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Query Match
Best Local Similarity    80.7%;    Score 1777.8;    DB 2;    Length 1926;
Matches 1844;    Conservative    97.9%;    Pred. No. 0;
                 Conservative    1;    Mismatches    4;    Indels    35;    Gaps    3;

Qy    347  AGGGAGCTGGCCGTGCGACTGGGCTTCGGGCCCTGTG-CAGAGAGGAGCAGGCCTTCCTGAG  405
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Db     66  CAGGAGGAAGCAGGTGGTGCGCGGGCCTGAGGCAGGCAGGGCCCTGCAGCTGATGAGAGACCT  125

Qy    466  GCAGGAGGATGAGATCCAGTGGTAGCTATTATGGCCACTGGTGTGGTGGGATCCGGGCAAT  525
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Db    126  GCAGGAGGATGAGATCCCAGTGGTAGCTATTATGGCCACTGGTGTGGTGGGATCCGGGCAAT  185

Qy    526  GACTTCCCTGTATGGGCAGCTGGCTGGCCTGAAGGAGCTGGGCCTCTTGGATTGCGTCTC  585
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Db    786  CCAGGACAGCTTATACTGGGCTCCAGAGCCCAGTTCTCGGGACCGGCTGGGTCAGGAA  845

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Db    846  CCAGGCCAACCTGACAAGGAGCAGGTCCCCTTCGAAGATAGAAGAACCACCCTCAAC  905

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PR   23-MAY-1997;   97US-0047633P.
PR   06-JUN-1997;   97US-0048964P.
PR   06-JUN-1997;   97US-0048974P.
PR   22-AUG-1997;   97US-0056630P.
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PR   05-SEP-1997;   97US-0057650P.
PR   05-SEP-1997;   97US-0057761P.
XX
PA   (HUMA-) HUMAN GENOME SCI INC.
XX
PI   Ruben SM, Rosen CA, Fischer CL, Soppet DR, Carter KC;
PI   Bednarik DP, Endress GA, Yu G, Ni J, Feng P, Young PE, Greene JM;
PI   Ferrie AM, Duan R, Hu YJ, Florence KA, Olsen HS, Ebner R, Brewer LA;
PI   Moore PA, Shi Y, Lafleur DW, Li Y, Zeng Z, Kyaw H;
XX
DR   WPI, 1998-609887/51.
DR   P-PSDB; AAW75067.
XX
PT   New isolated human genes and the secreted polypeptides they encode -
PT   useful for diagnosis and treatment of e.g. cancers, neurological
PT   disorders, immune diseases, inflammation or blood disorders.
XX
PS   Claim 1; Page 171-172; 447pp; English.
XX
CC   This sequence represents a nucleic acid molecule which encodes a secreted
CC   human protein. The gene number, and the clone it is derived from, are
CC   detailed in the descriptor line. The gene can be used to generate fusion
CC   proteins by linking the gene to a human immunoglobulin Fc portion
CC   (e.g. AAV34145) for increasing the stability of the fused protein as
CC   compared to the human protein only. The invention relates to 70 novel
CC   genes and their fragments (nucleic acid sequences: AAV34154-V34276; amino
CC   acid sequences AAW75057-W75179) which are useful for preventing, treating
CC   or ameliorating medical conditions e.g. by protein or gene therapy. Also,
CC   pathological conditions can be diagnosed by determining the amount of the
CC   new polypeptides in a sample or by determining the presence of mutations
CC   in the new polynucleotides. Specific uses are described for each of the
CC   70 polynucleotides, based on which tissues they are most highly expressed
CC   in (see AAV34154 for described uses). (Updated on 25-MAR-2003 to correct
CC   PF field.) (Updated on 25-MAR-2003 to correct PI field.)
XX
SQ   Sequence 1926 BP; 388 A; 613 C; 545 G; 377 T; 0 U; 3 Other;

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Qy   1753 ATCGGACTCTCCCTACCACTACACGAAAGTGACCTACAGCCAGGAGGACGTGGACAAGCT 1812
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Qy   1813 GCTGCACCTGACACATTACAATGTCTGCAACAACCAGCAGCAGGAGCAGCTGCTGGAGGCTCTGCGG 1872
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AC   ACD08035;
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DT   12-AUG-2003  (first entry)
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DE   cDNA encoding novel human secreted protein #11.
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KW   Human; immunoglobulin G; IgG; fragment of crystallisation; Fc;
KW   immune system disorder; haematopoietic cell disorder;
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KW   immunologic deficiency disorder; ataxia telangiectasia; HIV infection;
KW   Wiskott-Aldrich disorder; thrombocytopenia; haemoglobinuria;
KW   blood coagulation disorder; blood platelet disorder; autoimmune disorder;
KW   Addison's disease; haemolytic anaemia; rheumatoid arthritis; dermatitis;
KW   glomerulonephritis; Grave's disease; allergic reaction;
KW   graft-versus-host disease; hyperproliferative disorder; neoplasm;
KW   infectious disease; nervous system disease; spinal cord disorder;
KW   head trauma; stroke; tissue regeneration; congenital defect; trauma;
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KW   food additive; preservative; secreted protein; gene; ss.
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PN   US2003027132-A1.
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PD   06-FEB-2003.
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PR  06-MAR-1998;  98WO-US004482.
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PA  (CART/)  CARTER K C.
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PI  Bednarik DR, Endress GA, Yu G, Ni J, Feng P, Young PE, Greene JM;
PI  Ferrie AM, Duan R, Hu J, Florence KA, Olsen HS, Ebner R, Brewer LA;
PI  Shi Y;
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DR  WPI; 2003-466138/44.
DR  P-PSDB; ABO01943.
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PT  Novel isolated human secreted HODAZ50 polypeptide useful for diagnosing
PT  or treating deficiencies or disorders of the immune system, autoimmune
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PT  disorders, hyperproliferative disorders, and infectious diseases.
XX
PS  Claim 4; Page 85-86; 243pp; English.
XX
CC  The invention describes an isolated human secreted HODAZ50 polypeptide
CC  (I) comprising a sequence at least 95% identical to a sequence selected
CC  from polypeptide fragment of any one of the 123 polypeptide sequences
CC  (PS) fully defined in the specification and having biological activity,
CC  polypeptide domain or epitope of PS, secreted form of PS, full-length
CC  protein of PS, or variant, allelic variant or species homologue of PS.
CC  (I) or a polynucleotide (II) encoding (I) is useful for preventing,
CC  treating, or ameliorating a medical condition in a mammalian subject. (I)
CC  or (II) is also useful for diagnosing a pathological condition or a
CC  susceptibility to a pathological condition in a subject. (I) is useful
CC  for identifying a binding partner which involves contacting the
CC  polypeptide with the binding partner and determining whether the binding
CC  partner affects the activity of the polypeptide. (I) or (II) is useful
CC  for diagnosing or treating deficiencies or disorders of the immune
CC  system, deficiencies or disorders of haematopoietic cells, to treat
CC  immunologic deficiency disorders, ataxia telangiectasia, HIV infection,
CC  Wiskott-Aldrich disorders, thrombocytopenia or haemoglobinuria, blood
CC  coagulation disorders, blood platelet disorders, autoimmune disorders
CC  (e.g., Addison's disease, haemolytic anaemia, rheumatoid arthritis,
CC  dermatitis, glomerulonephritis, Grave's disease), allergic reactions,
CC  graft-versus-host disease, hyperproliferative disorders (e.g., neoplasms
CC  located in the abdomen, bone, breast, digestive system, liver, pancreas,
CC  peritoneum, endocrine glands), infectious diseases (e.g., viral,
CC  bacterial, fungal or parasitic infection), central and peripheral nervous
CC  system diseases (e.g., spinal cord disorders, head trauma or stroke), to
CC  differentiate, proliferate and attract cells leading to the regeneration
CC  of tissues to repair, replace or protect tissue damaged by congenital
CC  defects, trauma (wounds, burns, incisions, or ulcers) age disease (e.g.,
CC  osteoporosis, periodontal disease, liver failure) or surgery. (I) or (IV)
CC  is useful to modulate mammalian characteristics, to modulate mammalian
CC  metabolism affecting catabolism, anabolism, processing, utilisation, and
CC  storage of energy, to change a mammal's mental state or physical state,
CC  or as a food additive or preservative, such as to increase or decrease
CC  storage capabilities, fat content, lipid, protein, carbohydrate,
CC  vitamins, minerals, cofactors or other nutritional components. This
CC  sequence encodes a novel human secreted protein
XX
SQ  Sequence 1926 BP; 388 A; 613 C; 545 G; 377 T; 0 U; 3 Other;

Query Match             80.7%;  Score 1777.8;  DB 7;  Length 1926;
Best Local Similarity   97.9%;  Pred. No. 0;
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Qy    347 AGGGAGCTGGCCGTGCGACTGGGCTTCGGGCCCTG-CAGAGGAGGAGGAGGCCTTCCTGAG 405
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Db      6 AGGGAGCTGGCCGTGCGACTGGGCTTCGGGCCCTGCCCAGAGGAGGAGCANGCCTTCCTGAG 65

Qy    406 CAGGAGGAAGCAGGTGGTGCGCGGCCTTGAGCGAGGAGGCCTGCAGCTGGATGAGGAGACCT 465
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Qy    586 CTACATCACCGGGGCCTCGGGGCTCCACCTGGCCTTGGCCAACCTTATGAGGACCCAGA 645
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Db   366 CAAGCTGGGTGTGCTGGCCCCGAGCTGCGAGCGCGTACCGGCAGGAGCTGCGAGGCG  425
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Job time : 959.252 secs

OM nucleic - nucleic search, using sw model

Run on: October 7, 2004, 11:15:59 ; Search time 8928.72 Seconds
(without alignments)
10698.960 Million cell updates/sec

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Listing first 45 summaries

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41: em_hgo_other:*

SUMMARIES

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	2118.6	96.1	3038	9	AK124489	AK124489 Homo sapi
	2	1816.8	82.4	3085	6	AR137923	AR137923 Sequence
	3	1816.8	82.4	3085	6	AR137924	AR137924 Sequence
	4	1816.8	82.4	3085	6	AR156370	AR156370 Sequence
	5	1816.8	82.4	3085	6	AR156371	AR156371 Sequence
	6	1816	82.4	3352	9	AF065215	AF065215 Homo sapi
	7	1814	82.3	3193	9	BC013415	BC013415 Homo sapi
	8	1806.2	82.0	2699	6	AR168355	AR168355 Sequence
	9	1806.2	82.0	2699	6	AR255869	AR255869 Sequence
	10	1806.2	82.0	3339	9	AF121908	AF121908 Homo sapi
	11	1806.2	82.0	4183	6	AR168354	AR168354 Sequence
	12	1806.2	82.0	4183	6	AR255868	AR255868 Sequence
	13	1788.8	81.2	1925	6	BD195624	AR352679 70 human
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c	17	1676.6	76.1	1818	6	AR352680	AR352680 Sequence
c	18	1676.6	76.1	1818	6	BD195625	BD195625 70 human
	19	1422	64.5	7252	9	AF065216	AF065216 Homo sapi
	20	1408.6	63.9	8517	9	AR137922	AR137922 Sequence
	21	1408.6	63.9	8517	6	AR156369	AR156369 Sequence
	22	1320.2	59.9	3775	9	BX648318	BX648318 Homo sapi
	23	918.4	41.7	1712	10	BC042758	BC042758 Mus muscu
	24	602	27.3	2409	6	AX417785	AX417785 Sequence
	25	602	27.3	3197	6	AX402962	AX402962 Sequence
	26	602	27.3	3587	9	AB090876	AB090876 Homo sapi
c	27	509.2	23.1	168413	2	AC009877	AC009877 Homo sapi
	28	507.6	23.0	139376	2	AC020659	AC020659 Homo sapi
	29	507.6	23.0	180304	2	AC012541	AC012541 Homo sapi
c	30	494.8	22.5	58152	2	AC087582	AC087582 Homo sapi
	31	444.2	20.2	3998	9	HSM808630	HSM808630 Homo sapi
	32	441	20.0	4066	9	AK127558	AK127558 Homo sapi
	33	429.6	19.5	3879	6	AX512947	AX512947 Sequence
	34	399.8	18.1	3370	6	BC035335	BC035335 Homo sapi
	35	398.2	18.1	3460	6	BD141861	BD141861 Polypepti
	36	393.2	17.8	3032	9	AK122623	AK122623 Homo sapi
	37	385.8	17.5	2547	6	AX402959	AX402959 Sequence
	38	380.2	17.3	4459	10	BC060600	BC060600 Mus muscu
	39	365	16.6	2694	6	BD141893	BD141893 Polypepti
	40	358.6	16.3	3006	10	BC039947	BC039947 Mus muscu
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	42	336.2	15.3	2397	6	AX490840	AX490840 Sequence
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	45	184.8	8.4	237806	2	AC097746	AC097746 Rattus no

ALIGNMENTS

RESULT 1
AK124489
LOCUS   AK124489   3038 bp   mRNA   linear   PRI 09-SEP-2003
DEFINITION Homo sapiens cDNA FLJ42498 fis, clone BRACE2035381, highly similar
            to Homo sapiens phospholipase A2, group IVB (cytosolic) (PLA2G4B).
ACCESSION   AK124489
VERSION   AK124489.1 GI:34530282
KEYWORDS   oligo capping; fis (full insert sequence).
SOURCE   Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
AUTHORS   Tanigami,A., Fujiwara,T., Shibahara,T., Goto,Y., Hirao,M.,
            Shimizu,F., Wakebe,H., Ono,T., Hishigaki,H., Watanabe,T., Ozaki,K.,

Pred. No. is the number of results predicted by chance to have a

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        Sugiyama,T., Irie,R., Otsuki,T., Sato,H., Wakamatsu,A., Ishii,S.,
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        Sugano,S., Nagahari,K., Masuho,Y., Nagai,K. and Isogai,T.
  TITLE  NEDO human cDNA sequencing project
  JOURNAL Unpublished
REFERENCE 2 (bases 1 to 3038)
  AUTHORS Isogai,T. and Yamamoto,J.
  TITLE  Direct Submission
  JOURNAL Submitted (15-JUL-2003) Takao Isogai, FLJ Project (HRI Team); 2-6-7
        Kazusa-Kamatari, Kisarazu, Chiba 292-0818, Japan
        (E-mail:genomics@hri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986)
COMMENT  NEDO human cDNA sequencing project supported by Ministry of
        Economy, Trade and Industry of Japan; cDNA full insert sequencing:
        Research Association for Biotechnology (RAB); cDNA library
        construction: Helix Research Institute (HRI) (supported by Japan
        Key Technology Center etc.); 5'- & 3'-end one pass sequencing: RAB,
        HRI, and Biotechnology Center, National Institute of Technology and
        Evaluation; clone selection for full insert sequencing: HRI and
        RAB; annotation: HRI and RAB.
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                     /clone_lib="BRACE2"
                     /note="cloning vector: pME18SFL3"
ORIGIN

Query Match      96.1%;  Score 2118.6;  DB 9;  Length 3038;
Best Local Similarity  97.8%;  Pred. No. 0;
Matches 2181;  Conservative 0;  Mismatches 11;  Indels 37;  Gaps 2;

Qy    1 CATGGTTTGGGGCGCAGAGAGGGCCAGAGAGGGCCAGGANACCAAGGAGGAGAGAGAGGGGAATTGCGCC   60
          |||||||||||||||||||||||||||||||||||||| ||||||| |||||||| ||||||||||||||
Db  810 CATGGTTTGGGGCGCAGAGAGGGCCAGAGAGGGCCAGGAAAACCAAGGAGAGAGGGGAAATTGCGCC  869

Qy   61 CTTTTGGGGTGGAAGCTGTGTTATGGGTGGACCTTAAATGATCTTCGTAGAGTTGTCGCCCAC  120
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Db  930 CCTGGCCCCTCGTGTTGAGAGAGTGGCTTCTCACCTCACAGACACCAGGATTATTGGTCCT  989

Qy  181 TTTCTGCCCCGCCCCCTGCCCCTTTTTTTTTTTTTT----TGAGATGGAGTCTCTCTCTG  236
          |||||||||||||||||||||||||||||||||||    |||||||||||| |||||||||
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                                                                              Db  1246 TGAGCAGGAGGAAGCAGGTGGTGGCGGCCGGCCCTGAGGCAGGCCCTGCGCAGCTGGATGGAG 1305

Qy  1677 CTGCGGTGCTGCACTTT------------------------TCCTCTGGGG 1703             Qy   462 ACCTGCAGGAGGATGAGATCCCAGTGGTAGCTATTATGGCCACTGGTGTGTGGGGATCCGGG  521
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Qy  1704 TCCGGGCCGACACCCGAGGAGGGGCAGCTGGGAGGTGAACCTGTCTTCATCGGACTCTC 1763       Qy   522 CAATGACTTCCCTGTATGGCAGCTGGCTGGCCTGAAGGAGCTGGGCCTCTTGGATTGCG  581
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Qy  1884 AGCGGAGGCGGCAGCGCCAGGCCCCACTGATGGCCGGGGCCCCTGCACCCCTAACTCTCA 1943     Qy   702 AGAACAAGCTGGGTGTGGCCTACCCAGTGCAGCGGTACCGGAGAGCTGGCCG 761
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Qy  2004 CGGGCTTCAGGTGGCACTGTCCCAGGGTCCAGGCTGGGGGTCGGGAGTTCCCTGCGCTC 2063     Qy   822 CGCTGCTGCATGATGAGCCCCATGATCACAAGCTCTCAGATCAACGGAGGCCCTGAGTC  881
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Qy  2064 AGCAGTTGCAGTGGGGTAAGGAGGCCAAGCCCATTTGTGTAATCACCCAAAACCCCCG 2123      Qy   882 ATGGCCAGAACCCTCTGCCCTACTGTGCCCTCAACACCACAAAGGGCCAGAGCCTGACCA  941
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Qy  2124 GCCTGTGCCTGTTTCCCTTCTGCGCTACCTTGAGTAGTTGGAGCACTTGATACATCACA 2183     Qy   942 CTTTTGAATTGGGGAGTGGTGCGGAGTCTCCTCCTAGAGTGTCGGCTTCCCCAAGTACG 1001
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Qy  2184 GACTCATAC 2192                                                      Qy  1002 GGGCCTTCATCCCCTCTGAGCTCTTTGGCTCCGAGTTCTTTATGGGGCAGCTGATGAAGA 1061
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Db  3030 GACTCATAC 3038                                                      Db  1846 GGGCCTTCATCCCCTCTGAGCTCTTTGGCTCCGAGTTCTTTATGGGGCAGCTGATGAAGA 1905

                                                                              Qy  1062 GGCTTCCTGAGTCCGATCTCCGCATCTGCTTCTTAGAGAAGTGAGCAACCTGTATGCAGCA 1121
                                                                                      |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
RESULT 2                                                                Db  1906 GGCTTCCTGAGTCCGATCTCCGCATCTGCTTCTTAGAGAAGTGAGCAACCTGTATGCAGCA 1965
AR137923
LOCUS       AR137923      3085 bp    DNA     linear    PAT 16-JUN-2001      Qy  1122 ACCTCCAGGACAGCTTATACTGGGCCTCCAGCCAGTTCGGGACCGCGTCGGGTCA 1181
DEFINITION  Sequence 2 from patent US 6197569.                                     |||||||||||||||||||||||||||||||||||||||||||||||||||||||
ACCESSION   AR137923                                                     Db  1966 ACCTCCAGGACAGCTTATACTGGGCCTCCAGCCAGTTCGGGACCGCGTCGGGTCA 2025
VERSION     AR137923.1   GI:14479432
KEYWORDS    .                                                           Qy  1182 GGAACCAGGCCAACCTGGACAACAGGAGCAGGTCCCCCTTCTGAAGATAGAAGAACCACCCT 1241
SOURCE      Unknown.                                                             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
ORGANISM    Unknown.                                                     Db  2026 GGAACCAGGCCAACCTGGACAAGGAGCAGGTCCCCCTTCTGAAGATAGAAGAACCACCCT 2085
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REFERENCE   1 (bases 1 to 3085)                                          Qy  1242 CAACAGCCGGCAGAATAGCTGAGTTTTCACCGATCTTCTGACGTGGCGTCCACTGGCCC 1301
AUTHORS     Choiu,X.-C., Kramer,R.M., Pickard,R.T., Sharp,J.D. and               |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
            Strifler,B.A.                                                Db  2086 CAACAGCCGCAGAATAGCTGAGTTTTCACCGATCTTCTGACGTGGCGTCCACTGGCCC 2145
TITLE       Human phospholipase A2 and related nucleic acid compounds
JOURNAL     Patent: US 6197569-A 2 06-MAR-2001;                          Qy  1302 AGCCACACATAATTTCCTGCGTGGCCTCCATTTCCACAAAGACTACTTTCAGCATCCTC 1361
FEATURES    Location/Qualifiers                                                  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
source      1..3085                                                      Db  2146 AGCCACACATAATTTCCTGCGTGGCCTCCATTTCCACAAAGACTACTTTCAGCATCCTC 2205
            /organism="unknown"
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ORIGIN                                                                           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
                                                                         Db  2206 ACTTCTCCACATGGAAAGCTACCACTCTGGATGGGCTTCCCCAACCAGCTGACACCCTCGG 2265

Query Match    82.4%;   Score 1816.8;   DB 6;   Length 3085;             Qy  1422 AGCCCCACCTGTCGCCTGCTGATGTTGGCTACTCTCATCAATACCAGCTGCCTCGCCCCTCC 1481
Best Local Similarity   98.2%;   Pred. No. 0;                                    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Matches 1861;   Conservative   0;  Mismatches   2;  Indels   33;  Gaps  1;  Db  2266 AGCCCCACCTGTCGCCTGCTGATGTTGGCTACCTCATCAATACCAGCTGCCTCGCCCCTCC 2325

Qy   342 GACTGAGGGAGGTCGGCCGTGCGACTGGGCTTCGGGCTTCGGGGCTTCGCAGAGGAGGCAGGCCTTCG 401   Qy  1482 TGCAGCCCACCTCGGGACGTGGACCTCATCCTGCTCATTGGACTACACAACCTCCACGGAGGCCT 1541
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1186 GACTGAGGGAGGTCGGCCGTGCGACTGGGCTTCGGGCTTCGGGGCTTCGCAGAGGAGGCAGGCCTTCC 1245
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Query Match            82.4%;   Score 1816.8;   DB 6;   Length 3085;
Best Local Similarity  98.2%;   Pred. No: 0;
Matches 1861;   Conservative 0;   Mismatches 0;   Indels 2;   Gaps 1;

Qy   342 GACTGAGGGAGCTGGCCGTGCGACTGGGCTTCGGCGCTCGGGACTGGCCCTGTGCAGAGGAGCAGGCCTTCC  401
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1186 GACTGAGGGAGCTGGCCGTGCGACTGGGCTTCGGCGCTCGGGACTGGCCCTGTGCAGAGGAGCAGGCCTTCC 1245

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Db  1306 ACCTGCAGGAGGATGAGATCCCAGTGGTAGCTATTATGGCCACTGGTGCTGGTGGGATCCCGGG 1365

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Db  1726 ATGGCCAGAACCCTGCCCATCTACTGTGCCCTCAACACACCAGGGCAGAGCCAGACCTGACCA 1785

Qy   942 CTTTTGAATTTGGGGAGTGTGCGAGTTCTCTCCGAGGTGCCCTTCCCAAGTACG 1001
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Db  1786 CTTTTGAATTTGGGGAGTGTGCGAGTTCTCTCCGAGGTGCCCTTCCCAAGTACG 1845

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Db  2086 CAACAGCCGCAGAATAGCTGAGTTTTCACCGATCTTCTGGACTTCTGGAGTATCTGGCCC 2145

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Qy  1694 -----TCCTCTGGGGTCCGGCGGACACCCGGAGGAGGCGGCAGTGGCTGGGCGGAGGTGAACCTGT 1748
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Db  2566 ACTCGGCCCCTGGGGTCCGGCGGACACCCGGAGGAGGCGGCAGTGGCTGGGCGGAGGTGAACCTGT 2625

Qy  1749 CTTCATCGGACTCTCCCTACCACTACACGAAGGTGACCTACAGCCAGGAGGACGTGACA 1808
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RESULT 3
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LOCUS   AR137924   3085 bp   DNA   linear   PAT 16-JUN-2001
DEFINITION Sequence 4 from patent US 6197569.
ACCESSION   AR137924
VERSION   AR137924.1 GI:14479433
KEYWORDS
SOURCE   Unknown.
  ORGANISM Unknown.
            Unclassified.
REFERENCE   1 (bases 1 to 3085)
  AUTHORS   Choiu,X.-C., Kramer,R.M., Pickard,R.T., Sharp,J.D. and
            Strifler,B.A.
  TITLE   Human phospholipase A2 and related nucleic acid compounds
  JOURNAL   Patent: US 6197569-A 4 06-MAR-2001;
FEATURES   Location/Qualifiers
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TITLE      Human phospholipase A2 and related nucleic acid compounds
JOURNAL    Patent: US 6242206-A 2 05-JUN-2001;
FEATURES   source
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ORIGIN

Query Match          82.4%;    Score 1816.8;   DB 6;   Length 3085;
Best Local Similarity 98.2%;   Pred. No. 0;
Matches 1861;  Conservative  0;  Mismatches  2;  Indels  33;  Gaps  1;

Qy    342 GACTGAGGGAGCTGCCGTGCGGGACTGGCGTTCGGGACTGCAGAGGAGGAGGCCTCC 401
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Db   1186 GACTGAGGGAGCTGCCGTGCGGGACTGGCGTTCGGGACTGCAGAGGAGGAGGCCTTCC 1245

Qy    402 TGAGCAGGAGGAAGCAGGTGGTGCCGCGGTGGGCCTTGAGGCAGGCCCTGAGCTGGATGGAG 461
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Db   2806 CACCCCTAACTCTCATTCATTCCCTGGCTGCTGAGTTGCAGGTGGGAACTGTCATCACGC 2865

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Qy   2049 GCTCCCTTGCGCCTCAGCAGTTTGCAGTTGGGGTAAGGAGGCCAAGCCCCATTGTGTAATC 2108
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Db   2926 GCTCCCTTGCGCCTCAGCAGTTTGCAGTTGGGGTAAGGAGGCCAAGCCCCATTGTGTAATC 2985

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RESULT 4
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DEFINITION Sequence 2 from patent US 6242206.
ACCESSION   AR156370
VERSION   AR156370.1 GI:15125074
KEYWORDS   .
SOURCE   Unknown.
  ORGANISM Unknown.
            Unclassified.
REFERENCE   1 (bases 1 to 3085)
  AUTHORS   Chciu,X.-C.C., Kramer,R.M., Pickard,R.T., Sharp,J.D. and
            Strifler,B.A.

VERSION   AR156371.1 GI:15125075
KEYWORDS   .
SOURCE   Unknown.
  ORGANISM Unknown.
            Unclassified.
REFERENCE   1 (bases 1 to 3085)
  AUTHORS   Choiu,X.-C.C., Kramer,R.M., Pickard,R.T., Sharp,J.D. and
            Strifler,B.A.
  TITLE   Human phospholipase A2 and related nucleic acid compounds
  JOURNAL   Patent: US 6242206-A 4 05-JUN-2001;
FEATURES   Location/Qualifiers
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ORIGIN

Query Match   82.4%; Score 1816.8; DB 6; Length 3085;
Best Local Similarity 98.2%; Pred. No. 0;
Matches 1861; Conservative 0; Mismatches 0; Indels 33; Gaps 1;

Qy   342 GACTGAGGAGGAGCTGCGCCGTGCGACTGGCTTCGGGCTTCGGGCTCGTGCAGAGGAGCAGGCCTTCC 401
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Db   1186 GACTGAGGAGGAGCTGCGCCGTGCGACTGGCTTCGGGCTTCGGGCTCGTGCAGAGGAGCAGGCCTTCC 1245

Qy   402 TGAGCAGGAGGAAGCAGCAGGTGGTGCGCCGGCGGCCTTGAGGCAGGCAGGCAGGCAGGCAGGGAG 461
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy   522 CAATGACTTCCTGTATGGGCAGCTGGCTGGCTGGCCTGAAGGAGCTGGGCTTCTTGGATTGCG 581
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Db   1366 CAATGACTTCCTGTATGGGCAGCTGGCTGGCTGGCCTGAAGGAGCTGGGCTTCTTGGATTGCG 1425

Qy   582 TCTCCTACATCACCGGGGCCTCGGGCCTGGCCTGGCCAACCTTTATGAGACC 641
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1426 TCTCCTACATCACCGGGGCCTCGGGCCTGGCCTGGCCAACCTTTATGAGACC 1485

Qy   642 CAGAGTGGTCTCAGAAGGACCACTGAGTTGCTCAGCGGTACCGGCTGGCCG 701
          |||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1486 CAGAGTGGTCTCAGAAGGACCACTGAGTTGCTCAGCGGTACCGGCTGGCCG 1545

Qy   702 AGAACAAGCTGGGTGTGCTGCGTGTGCTGGCTACCAAGTGCTTCACCAACCTGTGGGCCCTCATCAAGAGG 761
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Db   1546 AGAACAAGCTGGGTGTGCTGCGTGTGCTGGCTACCAAGTGCTTCACCAACCTGTGGGCCCTCATCAAGAGG 1605

Qy   762 AGCGGTGCCCGGTGCCGGTGCCACTGGGCTGAGTTGCAGGTGGCACTGTCCCAGGGTCGGGA 821
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Db   1606 AGCGGTGCCCGGTGCCGGTGCCACTGGGCTGAGTTGCAGGTGGCACTGTCCCAGGGTCGGGA 1665

Qy   822 CGCTGCTGCATGATGAGCCCATGATCACAAGCTCTCAGATCACAAGCTCTCAGAGTC 881
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Db   1666 CGCTGCTGCATGATGAGCCCATGATCACAAGCTCTCAGATCACAAGCTCTCAGAGTC 1725

Qy   882 ATGGCCAGAACCCTCTGCCCATCACTACTGTGCCCTCAACACCCAAAGGGCAGAGCCTGACCA 941
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Db   1726 ATGGCCAGAACCCTCTGCCCATCACTACTGTGCCCTCAACACCCAAAGGGCAGAGCCTGACCA 1785

Qy   942 CTTTTGAATTTGGGAGTGGTGCGAGTTCTTTGGCTCCGAGTTCTTTATGGGCAGCTGATGAAGA 1001
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Db   1786 CTTTTGAATTTGGGAGTGGTGCGAGTTCTTTGGCTCCGAGTTCTTTATGGGCAGCTGATGAAGA 1845

Qy   1002 GGGCCTTCATCCCCTCGAGTCCGCATCGTCTTGTTCTTAGAAGGTATCGTGAGCAACCTGTATGCAGCCA 1061
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Db   1846 GGGCCTTCATCCCCTCGAGTCCGCATCGTCTTGTTCTTAGAAGGTATCGTGAGCAACCTGTATGCAGCCA 1905

Qy   1062 GGCTTCCTGAGTCCCGCATCGTCTTGTTCTTAGAAGGTATCGTGAGCAACCTGTATGCAGCCA 1121

Db   1906 GGCTTCCTGAGTCCCGCATCGTCTTGTTCTTAGAAGGTATCGTGAGCAACCTGTATGCAGCCA 1965

Qy   1122 ACCTCCAGGACAGCTTATACTGGGCCTCAGCACCCAGCCAGTTCTCGAGACCGCTGGGTCA 1181

Db   2086 CAACAGCCGGCAGAATAGCTGAGTTTTTCACCGATCTTCTGACGTGGCGTCCACTGGCCC 2145
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Qy   1302 AGGCCACCACATAATTTCCTGCGTGGCCTCCATTTCCACAAAGACTACTTCAGCATCTC 1361
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Db   2146 AGGCCACCACATAATTTCCTGCGTGGCCTCCATTTCCACAAAGACTACTTCAGCATCTC 2205

Qy   1362 ACTTCTCCACATGGAAAGCTACCACTCTGGATGGCCTCCCCAACCAGTGACACCCTCGG 1421
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Db   2206 ACTTCTCCACATGGAAAGCTACCACTCTGGATGGCCTCCCCAACCAGTGACACCCTCGG 2265

Qy   1422 AGCCCCACCTGTGCCTGCTGGATGTTGGCTACCTCATCAATACCAGCTGCTCCTGCCCCTCC 1481
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Db   2266 AGCCCCACCTGTGCCTGCTGGATGTTGGCTACCTCATCAATACCAGCTGCTCCTGCCCCTCC 2325

Qy   1482 TGCAGCCCACTCGGGACGTGGACCTGACCTCATCCTGTCATTGACTACAACCTCCACGGAGCCT 1541
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Db   2326 TGCAGCCCACTCGGGACGTGGACCTGACCTCATCCTGTCATTGACTACAACCTCCACGGAGCCT 2385

Qy   1542 TCCAGCAGTTGCAGCTCTCGGGCCGGTTCTGCCAGGAGCAGGGGGATCCCGTTCCCACCCA 1601
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Qy   1602 TCTCGCCCCAGCCCCCCGAAGAGCAGCTCCAGCTCCGGGAGTGCCCACACCTTCTCGACCCCA 1661
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Db   2446 TCTCGCCCCAGCCCCCCGAAGAGCAGCTCCAGCTCCGGGAGTGCCCACACCTTCTCGACCCCA 2505

Qy   1662 CCTGCCCCGGAGCCCTGCGGTGCTGCACTTT------------------------------ 1693

Db   2506 CCTGCCCCGGAGCCCTGCGGTGCTGCACTTTCCTCTGGTCAGCGGGACTCCTTCCGGGAGT 2565

Qy   1694 -----TCTCTGGGGTCCGGCGGACACCCGAGGAGGCGGCAGTTGGGAGGTGAACCTGT 1748

Db   2566 ACTCGGCCCCTGGGGTCCGGCGGACACCCGAGGAGGCGGCAGTTGGGAGGTGAACCTGT 2625

Qy   1749 CTTCATCGGACTCTCTCCCTACCACTACACGAAGTGACTACCAGGAGGACGTGGACA 1808

Db   2626 CTTCATCGGACTCTCTCCCTACCACTACACGAAGTGACTACCAGGAGGACGTGGACA 2685

Qy   1809 AGTCTGCTGCACTCGACACATTACAATGTCTGCAACAACCAGGAGCAGCTCTGGAGGCTC 1868

Db   2686 AGTCTGCTGCACTCGACACATTACAATGTCTGCAACAACCAGGAGCAGCTCTGGAGGCTC 2745

Qy   1869 TGGCCAGGCAGTGCAGCCGGAGGGGCCACTGATGGCCGGGGCCCCTGC 1928

Db   2746 TGCGCCAGGCAGTGCAGCCGGAGGGGCCACTGATGGCCGGGGCCCCTGC 2805

Qy   1929 CACCCCTAACTCTCATTCATTCCCTGGCTTGCAGGTGGAACTGTCATCACGC 1988

Db   2806 CACCCCTAACTCTCATTCATTCCCTGGCTTGCAGGTGGAACTGTCATCACGC 2865

Qy   1989 AGTGCTTCAGAGCCTCGGGCTCAGGTGGCACTGTCCCAGGGTCGGGA 2048

Db   2866 AGTGCTTCAGAGCCTCGGGCTCAGGTGGCACTGTCCCAGGGTCGGGA 2925

Qy   2049 GCTCCCTTGCGCCTCAGCAGTTGCAGTGGGTAAGGAGGCCAAGCCATTTGTGTAATC 2108

Db   2926 GCTCCCTTGCGCCTCAGCAGTTGCAGTGGGTAAGGAGGCCAAGCCATTTGTGTAATC 2985

Qy   2109 ACCCAAAACCCCCGGCCTGTGCCCTGTTTCCCTTCTGCGCCTTGAGTGTTGGAGC 2168

Db   2986 ACCCAAAACCCCCGGCCTGTGCCCTGTTTCCCTTCTGCGCCTTGAGTGTTGGAGC 3045

Qy   2169 ACTTGATACATCACAGACTCATACAAAAAAAAAA 2204

Db   3046 ACTTGATACATCACAGACTCATACAAAAAAAAAAAA 3081

RESULT 5
AR156371
LOCUS   AR156371   3085 bp   DNA   linear   PAT 08-AUG-2001
DEFINITION Sequence 4 from patent US 6242206.
ACCESSION   AR156371

Db   3046 ACTTGATACATCACAGACTCATACAAAAAAAAAAA 3081

RESULT 6
AF065215
LOCUS   AF065215   3352 bp   mRNA   linear   PRI 23-MAR-1999
DEFINITION   Homo sapiens cytosolic phospholipase A2 beta (cPLA2 beta) mRNA,
                complete cds.
ACCESSION   AF065215
VERSION   AF065215.1 GI:3811346
KEYWORDS   .
SOURCE   Homo sapiens (human)
  ORGANISM   Homo sapiens
                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 3352)
  AUTHORS   Pickard,R.T., Strifler,B.A., Kramer,R.M. and Sharp,J.D.
  TITLE   Molecular cloning of two new human paralogs of 85-kDa cytosolic
                phospholipase A2
  JOURNAL   J. Biol. Chem. 274 (13), 8823-8831 (1999)
  MEDLINE   99185108
  PUBMED   10085124
REFERENCE   2 (bases 1 to 3352)
  AUTHORS   Pickard,R.T., Strifler,B.A., Kramer,R.M. and Sharp,J.D.
  TITLE   Direct Submission
  JOURNAL   Submitted (15-MAY-1998) Lilly Research Laboratory, Lilly Corporate
                Center, Indianapolis, IN 46285, USA
FEATURES   Location/Qualifiers
     source   1..3352
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /chromosome="15"
                     /note="spliced mRNA is rare in all tissues examined, and
                     was obtained by PCR; more abundant unspliced RNA form can
                     be found in GenBank Accession Number AF065216"
     gene   1..3352
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     CDS   16..3054
                     /gene="cPLA2 beta"
                     /codon_start=1
                     /product="cytosolic phospholipase A2 beta"
                     /protein_id="AAC78836.1"
                     /db_xref="GI:3811347"
                     /translation="MAEAALEAVRSELREFPAAARELCVPLAVPYLDKPPTPLHFYRD
                     WVCPNRPCIIRNALQHWPALQKWSLPYFRATVGSTEVSVAVTPDGYADAVRGDRFMMP
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                     PDAVNFWLGEAAAVTSLHKDHYENLYCVVSGEKHFLPHPPSDRPFIPYELYTPATYQL
                     TEEGTFKVKHFWLDEAMEKAEVSRTCLLTVRLQAHRLPSKDLVTPSDCVTLWLPTACSH
                     RLQTRTVKNSSSPVWNQSFHFRIHRQLKNVMELKVFPDQDLVTGDDPVLSVLFDAGTLR
                     AGEFRRESFSLSPQGGRLEVEFRLQSLADRGEWLVSNGVLVARELSCLHVQEETGD
                     QKSSEHRVQLVPGSCGPQEASVGTGTFRFHCPACWEQELSIRLQDAPEEOLKAPLS
                     ALPSGQVVRLVFPTSOEPLMRVELKKEAGLRELAVRLGFGPCAEEQAFLSRRKQVVAA
                     ALRQALQLDGDLQEDBIPVVAIMATGGIRAMTSLYGQLAGLKELGLLDCVSYITGAS
                     GSTWALANLYEDPEWSQKDLAGPTELLKTOVTKNKLGVLAPSQLQRYRQELAERARLG
                     YPSCFNLWALINEALLHDEPHDHKLSDQREALSHGQNPLPIYCALNTKGQSLITFEF
                     GEWCEFSPYEVGFPKYGAFIPSELFGSEFFMGQLMKRLPESRICFLEGIWSNLYAANL
                     QDSLYWASEPSQFWDRWVRNQANLDKEQVPLLKIEEPPSTAGRIAEFTDLLTWRPLA
                     QATHNFLRGLHFHKDYFQHPHFSTWKATTLDGLPNQLTPSEPHLCLLDVGYLINTSCL
                     PLLQPTRDVDLILSLDYNLHGAFQQLQLLGRFCQEQGIPFPFISPSPEEQLQPRECHT
                     FSDPTCPGAPAVLHFPLVSDSFREYSAPGVRRTPEEAAAGEVNLSSSDSPYHYTKVTY
                     SQEDVDKLLHLTHYNVCNNQEQLLEALRQAVQRRRQRRPH"

ORIGIN

Query Match   82.4%; Score 1816; DB 9; Length 3352;
Best Local Similarity   98.0%; Pred. No. 0;
Matches 1859; Conservative 2; Mismatches 2; Indels 33; Gaps 1;

Qy   342 GACTGAGGGAGCTGGCCGTGCGACTGGGCTTCGGGCCTTCGGGCCCCGTGTGCGAGGAGCAGCAGCCTTCC 401
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1451 GACTGAGGGAGCTGGCCGTGCGACTGGGCTTCGGGCCTTCGGGCCCCGTGTGCGAGGAGCAGCAGCCTTCC 1510

Qy   402 TGAGCAGGAGGAAGCAGGTGGTGGCCGCGGCCGCCTGAGGCAGCAGCCCTGAGCTGGATGGAG 461

Db   2591 TGCAGCCCACTCGGGACGTGGACCTCATCCTCTGTCATTGGACTACAACCTCCACGGAGCCT 2650
Qy   1542 TCCAGCAGTTGCAGCTCCTCGGGGCCGGTTCTGCGCCAGGAGCAGGGGATCCCGTTCCACCCA 1601
Db   2651 TCCAGCAGTTGCAGCTCCTCGGGGCCGGTTCTGCGCCAGGAGCAGGGGATCCCGTTCCACCCA 2710
Qy   1602 TCTCGCCCAGCCCGGAAGAGCAGCTCCAGCCTCGGGAGTGCCACACCTTCTCCGACCCCA 1661
Db   2711 TCTCGCCCAGCCCGAAGAGCAGCAGCTCCAGCCTCCGGGAGTGCCACACCTTCTCCGACCCCA 2770
Qy   1662 CCTGCCCCGGGAGCCCTCGCGGTGCTGCACTT--------- 1693
Db   2771 CCTGCCCCGGAGCCCCTCGCGGTGCTGCACTTTCCTCTGTCAGCGGACTCCTTCCGGGAGT 2830
Qy   1694 -----TCCCTGGGGTCCGGCGACACCCGGACAGCCGGCAGCCGGAGGTGAACCTGT 1748
Db   2831 ACTCGGCCCCTGGGGTCCGGCGACACCCGGACAGCCGGCAGCCGGGAGGTGAACCTGT 2890
Qy   1749 CTTCATCGGACTCTCCCTACCACTACACGAAGGTGACCTACAGCCAGCAGGAGGACGTGGACA 1808
Db   2891 CTTCATCGGACTCTCCCTACCACTACACGAAGGTGACCTACAGCCAGCAGGAGGACGTGGACA 2950
Qy   1809 AGCTGCTGCACCTGACACATTACAATGTCTGCAACAACCAGGAGGCAGCTGCTGAGGCTC 1868
Db   2951 AGCTGCTGCACCTGACACATTACAATGTCTGCAACAACCAGGAGGCAGCTGCTGAGGGCTC 3010
Qy   1869 TGCGGCAGGCAGTGCAGCGGCGGCCAGCGCCCCACTGATGGCCCGGGGCCCCCTGC 1928
Db   3011 TGCGGCCAGGCAGTGCAGCGGCGGCCAGCGCCCCACTGATGGCCCGGGGCCCCCTGC 3070
Qy   1929 CACCCCTAACTCTCATTCATTCCCTGGCTGCAGTTGCAGGTGGGAACTGTCATCACGC 1988
Db   3071 CACCCCTAACTCTCATTCATTCCCTGGCTGCAGTTGCAGGTGGGAACTGTCATCACGC 3130
Qy   1989 AGTGCTTCAGAGCCTTCAGAGGCTCAGGTGGCACTGTCGTCCCAGGGCTGAGGGGCTGGGA 2048
Db   3131 AGTGCTTCAGAGCCTTCAGAGGCTCAGGTGGCACKGTCGTCCCAGGGCTGAGGGGCTGGGA 3190
Qy   2049 GCTCCCTTGCGCTCAGCAGTTTGCAGTGGGGTAAGGAGGCCAAGCCCATTGTGTAATC 2108
Db   3191 GCTCCCTTGCGCTCAGCAGTTTGCAGTGGGGTAAGGAGGCCAAGCCCATTGTGTAATC 3250
Qy   2109 ACCCAAAACCCCCGGCCTGTGCCTGTTTCCCTTCGCGCTCTCGCCTACCTTGAGTAGTTGGAGC 2168
Db   3251 ACCCAAAACCCCCGGCCTGTGCCTGTTTCCCTTCGCGCTCTCGCCTACCTTGAGTAGTTGGAGC 3310
Qy   2169 ACTTGATACATCACAGACTCATACAGAGAGAAA 2204
Db   3311 ACTTGATACATCACAGACTCATACAGAGAGAAA 3346

RESULT 7
BC013415
LOCUS   BC013415   3193 bp   mRNA   linear   PRI 19-AUG-2003
DEFINITION   Homo sapiens phospholipase A2, group IVB (cytosolic), mRNA (cDNA
             clone IMAGE:3528417), partial cds.
ACCESSION   BC013415
VERSION   BC013415.2 GI:33604011
KEYWORDS   .
SOURCE   Homo sapiens (human)
ORGANISM   Homo sapiens
             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
             Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 3193)
AUTHORS   Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G.,
             Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D.,
             Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K.,
             Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F.,
             Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L.,
             Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L.,
             Scheetz,T.E., Brownstein,M.J., Usdin,T.B., Toshiyuki,S.,
             Carninci,P., Prange,C., Raha,S.S., Loquellano,N.A., Peters,G.J.,
             Abramson,R.D., Mullahy,S.J., Bosak,S.A., McEwan,P.J.,

Qy   1511 TGAGCAGGAGGAAGCAGGTGTGGTGCCGCGGCCCTTGAGGCAGGCCCTGCAGCTGGATGGAG 1570
Qy   462 ACCTGCAGGAGGATGAGATCCAGTGGTAGCTATTATGCCACTGGTGGTGGGATCCGGG 521
Db   1571 ACCTGCAGGAGGATGAGATCCAGTGGTAGCTATTATGCCACTGGTGGTGGGATCCGGG 1630
Qy   522 CAATGACTTCCCTGTATGGGCAGCTGGCTGGCTGGGGCTCTTGGATTGCG 581
Db   1631 CAATGACTTCCCTGTATGGGCAGCTGGCTGGCTGGGGCTCTTGGATTGCG 1690
Qy   582 TCTCCTACATCACCGGGGCCTTGCTGGGGCTTCCACTGGGCCTTTATGAGACC 641
Db   1691 TCTCCTACATCACCGGGGCCTTGCTGGGGCTTCCACTGGGCCTTTATGAGACC 1750
Qy   642 CAGAGTGTCTCAGAAGACACCTGCAGGGCCCACTGAGTTGCTGAGAGACCCAGGTGACCA 701
Db   1751 CAGAGTGTCTCAGAAGACACCTGCAGGGCCCACTGAGTTGCTGAGAGACCCAGGTGACCA 1810
Qy   702 AGAACAAGCTGGGTGTCTGGCTGGCGTACCGGCAGGGAGCTGGCCG 761
Db   1811 AGAACAAGCTGGGTGTGTCTGGCTGGCGTACCGGCAGGGAGCTGGCCG 1870
Qy   762 AGCGGTGCCCGCTGGGTACCTGCTTCCACCAAGCTGTTCCAACCTGTGGGCCCTCATCAACGAGG 821
Db   1871 AGCGGTGCCCGCTGGGTACCTGCTTCCACCAAGCTGTTCCAACCTGTGGGCCCTCATCAACGAGG 1930
Qy   822 CGCTGCTGCATGATGAGCCCATGATCACAAGCTCTCAGATCAACGGGAGGCCCTGAGTC 881
Db   1931 CGCTGCTGCATGATGAGCCCATGATCACAAGCTCTCAGATCAACGGGAGGCCCTGAGTC 1990
Qy   882 ATGGCCAGAGAACCCTCTGCCCATCTACTGTGCCCTCAACACCAAAGGGCAGAGCCTGACCA 941
Db   1991 ATGGCCAGAGAACCCTCTGCCCATCTACTGTGCCCTCAACACCAAAGGGCAGAGCCTGACCA 2050
Qy   942 CTTTTGAATTGGGGAGTGGTGCGAGTTGTGCGAGTTCTCTCCCTAGGAGGTCGGCTCCCAAGTACG 1001
Db   2051 CTTTTGAATTGGGGAGTGGTGCGAGTTGTGCGAGTTCTCTCCCTAGGAGGTCGGCTCCCAAGTACG 2110
Qy   1002 GGGGCCTTCATCCCCTCTGAGTCTTTGGCTCCGAGTTCTTTATGGGCAGCTGATGAAGA 1061
Db   2111 GGGGCCTTCATCCCCTCTGAGTCTTTGGCTCCGAGTTCTTTATGGGCAGCTGATGAAGA 2170
Qy   1062 GGCTTCCTGAGTCCGATCTCGTCTTCTTAGAAGTATCTGGAGCAACCTGTATGCAGCCA 1121
Db   2171 GGCTTCCTGAGTCCGATCTCGTCTTCTTAGAAGTATCTGGAGCAACCTGTATGCAGCCA 2230
Qy   1122 ACCTCCAGGACAGCAGTTATACTGGGCCTCAGAGCCCAGAGGACCGCTGGGTCA 1181
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Db   2291 GGAACCAGGCCAACCTGGACAAGGAGCCAGGTCCCCCTTCTGAAGATAGAGAACCACCCT 2350
Qy   1242 CAACAGCCGGCAGAATAGCTGAGTTTTTCACCGATCTTCTGACGTGGCCTCCACTGGCCC 1301
Db   2351 CAACAGCCGGCAGRATAGCTGAGTTTTTCACCGATCTTCTGACGTGGCCGTCCCACTGGCCC 2410
Qy   1302 AGGGCCACACATAATTTCCGTGCCTGCCCTCCATTTCCACAAAGACTACTTTCAGCATCCTC 1361
Db   2411 AGGGCCACACATAATTTCCTGCCGTGCCCTCCATTTCCACAAAGACTACTTTCAGCATCCTC 2470
Qy   1362 ACTTCTCCACATGGAAAGCTACCACTCTGGATGGGCTCCCCAACCAGCTGACACCCTCG 1421
Db   2471 ACTTCTCCACATGGAAAGCTACCACTCTGGATGGGCTCCCCAACCAGCTGACACCCTCG 2530
Qy   1422 AGCCCCACCTTGCCTGTCGCTGTCGGATGTTGGCTACCTCATCAATAACCAGCAGTCGCCCTCC 1481
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Qy   1482 TGCAGCCCACTCGGGACGTGGACCTCATCCTCTGTCATTGGACTACAACCTCCACGGAGCCT 1541

McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S.,
Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W.,
Villalon,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A.,
Fahey,J., Helton,E., Ketteman,M., Madan,A., Rodrigues,S.,
Sanchez,A., Whiting,M., Madan,A., Young,A.C., Shevchenko,Y.,
Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D.,
Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M.,
Butterfield,Y.S., Krzywinski,M.I., Skalska,U., Smailus,D.E.,
Schnerch,A., Schein,J.E., Jones,S.J. and Marra,M.A.

TITLE   Generation and initial analysis of more than 15,000 full-length
          human and mouse cDNA sequences

JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
MEDLINE   22388257
PUBMED   12477932
REFERENCE 2 (bases 1 to 3193)
AUTHORS   Strausberg,R.
TITLE   Direct Submission
JOURNAL   Submitted (31-AUG-2001) National Institutes of Health, Mammalian
          Gene Collection (MGC), Cancer Genomics Office, National Cancer
          Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
          USA
REMARK   NIH-MGC Project URL: http://mgc.nci.nih.gov
COMMENT   On Aug 12, 2003 this sequence version replaced gi:16807142.
          Contact: MGC help desk
          Email: cgapbs-r@mail.nih.gov
          Tissue Procurement: ATCC
          cDNA Library Preparation: Rubin Laboratory
          cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
          DNA Sequencing by: Institute for Systems Biology
          http://www.systemsbiology.org
          contact: amadan@systemsbiology.org
          Amup Madan, Jessica Fahey, Erin Helton, Mark Ketteman, Anuradha
          Madan, Stephanie Rodrigues, Amy Sanchez and Michelle Whiting

          Clone distribution: MGC clone distribution information can be found
          through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
          Series: IRAL Plate: 11 Row: a Column: 11
          This clone was selected for full length sequencing because it
          passed the following selection criteria: Hexamer frequency ORF
          analysis.
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ORIGIN

Query Match   82.3%;   Score 1814;   DB 9;   Length 3193;
Best Local Similarity   98.0%;   Pred. No. 0;
Matches 1860;   Conservative   0;   Mismatches   5;   Indels   33;   Gaps   1;

Qy   340 CAGACTGAGGAGGAGCTGCCGTGCGACTGGGCTTCGGGCCTTGAGGGCCCTGTGCAGGAGGAGGAGCAGGCCTT 399
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Db   1290 CAGACTGAGGAGGAGCTGCCGTGCGACTGGGCTTCGGGCCTTGAGGGCCCTGTGCAGGAGGAGGAGCAGGCCTT 1349

Qy   400 CCTGAGCAGCAGGAAGCAGCAGGTGGTGCCGCGGCCGCGGCCTTGAGGACAGGCGCCCTGAGCGACTGAGCTGG 459
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Db   1350 CCTGAGCAGCAGGAAGCAGCAGGTGGTGCCGCGGCCGCGGCCTTGAGGACAGGCGCCCTGAGCGACTGAGCTGG 1409

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Qy   520 GGCAATGACTTCCCTGTATGGGCAGCTGGCTGGCCTGAAGGAGCTGGGCCTCTTGGATTG 579
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Db   1470 GGCAATGACTTCCCTGTATGGGCAGCTGGCTGGCCTGAAGGAGCTGGGCCTCTTGGATTG 1529

Qy   580 CGTCTCCTACATCACCGGGGGCTCCACCTGGGCTCCACCTTTGGCCAACCTTTATGAGGA 639

Db   1530 CGTCTCCTACATCACCGGGGGCTCCACCTGGGCTCCACCTTTGGCCAACCTTTATGAGGA 1589
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   640 CCCAGAGTGTGCTCAGAAGACCTGGCAGGGCCCACTGAGTTGCTGAAGACCCAGGTGAC 699
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1590 CCCAGAGTGTGCTCAGAAGACCTGGCAGGGCCCACTGAGTTGCTGAAGACCCAGGTGAC 1649

Qy   700 CAAGAACAAGCTGGGTGTGCTGGCCCCAGCCAGCTGCAGCGGGTACCGGCAGGAGCTGGC 759
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1650 CAAGAACAAGCTGGGTGTGCTGGCCCCAGCCAGCTGCAGCGGGTACCGGCAGGAGCTGGC 1709

Qy   760 CGAGCGTGCCCGCCTTGGGCTACCCAAGCTGCTTCACCAACCTGTGGCCCTCATCAACGA 819
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Db   1710 CGAGCGTGCCCGCCTTGGGCTACCCAAGCTGCTTCACCAACCTGTGGCCCTCATCAACGA 1769

Qy   820 GGGCGTGCTGCATGATGAGCCCCATGATCACAAGCTCTCAGATACACGGAGGCCCTGAG 879
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Db   1770 GGGCGTGCTGCATGATGAGCCCCATGATCACAAGCTCTCAGATCACGGAGGCCCTGAG 1829

Qy   880 TCATGGCCAGAACCCTGCCCATCTACTGTGCCCTCAACACCAAAGGGCAGAGCCTGAC 939
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Db   1830 TCATGGCCAGAACCCTGCCCATCTACTGTGCCCTCAACACCAAAGGGCAGAGCCTGAC 1889

Qy   940 CACTTTTGAATTGGGAGTGGTGCGAGTTCTCTCCCTACGAGTTCGGCTTCCCCAAGTA 999
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1890 CACTTTTGAATTGGGAGTGGTGCGAGTTCTCTCCCTACGAGTTCGGCTTCCCCAAGTA 1949

Qy   1000 CGGGGCCTTCATCCCCTCGAGCTTTTGGCTCGGAGTTCTTTATGGGAGTCGTGATGAA 1059
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Db   1950 CGGGGCCTTCATCCCCTCGAGCTTTTGGCTCGGAGTTCTTTATGGGAGTCGTGATGAA 2009

Qy   1060 GAGGCTTCCTGAGTCCCGATCGTTCTTAGAAGGTATCTGAGCAACCTGTATGCAGC 1119
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Db   2010 GAGGCTTCCTGAGTCCCGATCGTTCTTAGAAGGTATCTGAGCAACCTGTATGCAGC 2069

Qy   1120 CAACCTCCAGGACAGCAGCTTATACTGGGCCTCAGAGCCCAGTTCTGGGACCCGTGGGT 1179
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Db   2070 CAACCTCCAGGACAGCAGCTTATACTGGGCCTCAGAGCCCAGTTCTGGGACCCGTGGGT 2129

Qy   1180 CAGGAACCAGGCCAACCTGGACAAGGAGGAGCAGGTCCCCCTTCTGAAGATAGAAGAACCACC 1239
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Db   2130 CAGGAACCAGGCCAACCTGGACAAGGAGGAGCAGGTCCCCCTTCTGAAGATAGAAGAACCACC 2189

Qy   1240 CTCAACAGCCGCAGAATAGCTGAGTTTTCACCGATCTTCTGACGTGGCGTCCACTGGC 1299
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Db   2190 CTCAACAGCCGCAGGATAGCTGAGTTTTTCACCGATCTTCTGACGTGGCGTCCACTGGC 2249

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Qy   1360 TCACTTCTCCACATGGAAAGCTACCACTCTGGATGGGCTACCACCTGACACCCCTC 1419
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Qy   1420 GGAGCCCCACCTGTGCTCGCTGCGATGTTGGCTACCTCATCAATACCAGCTGCTGCCCCCT 1479
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2370 GGAGCCCCACCTGTGCTCGCTGCGATGTTGGCTACCTCATCAATACCAGCTGCTGCCCCT 2429

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Db   2430 CCTGCAGCCACACTCGGGAGACGTGGACCTCATCGTTCATTGGACTACAACCTCACGCGAGC 2489

Qy   1540 CTTTCAGCAGTTGCAGCTCTCTGGGCCGTTCTGCCAGAGCAGGGGATCCGGTTCCCACCG 1599
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2490 CTTTCCACAGTTGCAGCTCTCTGGGCCGTTCTGCCAGAGCAGGGGATCCGGTTCCCACC 2549

Qy   1600 CATCTGCCCAGCCCCGAAGAGCAGCTCCACACTTCTCCGACCC 1659
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Db   2550 CATCTGCCCAGCCCCGAAGAGCAGCTCCACACTTCTCCGACCC 2609

Qy   1660 CACCTGCCCCCGAGCCCCTGCCGTGCTGCACTTT---------- 1693
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Db   929  ACCTGCAGGAGGATGAGATCCCAGTGGTAGCTATTATGGCCACTGGTGGTGGGATCCGGG  988
Qy   522  ------TCCTGGGGTCCGGCGGCACCCCGGACACCCGGCGGCAGCGGCCTGGCCTTGATTGCG  581
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Qy   642  CAGAGTGGTCTCAGAAGGACCTGCGCAGGGGCCCACTGAGTTGCTGAAGACCCAGTGACCA  701
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Qy   702  AGAACAAGCTGGGTGTGCTGGCCCCAGCCAGCTGCTCACCCAACCTGTGGGCCCTCATCAACGAGG  761
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Db  1169  AGAACAAGCTGGGTGTGCTGGCCCCAGCCAGCTGCTCACCCAACCTGTGGGCCCTCATCAACGAGG 1228

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Db  1409  CTTTTGAATTTGGGGAGTGGTGTGCGAGTTCTCTCGCCTACTTTGAGTTAGTTGGA 1468

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Db  1469  GGGCCTTCATCCCCTCGAGCTCTTTGGGCTCGAGTTCTTTATGGGGCAGCTGATGAAGA 1528

Qy  1062  GGCTTCCTGAGTCCCGCATCTGCTTCTTAGAAGTATCTGAGCAACCTGTATGCAGCCA 1121
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Qy  1122  ACCTCCAGACAGCTTATACTGGGCCTCAGAGCCCCAGTTCTGGACCGCTGGGTCA 1181
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Db  1649  GGAACCAGGCCAACCTGGACAAGGAGCAGTCCCCCTTCTGAAGATAGAAGAACCACCCT 1708

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Qy  1302  AGGCCACACATAATTTCCTGCGTGGCCTCCATTTCCACAAAGACTACTTTCAGCATCCTC 1361
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Qy  1747  GTCTTCATCGGACTCTCCCTACCACTACACGAAGAGGTGACCTACAGCCAGGAGACGTGGA 1806
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Db  2730  GTCTTCATCGGACTCTCCCTACCACTACACGAAGAGGTGACCTACAGCCAGGAGACGTGGA 2789

Qy  1807  CAAGTGGTCTCGACACATTACAATGTCTGCAACAACCAGGAGGAGCAGCGTGCTGCTGAGGC 1866
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2790  CAAGTGGTCTCGACCTGACCTGCAACAACCAGGAGGAGCAGCGTGCTGCTGAGGC 2849

Qy  1867  TCTGCGGCCAGCAGTCGAGCGGCGGAGGCGGCAGCGCGCCCACTGATGGCGCGGGGCCCT 1926
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Db  2850  TCTGCGGCCAGCAGTCGAGCGGCGGAGGCGGCAGCGCGCCCACTGATGGCGCGGGGCCCCT 2909

Qy  1927  GCCACCCTAACTCTCATTCATTCCCTGGCTGCGCTGGAGTTGCAGGTGGGAACTGTCATCAC 1986
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Db  2910  GCCACCCTAACTCTCATTCATTCCCTGGCTGCGCTGGAGTTGCAGGTGGGAACTGTCATCAC 2969

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Db  2970  GCAGTGCTTCAGAGCCTCGGGTCAGGTGGCACGGTCCCAGGGTCCAGGGCTGGG 3029

Qy  2047  GAGCTCCCCTTGCGCCTCCAGCAGTTGCAGTTGGGGTAAGGAGGCCAAGCCCATTTGTGTAA 2106
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Db  3030  GAGCTCCCCTTGCGCCTCCAGCAGTTGCAGTTGGGGTAAGGAGGCCAAGCCCATTTGTGTAA 3089

Qy  2107  TCACCCAAAACCCCCGGCCTGTGCCTGTTTTCCCTTCCTTCGCTGCTCCACTTGAGTAGTTGGA 2166
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3090  TCACCCAAAACCCCCGGCCTGTGCCTGTTTTCCCTTCCTTCGCTGCTCCACTTGAGTAGTTGGA 3149

Qy  2167  GCACTTGATCATCACAGACTCATACACAGAAAAAAAAAAA 2204
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RESULT 8
AR168355

LOCUS       AR168355                2699 bp    DNA        linear
DEFINITION  Sequence 3 from patent US 6287838.
ACCESSION   AR168355
VERSION     AR168355.1  GI:17904228
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1 (bases 1 to 2699)
  AUTHORS   Kriz,R. and Song,C.
  TITLE     Cytosolic phospholipase A2-Beta enzymes
  JOURNAL   Patent: US 6287838-A 3 11-SEP-2001;
FEATURES    Location/Qualifiers
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            /organism="unknown"
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ORIGIN

Query Match      82.0%;  Score 1806.2;  DB 6;  Length 2699;
Best Local Similarity   98.1%;
Matches 1851;  Conservative  0;  Mismatches  3;  Indels 33;  Gaps 1;
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(PAT 17-DEC-2001)

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Qy   342  GACTGAGGGAGCTGGCCGTGCCGCGACTGGGCTTCGGGCCTTGCAGAGGAGCAGGCCTTCC  401
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Db   809  GACTGAGGGAGCTGGCCGTGCCGTGCGACTGGGCTTCGGGCCTTGCAGAGGAGCAGGCCTTCC  868

Qy   402  TGAGCAGGGAGGAAGCAGGTGGTGCCGCGCCGCCGGCCTTGAGGCCAGCCCCTGCAGCTGATGGAG  461
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   869  TGAGCAGGGAGGAAGCAGGTGGTGCCGCGCCGCCGGCCTTGAGGCCAGCCCCTGCAGCTGATGGAG  928

Qy   462  ACCTGCAGGAGGATGAGATCCCAGTGGTAGCTATTATGGCCACTGGTGGTGGGATCCGGG  521
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy    402 TGAGCAGGAGGAAGCAGGTGGTGGCGCGGCCTTGAGGCAGGCCCTTGCAGCTGGATGGAG  461
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Db    989 CAATGACTTCCCTGTATGGGCAGCTGGGGAGGTGAACCTGT 1048

Qy    582 TCTCCTACATCACCGGGGCCTCGGGGTCCACCTGGGCCTTGGCCAACCTTTATGAGGACC  641
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Db   1049 TCTCCTACATCACCGGGGCCTCGGGGTCCACCTGGGCCTTGGCCAACCTTTATGAGGACC 1108

Qy    642 CAGAGTGGTCTCAGAAGGACTGGCAGGGGCCACTGAGTTGCTGAAGACCCAGTGACCA   701
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Db   1109 CAGAGTGGTCTCAGAAGGACTGGCAGGGGCCACTGAGTTGCTGAAGACCCAGTGACCA 1168

Qy    702 AGAACAAGCTGGGTGCTGCCCCAGCAGCGTGCTTCACCGGCTACCGCCCTCATCAACGAGG  761
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Qy   1302 AGGCCACCACATAATTTCCTGCGCTGGCCTCCATTTCCACAAAGACTACTTTCAGCATCCTC  1361
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Qy   1602 TCTCGCCCCAGCCCCGAAGAGCAGTTCCAGCCTTCGGGAGTGCCACACCTTCTCCGACCCCA 1661
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Qy   1694 ------TCCTCTGGGGTCCGGCGGACACCCGAGGAGGCGGCAGCTGGGGAGGTGAACCTGT 1748
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RESULT 9
AR255869
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DEFINITION Sequence 3 from patent US 6482625.
ACCESSION   AR255869
VERSION   AR255869.1 GI:27305099
KEYWORDS   .
SOURCE   Unknown.
  ORGANISM Unknown.
            Unclassified.
REFERENCE   1 (bases 1 to 2699)
  AUTHORS   Kriz,R. and Song,C.
  TITLE   Cytosolic phospholipase A2-beta enzymes
  JOURNAL   Patent: US 6482625-A 3 19-NOV-2002;
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ORIGIN

Query Match   82.0%; Score 1806.2; DB 6; Length 2699;
Best Local Similarity   98.1%;
Matches 1851; Conservative 0; Mismatches 3; Indels 33; Gaps 1;

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Qy   1482  TGCAGCCACTCGGGACGTGGACCTCATCCTGTCATTGGACTACAACCTCCACGGAGCCT  1541
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Db   1949  TGCAGCCACTCGGGACGTGGACCTCATCCTGTCATTGGACTACAACCTCCACGGAGCCT  2008

Qy   1542  TCCAGCAGTTGCAGCTCCTGGGCCGGTTCTGCCAGAGCAGCAGGCAGCCGGTCCACCCA  1601
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Db   2009  TCCAGCAGTTGCAGCTCCTGGGCCGGTTCTGCCAGAGCAGCAGGCAGCCGGTCCACCCA  2068

Qy   1602  TCTCGCCCAGCCCCGGAGAGCAGCTCCAGCTCCTGGGAGTGCCACACCTTCTCCGACCCA  1661
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Db   2069  TCTCGCCCAGCCCCGGAGAGCAGCTCCAGCTCCTGGGAGTGCCACACCTTCTCCGACCCA  2128

Qy   1662  CCTGCCCCGGAGCCCCTGCGGTGCTGCACTTT-----------------------  1693
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Db   2129  CCTGCCCCGGAGCCCCTGCGGTGCTGCACTTTCCTCCTGGTCAGCGACTCCTTCCGGGAGT  2188

Qy   1694  -----TCCTCTGGGGTCCGGCGACACCCGGAGGAGGCGGCAGCTGGGAGGTGAACCTGT  1748
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Db   2189  ACTCGGCCCCGTGGGTCCGGCGACACCCGGAGGAGGCGGCAGCTGGGAGGTGAACCTGT  2248

Qy   1749  CTTCATCGGACTCTCCTACCACTACACGAAGGTGACCTACAGCCAGGAGGACGTGGACA  1808
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Db   2249  CTTCATCGGACTCTCCTACCACTACACGAAGGTGACCTACAGCCAGGAGGACGTGGACA  2308

Qy   1809  AGTGCTGCACCTGACACATTACAATGTCTGCAACAACCAGGAGCAGCTGCTGAGGCTC  1868
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Db   2309  AGTGCTGCACCTGACACATTACAATGTCTGCAACAACCAGGAGCAGCTGCTGAGGCTC  2368

Qy   1869  TGCGCCAGGCAGTGCAGCGGAGCGGCGAGCGGCAGCGCAGCCCACTGATGGCCCGGGGC  1928
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Db   2369  TGCGCCAGGCAGTGCAGCGGAGCGGCGAGCGGCAGCGCAGCCCACTGATGGCCCGGGGC  2428

Qy   1929  CACCCCTAACTCTCATTCATTCCCTGGCTGTGAGTTGCAGGTTGGGAACTGTCATCACGC  1988
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2429  CACCCCTAACTCTCATTCATTCCCTGGCTGTGAGTTGCAGGTTGGGAACTGTCATCACGC  2488

Qy   1989  AGTGCTTCAGAGCCTCGGGCTCAGGCTGGCACTGTCCCAGGTCCAGGTCGAGGGCTGGGA  2048
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Db   2489  AGTGCTTCAGAGCCTCGGGCTCAGGCTGGCACTGTCCCAGGTCCAGGTCGAGGGCTGGGA  2548

Qy   2049  GCTCCCTTGCGCCTCAGCAGTTTGCAGTGGGGTAAGGAGGCCAAGCCCATTTGTGTAATC  2108
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Db   2549  GCTCCCTTGCGCCTCAGCAGTTTGCAGTGGGGTAAGGAGGCCAAGCCCATTTGTGTAATC  2608

Qy   2109  ACCCAAAAACCCCCGGCCCTGTGCCCTGTTTCCCTTCTCGCCTACCTTGACTTAGTTGGAGC  2168
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Db   2609  ACCCAAAAACCCCCGGCCCTGTGCCCTGTTTCCCTTCTCGCCTACCTTGACTTAGTTGGAGC  2668

Qy   2169  ACTTGATACATCACAGACTCATACAAA  2195
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RESULT 10

AF121908

LOCUS   AF121908   3339 bp   mRNA   linear   PRI 12-OCT-1999
DEFINITION   Homo sapiens cytosolic phospholipase A2 beta mRNA, complete cds.
ACCESSION   AF121908
VERSION   AF121908.1 GI:4886977
KEYWORDS   .
SOURCE   Homo sapiens (human)
  ORGANISM   Homo sapiens
             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
             Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 3339)
  AUTHORS   Song,C., Chang,X.J., Bean,K.M., Proia,M.S., Knopf,J.L. and
             Kriz,R.W.
  TITLE   Molecular characterization of cytosolic phospholipase A2-beta
  JOURNAL   J. Biol. Chem. 274 (24), 17063-17067 (1999)
  MEDLINE   99287906
  PUBMED   10358058
REFERENCE   2 (bases 1 to 3339)
  AUTHORS   Song,C., Chang,X.J., Bean,K.M., Proia,M.S., Knopf,J.L. and

TITLE   Kriz,R.W.
JOURNAL   Direct Submission
             Submitted (21-JAN-1999) Genetics Institute, 87 Cambridge Park
             Drive, Cambridge, MA 02140, USA
FEATURES   Location/Qualifiers
source   1..3339
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                /mol_type="mRNA"
                /db_xref="taxon:9606"
CDS   8..3046
                /note="cPLA2beta"
                /codon_start=1
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                PDAVNFWLGEAAAVTSLHKDHYENLYCVVSGEKHFLFHPPSDRPFIPYELYTPATYQL
                TEEGTFKVVDEEAMEKABVSRITCLLITVRVLQAHRLPSKDLVTPSDCYTLWLPTACSH
                RLQTRTVKNSSSPVWNQSFHFRIHRQLKNVMELKVFDQDLVTGDDPVLSVFDAGTLR
                AGEFRRESFSLSPQGEGRLEVEFRLQSLADRGEWFVSNGVLVARELSCLHVLEETGD
                QKSSEHRVQLVVPGSCEGPQEASVGTGTFRFHCPACWEQELSIRLQDAPEEQLKAPLS
                ALPSGQVVRLVFPTSQEPLMRVELVKKEAGLRELAVRLGFGPCAEEQAFLSRRRKQVVAA
                ALRQALQLDGLDLQEDEIPVVAIMATGGIRAMTSLYGQLAGLKELGLLDCVSYITGAS
                GSTWALANLYEDPEWSQKDLAGPTELLKTQVTKNKLGVLAPSQLQRYRQELAERARLG
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                GEWCEFSPYEVGFPKYGAFIPSELFGSEFFMGQLMKRLPESRICFLEGIWSNLYAANL
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                QATHNFLRGLHPHKDYFQHPHFSTWKATTLDGLPNQLTPSEPHICLLDVGYLINTSCL
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ORIGIN

Query Match   82.0%;   Score 1806.2;   DB 9;   Length 3339;
Best Local Similarity   98.1%;   Pred. No. 0;
Matches 1851; Conservative   0;   Mismatches   3;   Indels   33;   Gaps   1;

Qy   342 GACTGAGGAGCTGGAGCTGGACCTGCGACTGGCTTCGGGCCTGTGCAGAGCAGGAGCCTTCC 401
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Db   1443 GACTGAGGAGCTGGAGCTGGACCTGCGACTGGCTTCGGGCCTGTGCAGAGCAGGAGCCTTCC 1502

Qy   402 TGAGCAGGAGGAAGCAGCAGGTGTGGCCGGGCGCGGCCTGCAGCCAGGCAGGCCCTGCAGTGGAGCCCTGCAGCCTGCAGTCGAGTGGAG 461
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Db   1503 TGAGCAGGAGGAAGCAGCAGGTGTGGCCGGGCGCGGCCTGCAGCCAGGCAGGCCCTGCAGCTGGTGGAGCCCTGCAGCTGGTGGAG 1562

Qy   462 ACCTGCAGGAGGATGAGATCCCAGTGGTAGTATTATGGCCACTGGTGGTGGGATCCGGG 521
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Db   1563 ACCTGCAGGAGGATGAGATCCCAGTGGTAGTATTATGGCCACTGGTGGTGGGATCCGGG 1622

Qy   522 CAATGACTTCCCTGTATGGGCAGCTGCTGGCCTGGCTGCGTGGGCCTCTTGGATTGCG 581
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Db   1623 CAATGACTTCCCTGTATGGGCAGCTGCTGGCCTGGCTGCGTGGGCCTCTTGGATTGCG 1682

Qy   582 TCTCCTACATCACCGGGGCCTTGGACTTGCTTGCCCAACCTTTATGAGAGACC 641
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Db   1683 TCTCCTACATCACCGGGGCCTTGGACTTGCTTGCCCAACCTTTATGAGAGACC 1742

Qy   642 CAGAGGTGTTCAGAAGGACCTGGCAGGGCCCACTGAGTTGCTGAAGACCCCAGGTGACCA 701
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1743 CAGAGGTGTTCAGAAGGACCTGGCAGGGCCCACTGAGTTGCTGAAGACCCCAGGTGACCA 1802

Qy   702 AGAACAAGCTGGGTGTTGCTGGCCCCCAGCCAGCTGGCGGTACCGGTACCTGCCCG 761
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Db   1803 AGAACAAGCTGGGTGTTGCTGGCCCCCAGCCAGCTGGCGGTACCGGTACCTGCCCG 1862

Qy   762 AGCGTGCCCGCTTGGGCTACCCAAGTGCTTCACCAACCTGTGGGCCCTCATCAACGAGG 821
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Db   1863 AGCGTGCCCGCTTGGGCTACCCAAGTGCTTCACCAACCTGTGGGCCCTCATCAACGAGG 1922

Qy   822 CGCTGCTGCATGATGAGCCCCATGAACAAGCTCTCAGATCACAAGCTCCTGAGTC 881
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Db   1923 CGCTGCTGCTGCATGAGCCCCATGATCACAAGCTCTCAGATCAACGGGAGGCCCTGAGTC 1982

Qy    882 ATGGCCAGAGAACCCTGCCATCTACTGTGCCCTCAACACCAAAGGGCAGAGCTGACCA     941
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Db   1983 ATGGCCAGAGAACCCTGCCATCTACTGTGCCCTCAACACCAAAGGGCAGAGCCTGACCA   2042

Qy    942 CTTTTGAATTTGGGGAGTGGTGCGAGTTCTCTCCCTACGAGGTCGGCTTCCCAAGTACG   1001
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Db   2043 CTTTTGAATTTGGGGAGTGGTGCGAGTTCTCTCCCTACGAGGTCGGCTTCCCAAGTACG   2102

Qy   1002 GGGCCTTCATCCCCTGAGCTCTTTGGCTCCGAGTTCTTTATGGGGCAGCTGATGAAGA   1061
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Db   2103 GGGCCTTCATCCCCTGAGCTCTTTGGCTCCGAGTTCTTTATGGGGCAGCTGATGAAGA   2162

Qy   1062 GGCTTCCTGAGTCCGCATCTGCTTCTTAGAAGGTATCTGGAGCAACCTGTATGCAGCCA   1121
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Db   2163 GGCTTCCTGAGTCCGCATCTGCTTCTTAGAAGGTATCTGGAGCAACCTGTATGCAGCCA   2222

Qy   1122 ACCTCCAGGACAGCTTATACTTGGGCCTCAGAGCCCAGTTCTGGGACCCGCTGGGTCA   1181
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Db   2223 ACCTCCAGGACAGCTTATACTTGGGCCTCAGAGCCCAGTTCTGGGACCCGCTGGGTCA   2282

Qy   1182 GGAACCAGGCCAACCTGACAAGGAGGAGGAGGTCCCCCTTCTGAAGATAGAAGAACACCCCT   1241
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Db   2283 GGAACCAGGCCAACCTGACAAGGAGGAGGAGCAGGTCCCCCTTCTGAAGATAGAAGAACACCCCT   2342

Qy   1242 CAACAGCCGGCAGAATAGCTGAGTTTTTCACCGATCTTCTGACGTGGCCACTCGCCCC   1301
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Db   2343 CAACAGCCGGCAGGATAGCTGAGTTTTTCACCGATCTTCTGACGTGGCCACTCGCCCC   2402

Qy   1302 AGGCCACACATAATTTCCTGGGCCTCCATTCCACAAAGACTACTTTCAGCATCCTC   1361
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Db   2403 AGGCCACACATAATTTCCTGCGGCCTCCATTCCACAAAGACTACTTTCAGCATCCTC   2462

Qy   1362 ACTTCTCCACATGGAAAGCTACCACTCTGGATGGCTCCCAACCAGCTGACACCCTCGG   1421
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Db   2463 ACTTCTCCACATGGAAAGCTACCACTCTGGATGGCTCCCAACCAGCTGACACCCTCGG   2522

Qy   1422 AGCCCCACCTGTCTGCCTGCTTGGCTACCTCATCAATACCAGCTGCTGCCCCCTCC   1481
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Db   2523 AGCCCCACCTGTCTGCCTGCTTGGCTACCTCATCAATACCAGCTGCTGCCCCCTCC   2582

Qy   1482 TGCAGCCCACTCGGGACGTGACCTCATCCTGTCATTGGACTACAACCTCCACGGAGCCT   1541
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Db   2583 TGCAGCCCACTCGGGACGTGACCTCATCCTGTCATTGGACTACAACACCTCCACGGAGCCT   2642

Qy   1542 TCCAGCAGTTGCAGCTTCTGGCCCGGTTCTGCCAGAGCAGGCAGGGGATCCCCACCCA   1601
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Db   2643 TCCAGCAGTTGCAGCTTCTGGCCCGGTTCTGCCAGAGCAGGCAGGGGATCCCCACCCA   2702

Qy   1602 TCTCGCCCAGCCCCGAAGAGCAGCTCCAGCTCCAGCCTCGGGAGTGCCACACCTTCTCCGACCCC   1661
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Qy   1749 CTTCATCGGACTCTCCTCCCTACCACTACAGCGAGACGTGACCTACAGCCAGGACGTGACA   1808
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Db   2883 CTTCATCGGACTCTCCTCCCTACCACTACAGCGAGACGTGACCTACAGCCAGGACGTGACA   2942

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Db   2943 AGCTGCTGCACCTGACACAATTACAATGTCTGCAACAACCAGGAGCAGCTGCTGGAGGCTC   3002

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Db   3003 TGCGGCCAGGCAGTGCAGCCGGAGGGCGGCAGCGCCCACTGATGCCCGGGGCCCCTGC   3062
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Db   1929 CACCCCTAACTCTCATTCATTCCCTGGCTGCTGAGTTGCAGGTGGGAACTGTCATCACGC 1988
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Db   3063 CACCCCTAACTCTCATTCATTCCCTGGCTGCTGAGTTGCAGGTGGGAACTGTCATCACGC 3122

Qy   1989 AGTGCTTCAGAGCCTCGGGCTCAGGTGGCACTGTCCAGGGTCCAGGCTGGAGGGCTGGGA 2048
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Db   3123 AGTGCTTCAGAGCCTCGGGCTCAGGTGGCACTGTCCAGGGTCCAGGCTGGAGGGCTGGGA 3182

Qy   2049 GCTCCCTTGCGCCTCAGCAGTTTGCAGTGGGTAAGGAGGCCAAGCCCATTGTGTAATC 2108
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Db   3183 GCTCCCTTGCGCCTCAGCAGTTTGCAGTGGGTAAGGAGGCCAAGCCCATTGTGTAATC 3242

Qy   2109 ACCAAAACCCCCGGCCTGTGCCTGTTTCCCTTCTGCGCTACCTTGAGTAGTTGGAGC 2168
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Db   3243 ACCAAAACCCCCGGCCTGTGCCTGTTTCCCTTCTGCGCTACCTTGAGTAGTTGGAGC 3302

Qy   2169 ACTTGATACATCACAGACTCATACAAA 2195
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Db   3303 ACTTGATACATCACAGACTCATACAAA 3329
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RESULT 11
AR168354
LOCUS        AR168354                4183 bp    DNA        linear    PAT 17-DEC-2001
DEFINITION   Sequence 1 from patent US 6287838.
ACCESSION    AR168354
VERSION      AR168354.1  GI:17904226
KEYWORDS     .
SOURCE       Unknown.
  ORGANISM   Unknown.
             Unclassified.
REFERENCE    1 (bases 1 to 4183)
  AUTHORS    Kriz,R. and Song,C.
  TITLE      Cytosolic phospholipase A2-Beta enzymes
  JOURNAL    Patent: US 6287838-A 1 11-SEP-2001;
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ORIGIN

Query Match           82.0%;  Score 1806.2;  DB 6;  Length 4183;
Best Local Similarity 98.1%;  Pred. No. 0;
Matches 1851;  Conservative 0;  Mismatches 3;  Indels 33;  Gaps 1;
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Qy    762 AGGGTGCCCGCTTGGGCTACCCAAGTCGCTTCACCAACCTGCTTGGGCCCTCATCAACGAGG 821
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Qy    822 CGCTGCTGCATGATGAGCCCATGATGATCACAAGCTCTCAGATCACAAGCTCTCAGATCACAAGCCCTGAGTC 881
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Qy    882 ATGGCCAGAACCCTCTGCCCATCTACTGTGCCCTCAACACCCAAAGGCAGAGCCTGACCA 941
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Db   2833 ATGGCCAGAACCCTCTGCCCATCTACTACTGTGCCCTCAACACCCAAAGGCAGAGCCTGACCA 2892

Qy    942 CTTTTGAATTTGGGGAGTGGTGCGAGTTCTCCCTACGAGTGTCGGCTTCCCCAAGTACG 1001
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Db   2893 CTTTTGAATTTGGGGAGTGGTGCGAGTTCTCCCTACGAGTGTCGGCTTCCCCAAGTACG 2952

Qy   1002 GGGCCCTTCATCCCCTCTGAGCTCTTGGCTCCGAGTTCTTTATGGGGCAGCTGAGATGAAGA 1061
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Db   2953 GGGCCCTTCATCCCCTCTGAGCTCTTGGCTCCGAGTTCTTTATGGGGCAGCTGAGATGAAGA 3012

Qy   1062 GGCTTCCTGAGTCCCGCATCTGCTTCTTAGAAGGTATCTGGAGCAACCTGTATGCAGCCA 1121
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Db   3013 GGCTTCCTGAGTCCCGCATCTGCTTCTTAGAAGGTATCTGGAGCAACCTGTATGCAGCCA 3072

Qy   1122 ACCTCCAGGACAGCTTATACTGGGCCTCAGAGGCCCAGTTCTGGGACCGCTGGGTCA 1181
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Db   3073 ACCTCCAGGACACGCTTATACTGGGCCTCAGAGCCCAGTTCTGGGACCGCTGGGTCA 3132

Qy   1182 GGAACCAGGCCAACCTGGACAAGGAGCAGGTCCCCCTTCTGAAGATAGAAGAACCACCCT 1241
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Db   3193 CAACAGCCGGCAGGATAGCTGAGTTTTTCACCGATCTTCTGACGTGGCGTCCACTGGCCC 3252

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Db   3253 AGCCCACACATAATTTCCTGCGTGGCCTCCATTTCCACAAAGACTACTTTCAGCATCCTC 3312

Qy   1362 ACTTCTCCACATGGAAAGTACCACTCTGGATGGGCTCCCAACCAGCTGACACCCTCGG 1421
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Db   3313 ACTTCTCCACATGGAAAGTACCACTCTGGATGGGCTCCCAACCAGCTGACACCCTCGG 3372

Qy   1422 AGCCCCACCTGTCTGCTGGATGTTGGCTACCTCATCAATACCAGTCAGCTGCCTGCCCTCC 1481
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Db   3433 TGCAGCCCCACTGGGACGTGGACCTCATCCTGTCATTGGACTACAACCTCCACGGAGCT 3492

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Db   3493 TCCAGCAGTTGAGCTCTCGGCCGGTTCTGCCAGGAGCAGGGGATCCCGTTCCCACCCA 3552

Qy   1602 TCTCGCGGAAGAGCAGCTCCAGCCCTCGGGAGTCCACACCTTCTCCACACCTTCTCCGACCCCA 1661
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Db   3553 TCTCGCGGAAGAGCAGCTCCAGCCCTCGGGAGTCCACACCTTCTCCGACCCCA 3612

Qy   1662 CCTGCCCCGGAGCCCCTGCGGTCTGCACTTT----------- 1693
          |||||||||||||||||||||||||||||||
Db   3613 CCTCCCCCGGAGCCCCGGAGCTCCTTCCTCGTGTCAGCGACTCCTTCCGGGAGT 3672

Qy   1694 -----TCCTGTGGGTCCGGCGGACACCCGGACACCCGGCTGGGAGGTGAACCTGT 1748
          ||||||||||||||||||||||||||||||||||||||||||||||||
Db   3673 ACTTCCCCTGTGGGTCCGGCGGACACCCGGCTGGGAGGTGAACCTGT 3732

Qy   1749 CTTCATCGGACTCTCCCTACCACTACACACGAAGTGACCTACACAGCCAGGAGACGTGGACA 1808
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3733 CTTCATCGGACTCTCCCTACCACTACACACGAAGTGACCTACACAGCCAGGAGACGTGGACA 3792
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Qy   1809 AGCTGCTGCACCTGACACATTACAATGTCTGCAACAACCAGAGAGCAGCTGCTGCTCGAGGCTC 1868
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3793 AGCTGCTGCACCTGACACATTACAATGTCTGCAACAACCAGAGAGCAGCTGCTGCTCGAGGCTC 3852

Qy   1869 TGCGCCAGGCAGTGCAGCGGAGCGGAGGGCAGCGCAGCAGGCCCCCACTGATGGCCGGGGCCCCTGC 1928
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3853 TGCGCCAGGCAGTGCAGCGGAGCGGAGGGCAGCGCAGCAGGCCCCCACTGATGGCCGGGGCCCCTGC 3912

Qy   1929 CACCCCTAACTCACCTCCATTCCTGCTGCCTTGGCAGTTGCAGGTGGAACTGTCATCACGC 1988
          |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3913 CACCCCTAACTCATCCATTCCTGCTGCCTTGGCAGTTGCAGGTGGAACTGTCATCACGC 3972

Qy   1989 AGTGCTTCAGAGCCTCGGGCTCAGGTGGCCACTGTCCCAGGGTCCCAGGGCTGGGA 2048
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3973 AGTGCTTCAGAGCCTCGGGCTCAGGTGGCCACTGTCCCAGGGTCCCAGGGCTGGGA 4032

Qy   2049 GCTCCCTTGCGCCTCAGCAGTTTGCAGTGGGTAAGGAGCCAAGCCATTGTGTAATC 2108
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Db   4033 GCTCCCTTGCGCCTCAGCAGTTTGCAGTGGGTAAGGAGCCAAGCCATTGTGTAATC 4092

Qy   2109 ACCCAAAACCCCCGGCCGTGTGCCCTGTGTTTTCCCTTCTGCGCTACCTTGAGTAGTTGGAGC 2168
          |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4093 ACCCAAAACCCCCGGCCGTGTGCCCTGTGTTTTCCCTTCTGCGCTACCTTGAGTAGTTGGAGC 4152

Qy   2169 ACTTGATACATCACAGACTCATACAAA 2195
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Db   4153 ACTTGATACATCACAGACTCATACAAA 4179
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RESULT 12
AR255868
LOCUS        AR255868                4183 bp    mRNA            linear    PAT 20-DEC-2002
DEFINITION   Sequence 1 from patent US 6482625.
ACCESSION    AR255868
VERSION      AR255868.1  GI:27305098
KEYWORDS     Unknown.
SOURCE       Unknown.
  ORGANISM   Unclassified.
REFERENCE    1  (bases 1 to 4183)
  AUTHORS    Kriz,R. and Song,C.
  TITLE      Cytosolic phospholipase A2-beta enzymes
  JOURNAL    Patent: US 6482625-A 1 19-NOV-2002;
FEATURES             Location/Qualifiers
     source          1..4183
                     /organism="unknown"
                     /mol_type="mRNA"
ORIGIN

Query Match             82.0%;  Score 1806.2;  DB 6;  Length 4183;
Best Local Similarity   98.1%;  Pred. No. 0;
Matches 1851;  Conservative  0;  Mismatches  3;  Indels  33;  Gaps  1;
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Qy    342 GACTGAGGGAGCTGCGCCGTGCGACTGGCTTCGGCGCCCTGCGCAGAGGAGCAGGCCTTCC 401
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Db   2293 GACTGAGGGAGCTGCGCCGTGCGACTGGCTTCGGCGCCCTGCGCAGAGGAGCAGGCCTTCC 2352

Qy    402 TGAGCAGGAGGAAGCAGCAGGTGGTGGCCGCGGCCCCTGCAGCTGCAGCTGGATGGAG 461
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2353 TGAGCAGGAGGAAGCAGCAGGTGGTGGCCGCGGCCCTGCAGCTGCAGCTGGATGGAG 2412

Qy    462 ACCTGCAGGAGGATGAGATCCAGTGGTAGCTATTATGGCCACTGGTGTGGGATCCGGG 521
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2413 ACCTGCAGGAGGATGAGATCCAGTGGTAGCTATTATGGCCACTGGTGTGGGATCCGGG 2472

Qy    522 CAATGACTTCCCTGTATGGGAGCTGGCAGCTGGCTGCGCTGCGCCTCGAAGGAGCCTTCGG 581
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2473 CAATGACTTCCCTGTATGGGAGCTGGCAGCTGGCTGCGCTGCGCCTCGAAGGAGCCTTCGG 2532

Qy    582 TCTCCTACATCACCGGGGCCTTGGCCAACCTTTATGAGACC 641
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Db   2533 TCTCCTACATCACCGGGGCCTTGGCCAACCTTTATGAGACC 2592
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Qy   642 CAGAGTGGTCTTCAGAAGGACCTGGCAGGGCCCACTGAGTTGCTGAAGACCCAGGTGACCA  701
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2593 CAGAGTGGTCTTCAGAAGGACCTGGCAGGGCCCACTGAGTTGCTGAAGACCCAGGTGACCA 2652

Qy   702 AGAACAAGCTGGGTGTGCTGGCCCCCAGCCAGCTGCAGCGGTACCGGCAGGAGCTGGCCG  761
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2653 AGAACAAGCTGGGTGTGCTGGCCCCCAGCCAGCTGCAGCGGTACCGGCAGGAGCTGGCCG 2712

Qy   762 AGGCGTGCCCGCTTGGGCTACCAAGCTGCTTCACCAACCTGTGGGCCCTCATCATCAACGAGG  821
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2713 AGGCGTGCCCGCTTGGGCTACCAAGCTGCTTCACCAACCTGTGGGCCCTCATCATCAACGAGG 2772

Qy   822 CGCTGCTGCTGATGATGAGCCCCATGATCACAAGCTCTCAGATCAACGGGAGCCCTGAGTC  881
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Db  2773 CGCTGCTGCTGATGATGAGCCCCATGATCACAAGCTCTCAGATCAACGGGAGCCCTGAGTC 2832

Qy   882 ATGGCCAGAACCCTTCGCCCATCATCTGTGCCCTCAACACCAAAGGGCAGAGCCTGACCA  941
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Db  2833 ATGGCCAGAACCCTTCGCCCATCATCTGTGCCCTCAACACCAAAGGGCAGAGCCTGACCA 2892

Qy   942 CTTTTGAATTGGGGAGTGGTGCGAGTTCTCTCCCTACGAGGTCGGCAGTCTTTATGGGCAGCTGATGAAGA 1001
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Db  2893 CTTTTGAATTGGGGAGTGGTGCGAGTTCTCTCCCTACGAGGTCGGCAGTCTTTATGGGCAGCTGATGAAGA 2952

Qy  1002 GGGCCTTCATCCCCTCTGAGCTCTTTGGCTCCGAGTTCTTATGGGGCAGCTGATGAAGA 1061
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2953 GGGCCTTCATCCCCTCTGAGCTCTTTGGCTCCGAGTTCTTATGGGGCAGCTGATGAAGA 3012

Qy  1062 GGCTTCCTGAGTCCCGATCTGCTTCTTAGAAAGTATCTGGAGCAACCTGTATGCAGCCA 1121
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3013 GGCTTCCTGAGTCCCGATCTGCTTCTTAGAAAGTATCTGGAGCAACCTGTATGCAGCCA 3072

Qy  1122 ACCTCCAGACAGCTTATACTGGCCTCAGAGCCCAGCCAGTTCTCGGGACCGCTGGGTCA 1181
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Db  3073 ACCTCCAGACAGCTTATACTGGCCTCAGAGCCCAGCCAGTTCTCGGGACCGCTGGGTCA 3132

Qy  1182 GGAACCAGGCCAACCTGACAACGAGGCCAACAAGGAGCAGGAGTCCCCCTTCTGAAGATAGAAGAACCACCCT 1241
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3133 GGAACCAGGCCAACCTGACAACGAGGCCAACAAGGAGCAGGAGTCCCCCTTCTGAAGATAGAAGAACCACCCT 3192

Qy  1242 CAACAGCGGCGGCAGAATAGCTGAGTTTTTCACCGATCTTCTGACGTGGCGTCCACTGGCCC 1301
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3193 CAACAGCGGCGGCAGAATAGCTGAGTTTTTCACCGATCTTCTGACGTGGCGTCCACTGGCCC 3252

Qy  1302 AGGCCACACATATTTCCTGCGTGGCCTCCATTTCCACAAAGACTACTTTCAGCATCCTC 1361
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Db  3253 AGGCCACACATATTTCCTGCGTGGCCTCCATTTCCACAAAGACTACTTTCAGCATCCTC 3312

Qy  1362 ACTTCTCCACATGGGAAAGCTACCACTCTGGAAGCTCTCCCAACCAGCTGACACCCTCGG 1421
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3313 ACTTCTCCACATGGGAAAGCTACCACTCTGGAAGCTCTCCCAACCAGCTGACACCCTCGG 3372

Qy  1422 AGGCCCACCTGTGCCTGCTGCTGAATGTTGGCTACCTCATCATCAATACCAGCTGCCTGCCCCTCC 1481
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3373 AGCCCCACCTGTGCCTGCTGCTGAATGTTGGCTACCTCATCATCAATACCAGCTGCCTGCCCCTCC 3432

Qy  1482 TGCAGCCCACTCGGGACGTGACCTCATCCTGTCATTGGACTACAACCTCACGGAGACGCCT 1541
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Db  3433 TGCAGCCCACTCGGGACGTGACCTCATCCTGTCATTGGACTACAACCTCACGGAGACGCCT 3492

Qy  1542 TCCAGCAGTTGCAGCTCTCGGGCCCGGTTCTGCCAGAGCAGCAGGGGATCCCGGTTCCCACCCA 1601
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3493 TCCAGCAGTTGCAGCTCTCGGGCCCGGTTCTGCCAGAGCAGCAGGGGATCCCGGTTCCCACCCA 3552

Qy  1602 TCTGCCCCAGAGCCCGAAGAGCAGCTCCAGCTTCGGGAGTGCCACACTTCTCCGACCCCA 1661
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3553 TCTGCCCCAGAGCCCGAAGAGCAGCTCCAGCTTCGGGAGTGCCACACTTCTCCGACCCCA 3612

Qy  1662 CCTGCCCCGGAGCCCCTGCGGTGCTGCACTTT-------------- 1693
         ||||||||||||||||||||||||||||||||
Db  3613 CCTGCCCCGGAGCCCCTGCGGTGCTGCACTTTCCTCGTCAGCGACTTCCTTCCGGGAGT 3672

Qy  1694 -----TCCTCTGGGGGTCCGGCGGACACCCGGAGGAGGCGGCAGCTGGGGACTCTATTATGCCCACTGGT 1748
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Db                                                                              
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Db  3673 ACTCGGCACCCTGGGGTCGGGCCGCCGGACACCCAGGTGGGGGAGGTGAACCTGT 3732
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Qy  1749 CTTCATCGGACTCTCCCTACCACTACGAGAGGTGACCTACAGCAGCGTGGACA 1808
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3733 CTTCATCGGACTCTCCCTACCACTACGAGAGGTGACCTACAGCAGCGTGGACA 3792

Qy  1809 AGTCTGCTGCACCTGACCATTACAATGTCTGCAACAACCAGGAGCAGCTGCTGTGGAGGTC 1868
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3793 AGTCTGCTGCACCTGACCATTACAATGTCTGCAACAACCAGGAGCAGCTGCTGTGGAGGTC 3852

Qy  1869 TGCGCCAGGCAGTGCAGCGGCGGCGGGCCGCAGCGGCCCCACTGATGCGCGGGCCCCTGC 1928
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3853 TGCGCCAGGCAGTGCAGCGGCGGCGGGCCGCAGCGGCCCCACTGATGCGCGGGCCCCTGC 3912

Qy  1929 CACCCCTAACTCTCATTCATTCCTGCTGCTGAGTTGCAGTGGGAACTGTCATCACGC 1988
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3913 CACCCCTAACTCTCATTCATTCCTGCTGCTGAGTTGCAGTGGGAACTGTCATCACGC 3972

Qy  1989 AGTGCTTCAGAGCCTCGGGCTCAGTGGCACTGTCCCAGGGTCCAGGCTGAGGGCTGGGA 2048
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3973 AGTGCTTCAGAGCCTCGGGCTCAGTGGCACTGTCCCAGGGTCCAGGCTGAGGGCTGGGA 4032

Qy  2049 GCTCCCTTGCGCCTCCAGCAGTTGCAGTGGGGTAAGGAGGCCAAGCCATTTGTGTAATC 2108
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Db  4033 GCTCCCTTGCGCCTCCAGCAGTTGCAGTGGGGTAAGGAGGCCAAGCCCATTTGTGTAATC 4092

Qy  2109 ACCCAAAACCCCCGCCTGTGCCTGTTTTCCCTTCTGCGCTACCTTGAGTAGTTGGAGC 2168
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4093 ACCCAAAACCCCCGCCTGTGCCTGTTTTCCCTTCTGCGCTACCTTGAGTAGTTGGAGC 4152

Qy  2169 ACTTGATACATCACAGACTCATACAAA 2195
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Db  4153 ACTTGATACATCACAGACTCATACAAA 4179
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RESULT 13
AR352679

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LOCUS       AR352679                1925 bp    DNA        linear   PAT 17-AUG-2003
DEFINITION  Sequence 86 from patent US 6590075.
ACCESSION   AR352679
VERSION     AR352679.1  GI:33757937
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1925)
  AUTHORS   Ruben,S.M., Rosen,C.A., Fischer,C.L., Soppet,D.R., Carter,K.C.,
            Bednarik,D.P., Endress,G.A., Yu,G.-L., Ni,J., Feng,P., Young,P.E.,
            Greene,J.M., Ferrie,A.M., Duan,R., Hu,J.-S., Florence,K.A.,
            Olsen,H.S., Ebner,R., Brewer,L.A. and Shi,Y.
  TITLE     Secreted protein HODAZ50
  JOURNAL   Patent: US 6590075-A 86 08-JUL-2003;
FEATURES             Location/Qualifiers
     source          1..1925
                     /organism="unknown"
                     /mol_type="genomic DNA"
ORIGIN

Query Match       81.2%;  Score 1788.8;  DB 6;  Length 1925;
Best Local Similarity   97.9%;  Pred. No. 0;
Matches 1844;  Conservative  1;  Mismatches  4;  Indels  34;  Gaps  2;

Qy   347 AGGGAGCTGGCCGTGCGACTGGCCTTCGGGCCTCCGTG-CAGAGGAGCAGGCCTTCCTGAG 405
         ||||||||||||||||||||||||||| ||||||||||| ||||||||||| ||||||||
Db     6 AGGGAGCTGGCCGTGCGACTGGCCTTCGGGCCTCCGCCTGCCAGAGGAGCANGCCTTCCTGAG 65

Qy   406 CAGGAGGAAGCAGGAGTGTGGCCGGGCCTTGAGGCAGGCCCCTGCAGCTGGATCGGAGACCT 465
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    66 CAGGAGGAAGCAGGAGTGGTGGCCGGGCCTTGAGGCAGGCCCCTGCAGCTGGATGATGAGACCT 125

Qy   466 GCAGGAGGATGAGATCCCAGTGGTAGCTATTATGGCCCACTGGTGTGGTGGGATCCGGGCAAT 525
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db                                                                       
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Db  1606 GCCCAGCCCGGAAGAGCAGCAGTCCAGCCTGCGGGAGTGCCACACCTTCTCCGACCCCACCTG 1665
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  1266 GCCCAGCCCGGAAGAGCAGCAGTCCAGCCTGCGGGAGTGCCACACCTTCTCCGACCCCACCTG 1325

Qy  1666 CCCCGGAGCCCGGTGCTGCACTTT------------------------------------ 1693
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Db  1326 CCCCGGAGCCCGGTGCTGCACTTTCCTCGTCAGCGACTTCCTTCGGGAGGTGAAGTACTC 1385

Qy  1694 -TCCTCTGGGGTCCGGCGGACACCCGAGGAGGGCGCAGCTGGGAGGTGAACCTGTCTTC 1752
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Db  1386 GGCCCCTGGGGTCCGGCGGACACCCGAGGAGGGCGCAGCTGGGAGGTGAACCTGTCTTC 1445

Qy  1753 ATCGGACTTCTCCTACCACTACGAAGTGACCTACGCCAGCCAGAGGACGTGGACAAGCT 1812
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Db  1446 ATCGGACTCTCCTACCACTACGAAGTGACCTACGCCAGCCAGAGGACGTGGACAAGCT 1505

Qy  1813 GCTGCACCTGACACATTACAAATGTCTGCAACAACGAGCAGCTGCTGAGGCTCTGCG 1872
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1506 GCTGCACCTGACACATTACAAATGTCTGCAACAACGAGCAGCTGCTGAGGCTCTGCG 1565

Qy  1873 CCAGGCAGTGCAGCGGAGGCGGCGAGCGAGGCCCCACTGATGGCCGCGGGCCCCTGCCACC 1932
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1566 CCAGGCAGTGCAGCGGAGGCGGCGAGCGAGGCCCCACTGATGGGCCGCGGGCCCCTGCCACC 1625

Qy  1933 CCTAACTCTCATTCATTCCTGGCTCGAGTGCTGAGTTGCAGGTCCAGGGCTGGGAGCTG 1992
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1626 CCTAACTCTCATTCATTCCTGGCTCGAGTGCTGAGTTGCAGGTCCAGGGCTGGGAGCTC 1685

Qy  1993 CTTCAGAGCCTCGGGCTCAGGTGGCACTGTCCCAGGTCAAGCCCATTTGTGTAAATCACCC 2052
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1686 CTTCAGAGCCTCGGGCTCAGGTGGCACTGTCCCAGGTCAAGCCCATTTGTGTAATCACCC 1745

Qy  2053 CCTTGCGCCTCAGCAGTTTGCAGTGGGGTAAGGAGGCCAAGCCCATTTGTGTAATCACCC 2112
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Db  1746 CCTTGCGCCTCAGCAGTTTGCAGTGGGGTAAGGAGGCCAAGCCCATTTGTGTAATCACCC 1805

Qy  2113 AAAACCCCGCGGCCTGTGCGCTGTTTCCCTTCGCGCTACCTTGGAGTAGTTGGAGCACTT 2172
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1806 AAAACCCCGCGGCCTGTGCGCTGTTTCCCTTCGCGCTACCTTGGAGTAGTTGGAGCACTT 1865

Qy  2173 GATACATCACAGACTCATACAAA 2195
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Db  1866 GATACATCACAGACTCATACAAA 1888
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RESULT 14
BD195624

LOCUS   BD195624   1925 bp   DNA   linear   PAT 17-JUL-2003
DEFINITION   70 human secreted proteins.
ACCESSION   BD195624
VERSION   BD195624.1   GI:33005394
KEYWORDS   JP 2002519990-A/85.
SOURCE   unidentified
  ORGANISM   unidentified
             unclassified.
REFERENCE   1 (bases 1 to 1925)
  AUTHORS   Ruben,S.M., Rosen,C.A., Fischer,C.L., Soppet,D.R., Carter,K.C.,
             Bednarik,D.P., Endress,G.A., Yu,G.L., Feng,P., Young,P.E.,
             Greene,J.M., Ferrie,A.M., Duan,R., Hu,J.S., Florence,K.A.,
             Olsen,H.S., Ebner,R., Brewer,L.A., Moore,P.A., Shi,Y.,
             Lafleur,D.W., Li,Y., Zeng,Z. and Kyaw,H.
  TITLE   70 human secreted proteins
  JOURNAL   Patent: JP 2002519990-A 85 02-JUL-2002;
             HUMAN GENOME SCIENCES INC
COMMENT   OS   Unidentified
             PN   JP 2002519990-A/85
             PD   02-JUL-2002
             PF   06-MAR-1998 JP 1998538875
             PR   07-MAR-1997 US 60/040162,07-MAR-1997 US   60/040333 PR
             07-MAR-1997 US   60/038621,07-MAR-1997 US   60/040161 PR
             07-MAR-1997 US   60/040626,07-MAR-1997 US   60/040334 PR
             07-MAR-1997 US   60/040336,07-MAR-1997 US   60/040163 PR

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Db   126 GCAGGAGGATGAGATCCCAGTGGTAGCTATTATGGCCACTGCTGGTGGGATCCGGGCAAT 185

Qy   526 GACTTCCCTGTATGGGCAGCTGGCTGGCTGCCTGAAGGAGTCGGCTGGTGGGATTGCCGTCTC 585
         ||||||||||||||||||||||||||| ||| |||||||||||||||||||||||||||
Db   186 GACTTCCCTGTATGGGCAGCTGGCTGGCTGCCTGCCTGGATTGCKTKCTC 245

Qy   586 CTACATCACCGGGGCCTCGGGCTCCAACCTTTATGAGGACCAGA 645
         ||||||||||||||||||||||||||||||||||||||||||||
Db   246 CTACATCACCGGGGCCTCGGGCTCCAACCTTTATAAGGACCAGA 305

Qy   646 GTGGTCTCAGAAGGACCTGGCAGGGCCCACTGAGTTGCTGAAGACCCAGGTGACCAAGAA 705
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   306 GTGGTCTCAGAAGGACCTGGCAGGGCCCACTGAGTTGCTGAAGACCCAGGTGACCAAGAA 365

Qy   706 CAAGCTGGGTGCTGTGCTGGCCCCAGCAGCCGGTACCCGGCAGCAGGAGTCGGCCGAGCG 765
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   366 CAAGCTGGGTGCTGTGCTGGCCCCAGCAGCCGGTACCCGGCAGCAGGAGTCGGCCGAGCG 425

Qy   766 TGCCCGCTTGGGCTACCCAAGCTGCTTCACCCAACCTGTGGGGCCCTCATCAACGAGGCGCCT 825
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   426 TGCCCGCTTGGGCTACCCAAGCTGCTTCACCCAACCTGTGGGGCCCTCATCAACGAGGCGCCT 485

Qy   826 GCTGCATGATGAGCCCATGATCACAAGCTCTCAGATCAACGGGAGCCCTGAGTCATGG 885
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   486 GCTGCATGATGAGCCCATGATCACAAGCTCTCAGATCAACGGGAGCCCTGAGTCATGG 545

Qy   886 CCAGAACCCTCTGCCCATCTACTGTGCCCTCAACACCAAAGGGCAGAGCCTGACCACTTT 945
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   546 CCAGAACCCTCTGCCCATCTACTGTGCCCTCAACACCAAAGGGCAGAGCCTGACCACTTT 605

Qy   946 TGAATTTGGGGAGTGGTGCGAGTTCTCTCCCAGTGGCTCGGCTTCCCCAAGTACGGGGC 1005
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   606 TGAATTTGGGGAGTGGTGCGAGTTCTCTCCCAGTGGCTCGGCTTCCCCAAGTACGGGGC 665

Qy  1006 CTTCATCCCCTCTGAGTGTTCTTTGGCTCCGAGTTCTTTATGGGGCAGTGATGAAGAGAGCT 1065
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   666 CTTCATCCCCTCTGAGTGTTCTTTGGCTCCGAGTTCTTTATGGGGCAGTGATGAAGAGAGCT 725

Qy  1066 TCCTGAGTCCCGCATCTGCTTCTTAGAAGGTATCTGGAGCAACCTGTATGCAGCCAACCT 1125
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Db   726 TCCTGAGTCCCGCATCTGCTTCTTAGAAGGTATCTGGAGCAACCTGTATGCAGCCAACCT 785

Qy  1126 CCAGGACACAGCTTATATCTGGGCCTCAGAGCCCAGCCAGTTCTCGGACCGTCGGGTCAGGAA 1185
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   786 CCAGGACACAGCTTATATCTGGGCCTCAGAGCCCAGCCAGTTCTCGGACCGTCGGGTCAGGAA 845

Qy  1186 CCAGGCCAACCTGACACAGGAGCAGTCCCCCTTCTGAAGATGAAGAAGAACCACCCTCAAC 1245
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   846 CCAGGCCAACCTGACACAGGAGCAGTCCCCCTTCTGAAGATAGAAGAACCACCCTCAAC 905

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PI   STEVEN M RUBEN,CRAIG A ROSEN,CARRIE L FISCHER,DANIEL R SOPPET,
     KENNETH C CARTER,DANIEL P BEDNARIK,GREGORY
A ENDRESS,GUO LIANG
PI   YU,JIAN NI,
PI   PING FENG,PAUL E YOUNG,JOHN M GREENE,ANN
M FERRIE,ROXANNE DUAN,
PI   JING SHAN HU,KIMBERLY A FLORENCE,HENRIK
S OLSEN,REINHARD EBNER,
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,YI LI,ZHIZHEN ZENG,
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VERSION     AR352614.1  GI:33757872
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  AUTHORS   Ruben,S.M., Rosen,C.A., Fischer,C.L., Soppet,D.R., Carter,K.C.,
            Bednarik,D.P., Endress,G.A., Yu,G.-L., Ni,J., Feng,P., Young,P.E.,
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Qy     1813 GCTGCACTGACACATTACAATGTCTGCAACAACCAGGAGCAGCTGCTGGAGGCTCTGCG 1872
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Qy     2052 CCCTTGCGCGCTCAGCAGTTTGCAGTGGGGTAAGGAGGCCAAGCCCATTGTGTAATCACC 2111
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Search completed: October 7, 2004, 16:44:04
Job time : 8963.72 secs

OM nucleic - nucleic search, using sw model

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           Copyright (c) 1993 - 2004 Compugen Ltd.
           GenCore version 5.1.6
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Run on: October 7, 2004, 13:04:44 ; Search time 174.207 Seconds
                                            (without alignments)
                                            7021.008 Million cell updates/sec

Title: US-09-830-321A-5
Perfect score: 2204
Sequence: 1 catggttggggcgagaga........actccatacaaaaaaaaa 2204

Scoring table: IDENTITY_NUC
               Gapop 10.0 , Gapext 1.0

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   Issued Patents NA:*
          1: /cgn2_6/ptodata/2/ina/5A_COMB.seq:*
          2: /cgn2_6/ptodata/2/ina/5B_COMB.seq:*
          3: /cgn2_6/ptodata/2/ina/6A_COMB.seq:*
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          5: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
          6: /cgn2_6/ptodata/2/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Match Length	DB	ID	Description
1	1816.8	82.4	3085	3	US-08-827-208-2	Sequence 2, Appli
2	1816.8	82.4	3085	3	US-08-827-208-4	Sequence 2, Appli
3	1816.8	82.4	3085	3	US-09-500-358-2	Sequence 2, Appli
4	1816.8	82.4	3085	3	US-09-500-358-4	Sequence 4, Appli
5	1816.8	82.4	3085	3	US-09-498-809-2	Sequence 4, Appli
6	1816.8	82.4	3085	3	US-09-498-809-4	Sequence 4, Appli
7	1806.2	82.0	2699	3	US-09-460-145-3	Sequence 3, Appli
8	1806.2	82.0	2699	3	US-09-895-547-3	Sequence 3, Appli
9	1806.2	82.0	4183	3	US-09-460-145-1	Sequence 1, Appli
10	1806.2	82.0	4183	4	US-09-895-547-1	Sequence 1, Appli
11	1788.8	81.2	1925	4	US-09-148-545-86	Sequence 86, Appl
12	1777.8	80.7	1926	4	US-09-148-545-21	Sequence 21, Appl
c 13	1676.6	76.1	1818	4	US-09-148-545-87	Sequence 87, Appl
14	1408.6	63.9	8517	3	US-08-827-208-1	Sequence 1, Appli
15	1408.6	63.9	8517	3	US-09-500-358-1	Sequence 1, Appli
16	1408.6	63.9	8517	3	US-09-498-809-1	Sequence 1, Appli
17	128.8	5.8	74962	4	US-09-685-853A-3	Sequence 3, Appli
c 18	127.6	5.8	4668	3	US-09-045-301-1	Sequence 1, Appli
19	127.2	5.8	81001	4	US-09-750-580-1	Sequence 1, Appli
20	126.2	5.7	1001	4	US-09-641-638-629	Sequence 629, App
21	126.2	5.7	1001	4	US-09-641-638-630	Sequence 630, App
22	126.2	5.7	20674	4	US-09-641-638-651	Sequence 651, App
23	125.6	5.7	2932	4	US-09-016-434-1419	Sequence 1419, Ap
24	125.6	5.7	1656	1	US-08-324-465-2	Sequence 2, Appli
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26	125.6	5.7	1656	5	PCT-US93-11915-2	Sequence 2, Appli
27	125.6	5.7	1725	1	US-08-324-465-5	Sequence 5, Appli
28	125.6	5.7	1725	2	US-08-465-981-5	Sequence 5, Appli
29	125.6	5.7	1725	5	PCT-US93-11915-5	Sequence 5, Appli
30	125.6	5.7	319608	5	US-09-539-333D-1	Sequence 1, Appli
31	125.6	5.7	319608	4	US-09-679-409-1	Sequence 6, Appli
32	125.4	5.7	1000	3	US-09-018-584A-33	Sequence 33, Appl
33	125.4	5.7	1624	2	US-08-852-807-10	Sequence 10, Appl
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35	125.4	5.7	21968	4	US-09-851-985-3	Sequence 3, Appli
c 36	125	5.7	5581	4	US-08-973-544-1	Sequence 1, Appli
c 37	125	5.7	169998	4	US-09-676-610B-24	Sequence 24, Appl
c 38	125	5.7	197496	4	US-09-877-177A-10	Sequence 10, Appl
39	124.8	5.7	3804	2	US-08-483-488-5	Sequence 5, Appli
40	124.8	5.7	4066	4	US-09-367-750-1	Sequence 1, Appli
c 41	124.8	5.7	70000	4	US-09-851-896-3	Sequence 3, Appli
42	124.2	5.6	4421	4	US-08-257-963B-9	Sequence 9, Appli
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44	124.2	5.6	4421	4	US-08-520-373D-6	Sequence 6, Appli
45	124.2	5.6	4421	5	PCT-US95-07201-9	Sequence 9, Appli

ALIGNMENTS

RESULT 1
US-08-827-208-2
; Sequence 2 Application US/08827208
; Patent No. 6025178
; GENERAL INFORMATION:
; APPLICANT: Chiou, Xue-Chiou C.
; APPLICANT: Kramer, Ruth M.
; APPLICANT: Pickard, Richard T.
; APPLICANT: Sharp, John D.
; APPLICANT: Strifler, Beth A.
; TITLE OF INVENTION: HUMAN PHOSPHOLIPASE A2 AND RELATED
; TITLE OF INVENTION: NUCLEIC ACID COMPOUNDS
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Eli Lilly and Company
; STREET: Lilly Corporate Center
; CITY: Indianapolis
; STATE: Indiana
; COUNTRY: United States of America
; ZIP: 46285
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/827,208
; FILING DATE: 28-MAR-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/014,608
; FILING DATE: 29-MAR-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/041,264
; FILING DATE: 19-MAR-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Gaylo, Paul J.
; REFERENCE/DOCKET NUMBER: X-10610
; REGISTRATION NUMBER: 36,808
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (317) 276-0756
; TELEFAX: (317) 276-3861
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3085 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:

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;          NAME/KEY: CDS
;          LOCATION: 48..2786
US-08-827-208-2

Query Match       82.4%;   Score 1816.8;  DB 3;  Length 3085;
Best Local Similarity   98.2%;
Matches 1861;  Conservative   0;  Mismatches   0;  Indels  33;  Gaps   2;

Qy    342 GACTGAGGAGCTGGCCGTGCGACTGGGCTTCGGGCCTGTGCAGAGGAGCAGGCCTTCC 401
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Db   2806 CACCCCTAACTTCATTCATTCCTGGCTGCACTGTCCAGGTGGCACTGTGCTGAGGGCTGGGA 2865

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RESULT 2
US-08-827-208-4
; Sequence 4, Application US/08827208
; Patent No. 6025178

APPLICANT: Strifler, Beth A.
TITLE OF INVENTION: HUMAN PHOSPHOLIPASE A2 AND RELATED
TITLE OF INVENTION: NUCLEIC ACID COMPOUNDS
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
  ADDRESSEE: Eli Lilly and Company
  STREET: Lilly Corporate Center
  CITY: Indianapolis
  STATE: Indiana
  COUNTRY: United States of America
  ZIP: 46285
COMPUTER READABLE FORM:
  MEDIUM TYPE: Floppy disk
  COMPUTER: IBM PC compatible
  OPERATING SYSTEM: PC-DOS/MS-DOS
  SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
  APPLICATION NUMBER: US/08/827,208
  FILING DATE: 28-MAR-1997
  CLASSIFICATION: 435
PRIOR APPLICATION DATA:
  APPLICATION NUMBER: US 60/014,608
  FILING DATE: 29-MAR-1996
PRIOR APPLICATION DATA:
  APPLICATION NUMBER: US 60/041,264
  FILING DATE: 19-MAR-1997
ATTORNEY/AGENT INFORMATION:
  NAME: Gaylo, Paul J.
  REGISTRATION NUMBER: 36,808
REFERENCE/DOCKET NUMBER: X-10610
TELECOMMUNICATION INFORMATION:
  TELEPHONE: (317) 276-0756
  TELEFAX: (317) 276-3861
INFORMATION FOR SEQ ID NO: 4:
  SEQUENCE CHARACTERISTICS:
    LENGTH: 3085 base pairs
    TYPE: nucleic acid
    STRANDEDNESS: single
    TOPOLOGY: linear
    MOLECULE TYPE: mRNA
US-08-827-208-4

Query Match   82.4%; Score 1816.8; DB 3; Length 3085;
Best Local Similarity 78.9%; Pred. No. 0;
Matches 1496; Conservative 365; Mismatches 2; Indels 33; Gaps 1;

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          :|||(|||||||||||||||||||||||||||||||||||||||:||||||||||||||||
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          ||||||:||:|:|:|||:|:|||||||||||||||:|:|||||||||:|:||:|||||||
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Qy  1989  AGTGCTTCAGAGCCTCGGGCTCAGGTGCACTGTCCCAGGGTCCAGGCTGAGGGCTGGGA   2048
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          |||:|||||::|:|||:|||:|||||||||||||:|:||||||||||||:::|:||:|||
Db  2926  GCUCCCUUGCGCCUCAGCAGUUUGCAGUGGGUAAGGAGGCCAAGCCCAUUUGUGUAAUC   2985

Qy  2109  ACCCAAAACCCCCCGGCCTGTGCCTGTTTCCCTTGCGCTACCTTGAGTAGTTGGAGC   2168
          ||||||||||||||:|||||||||||||:|:|:|||||:|:||||||||||:|:|||||
Db  2986  ACCCAAAACCCCCCGGCCUGUGCCUGUUUCCCUUCGCUACCUUGAGUAGUUGGAGC   3045

Qy  2169  ACTTGATACATCAGACTCATCATCAAAAAAAAAAA   2204
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Db  3046  ACUUGAUACAUCACAGACUCAUCAUCAAAAAAAAAAA   3081
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INFORMATION FOR SEQ ID NO:  2:
    SEQUENCE CHARACTERISTICS:
        LENGTH:  3085 base pairs
        TYPE:  nucleic acid
        STRANDEDNESS:  single
        TOPOLOGY:  linear
    MOLECULE TYPE:  cDNA
    FEATURE:
        NAME/KEY:  CDS
        LOCATION:  48..2786
US-09-500-358-2

Query Match        82.4%;  Score 1816.8;  DB 3;  Length 3085;
Best Local Similarity  98.2%;  Pred. No. 0;
Matches 1861;  Conservative  0;  Mismatches  0;  Indels  33;  Gaps  1;
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Qy   342  GACTGAGGGAGCTGGCCGTGCGACTGGGCTTCGGGCCTGCGCAGAGGAGCAGGCCTTCC   401
          |||||||||||||||||||||||||||||||||||||| | |||||||||||||||||||
Db  1186  GACUGAGGGAGCUGGCCGUGCGACUGGGCUUCGGGCCUGUGCGAGAGGAGCAGGCCUUCC  1245

Qy   402  TGAGCAGGAGGAAGCAGGTGGTGCGCCGGCCCTGCAGCTGGCAGGCCCTGCAGCTGGATGAG  461
          ||||||||||||||||||||||||| |||||||||| ||||||||||||||||||||||||
Db  1246  UGAGCAGGAGGAAGCAGGUGGUGCGCCGGCCCUGCAGCUGGCAGGCCCUGCAGCUGGAUGAG  1305

Qy   462  ACCTGCAGGAGGATGAGATCCCAGTGGTAGCTATTATGGCCACTGGTGGTGGGATCCGGG   521
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1306  ACCUGCAGGAGGAUGAGAUCCCAGUGGUAGCUAUUAUGGCCACUGGUGGUGGGAUCCGGG   1365

Qy   522  CAATGACTTCCCTGTATGGGCAGTCAGCTGGCCTGGCCTGAAGGAGGTGGGCCTCTTGGATTGCG  581
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1366  CAAUGACUUCCCUGUAUGGGCAGUCAGCUGGCCUGGCCUGAAGGAGGUGGGCCUCUUGGAUUGCG  1425

Qy   582  TCTCCTACATCACCGGGGCCTTCGGGCTCAACCTTTATGAGGACC   641
          ||||||||||||||||||||||||||||||||||||||||||||
Db  1426  UCUCCUACAUCACCGGGGCCUUCGGGCUCAACCUUUAUGAGGACC  1485

Qy   642  CAGAGTGGTCTCAGAAGGACCTGCAGGGCCCACTGAGTTGCTGAAGACCCAGGTGACCA   701
          |||||||||||||||||||||||| |||||||||||||||||||||||||||||||||||
Db  1486  CAGAGUGGUCUCAGAAGGACCUGGCAGGGCCCACUGAGUUGCUGAAGACCCAGGUGACCA   1545

Qy   702  AGAACAAGCTGGGTGTGCTGCCCCAGCCAGCTGCAGCCGGTACCGGCAGGAGCTGGCCG   761
          |||||||||||||||||||||||||||||||| |||||||||||||||||||||||||||
Db  1546  AGAACAAGCUGGGUGUGCUGCCCCAGCCAGCUGCAGCCGGUACCGGCAGGAGCUGGCCG   1605

Qy   762  AGCGGTGCCCGCTTGGGCTACCCAAGTGCTTCACCAACCTGTCTTCCAACCTTTATGAGGAGG  821
          ||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||||||
Db  1606  AGCGGUGCCCGCUUGGGCUACCCAAGUGCUUCACCAACCUGUCUUCCAACCUUUAUGAGGAGG  1665

Qy   822  CGCTGCTGCATGATGAGACCCTGCCCATGGAGGCCCTGAGTC   881
          ||||||||||||||||||||||||||||||||||||||||||
Db  1666  CGCUGCUGCAUGAUGAGACCCUGCCCAUGGAGGCCCUGAGUC   1725

Qy   882  ATGGCCAGAACCCCTGCCCATCAGTCTGCCCCAACACCAAAGGCCAGAGCCTGACCA   941
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1726  AUGGCCAGAACCCCUGCCCAUCAGUCUGCCCCAACACCAAAGGCCAGAGCCUGACCA   1785

Qy   942  CTTTGAATTGGGAGTGGTGCGAGTTCTCTCCCTACGAGGTCGGCTTCCCCAAGTACG   1001
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1786  CUUUGAAUUGGGAGUGGUGCGAGUUCUCUCCCUACGAGGUCGGCUUCCCCAAGUACG   1845

Qy  1002  GGGCCTTCATCCCCTGAGTTCTTTGGCTCCGAGTTCTTTATGGGGCAGTCTGATGAAGA   1061
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1846  GGGCCUUCAUCCCCUGAGUUCUUUGGCUCCGAGUUCUUUAUGGGGCAGUCUGAUGAAGA   1905

Qy  1062  GGCTTCCTGAGTCCCCATCTGCTTCTTAGAAGTATCTGGAGCAACCTGTATGCAGCCA   1121
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1906  GGCUUCCUGAGUCCCCAUCUGCUUCUUAGAAGUAUCUGGAGCAACCUGUAUGCAGCCA   1965

Qy  1122  ACCTCCAGGACAGCTTATACTGGGCCTCAGAGCCCAGCCGCTGGGTCA   1181
          ||||||||||||||||||||||||||||||||||||||||||||||||
Db  1966  ACCUCCAGGACAGCUUAUACUGGGCCUCAGAGCCCAGCCGCUGGGUCA   2025

Qy  1182  GGAACCAGGCCAACCTGACAAGGAGCAGTGTCCCCTTCGAAGATAGAAGAACCACCCT   1241
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RESULT 3
US-09-500-358-2
; Sequence 2, Application US/09500358
; Patent No. 6197569
; GENERAL INFORMATION:
;   APPLICANT: Chiou, Xue-Chiou C.
;   APPLICANT: Kramer, Ruth M.
;   APPLICANT: Pickard, Richard T.
;   APPLICANT: Sharp, John D.
;   APPLICANT: Strifler, Beth A.
;   TITLE OF INVENTION: HUMAN PHOSPHOLIPASE A2 AND RELATED
;   TITLE OF INVENTION: NUCLEIC ACID COMPOUNDS
;   NUMBER OF SEQUENCES: 4
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE: Eli Lilly and Company
;   STREET: Lilly Corporate Center
;   CITY: Indianapolis
;   STATE: Indiana
;   COUNTRY: United States of America
;   ZIP: 46285
;   COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: PatentIn Release #1.0, Version #1.30
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/09/500,358
;   FILING DATE:
;   CLASSIFICATION:
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: US/08/827,208
;   FILING DATE: 28-MAR-1997
;   APPLICATION NUMBER: US 60/014,608
;   FILING DATE: 29-MAR-1996
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: US 60/041,264
;   FILING DATE: 19-MAR-1997
;   ATTORNEY/AGENT INFORMATION:
;   NAME: Gaylo, Paul J.
;   REGISTRATION NUMBER: 36,808
;   REFERENCE/DOCKET NUMBER: X-10610
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE: (317) 276-0756
;   TELEFAX: (317) 276-3861

```
US-09-500-358-4
; Sequence 4, Application US/09500358
; Patent No. 6197569
; GENERAL INFORMATION:
;   APPLICANT: Chiou, Xue-Chiou C.
;   APPLICANT: Kramer, Ruth M.
;   APPLICANT: Pickard, Richard T.
;   APPLICANT: Sharp, John D.
;   APPLICANT: Strifler, Beth A.
;   TITLE OF INVENTION: HUMAN PHOSPHOLIPASE A2 AND RELATED
;   TITLE OF INVENTION: NUCLEIC ACID COMPOUNDS
;   NUMBER OF SEQUENCES: 4
;   CORRESPONDENCE ADDRESS:
;     ADDRESSEE: Eli Lilly and Company
;     STREET: Lilly Corporate Center
;     CITY: Indianapolis
;     STATE: Indiana
;     COUNTRY: United States of America
;     ZIP: 46285
;   COMPUTER READABLE FORM:
;     MEDIUM TYPE: Floppy disk
;     COMPUTER: IBM PC compatible
;     OPERATING SYSTEM: PC-DOS/MS-DOS
;     SOFTWARE: PatentIn Release #1.0, Version #1.30
;   CURRENT APPLICATION DATA:
;     APPLICATION NUMBER: US/09/500,358
;     FILING DATE:
;     CLASSIFICATION:
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER: US/08/827,208
;     FILING DATE: 28-MAR-1997
;     APPLICATION NUMBER: US 60/014,608
;     FILING DATE: 29-MAR-1996
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER: US 60/041,264
;     FILING DATE: 19-MAR-1997
;   ATTORNEY/AGENT INFORMATION:
;     NAME: Gaylo, Paul J.
;     REGISTRATION NUMBER: 36,808
;     REFERENCE/DOCKET NUMBER: X-10610
;   TELECOMMUNICATION INFORMATION:
;     TELEPHONE: (317) 276-0756
;     TELEFAX: (317) 276-3861
; INFORMATION FOR SEQ ID NO: 4:
;   SEQUENCE CHARACTERISTICS:
;     LENGTH: 3085 base pairs
;     TYPE: nucleic acid
;     STRANDEDNESS: single
;     TOPOLOGY: linear
;   MOLECULE TYPE: mRNA
US-09-500-358-4

Query Match          82.4%;  Score 1816.8;  DB 3;  Length 3085;
Best Local Similarity 78.9%;  Pred. No. 0;
Matches 1496;  Conservative 365;  Mismatches 2;  Indels 33;  Gaps  1;

Qy    342 GACTGAGGGAGCTGGCCGTGCCGTGCCGACTGGGCTTCGGGCCCTTGGCCGCCGCCGTCCAGAGGAGCAGGCCTTCC 401
          ||||||||||||||||||||||||||||||||||||||||||      |::::||||||||||| |||
Db   1186 GACUGAGGGAGCUGGCCGUGCCGUGCCGACUGGGCUUCGGGCCCUUGAGGCAGGAGCGAGCAGGCCUUCC 1245

Qy    402 TGAGCAGGAGGAAGCAGGTGGTGCGCGGCCGGCAGCCCTGCAGCTGGATGAG 461
          |||||||||||||||||||||||::||||||||||||::|||||||||||||
Db   1246 UGAGCAGGAGGAAGCAGGUGGUGCGCGGCCGGCAGCCCUGCAGCUGGAUGGAG 1305

Qy    462 ACCTGACGAGGATGAGATCCCAGTGGTAGCTATTATGGGCACCACTCGGTTGGTGTGGGATCCGGG 521
          ||||:|||||||||||||:|:||||||||||||||||||||:|:||||||||||||||||||||||
Db   1306 ACCUGACGAGGAUGAGAUCCCAGUGGUAGCUAUUAUGGGCACUUAUUGGCCACUGGUGUGGGAUCCGGG 1365

Qy    522 CAATGACTTCCCTGTATGGGCAGCTGCTGCCTGAAGGAGCTGGGCCCTCTTGGATTGCG 581
          ||||:||||:|:||||:|::||||||||||||||||||||||||||||||||||||||
Db   1366 CAAUGACUUCCCUGUAUGGGCAGCUGCUGCCUGAAGGAGCUGGGCCCUCUUGGAUUGCG 1425

Qy    582 TCTCCTACATCACCGGGCGGCCTTCGGGCTTCCACCTGGCGCCTTGCCCAACCTTTATGAGGACC 641
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Db   2026 GGAACCAGGCCAACCTGGACAAGGAGCAGGTCCCCTTGAAGATAGAAGAACCACCCT 2085
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Qy   1242 CAACAGCCGGCAGAATAGCTGAGTTTTCACCGATCTTCTGACGTGGCGTCCACTGGCCC 1301
          ||||||||||||||||||||||||||||||||||||||  ||||||||||||||||||
Db   2086 CAACAGCCCGGCAGATAGCTGAGTTTTCACCGATCTTCACCGATCTGGACGTGGCGTCCACTGGCCC 2145

Qy   1302 AGGCCACACATAATTCCTGCGTGCCTCCATTCCACAAAGACTACTTCAGCATCCTC 1361
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2146 AGGCCACACATAATTCCTGCGTGCCTCCATTCCACAAAGACTACTTTCAGCATCCTC 2205

Qy   1362 ACTTCTCCACATGAAAGTACCACTCTGATGGGCTCCCAACCAGCTGACACCCTCCG 1421
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2206 ACTTCTCCACATGAAAGTACCACTCTGATGGGCTCCCAACCAGCTGACACCCTCCG 2265

Qy   1422 AGCCCCACCTGTGCCTGCTGGATGTTGGCTACCTCATCAATACCAGCTGCCCTCC 1481
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Db   2266 AGCCCCACCTGTGCCTGCTGGATGTTGGCTACCTCATCAATACCAGCTGCCCTCC 2325

Qy   1482 TGCAGCCCACTCGGGAGCGTGGACTGGACCTCATCCTTCATTGACTACAACCTCCACGGAGCT 1541
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Db   2326 TGCAGCCCACTCGGGAGCGTGGACTGGACCTCATCCTTCATTGACTACAACCTCCACGGAGCT 2385

Qy   1542 TCCAGCAGTTGCAGTCTCTGGGCGCGGTTCTGCCAGGAGCAGGGATCCCGTTCCCACCCA 1601
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Db   2386 TCCAGCAGTTGCAGTCTCTGGGCGCGGTTCTGCCAGGAGCAGGGATCCCGTTCCCACCCA 2445

Qy   1602 TCTCGCCAGCCCGAAGAGCAGCTCCAGGCCTCGGGAGTGCCACACCTTCTCCGACCCCA 1661
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2446 TCTCGCCAGCCCGAAGAGCAGCTCCAGGCCTCGGGAGTGCCACACCTTCTCCGACCCCA 2505

Qy   1662 CCTGCCCCGGAGCCCTTGCGGTGCTGCACTTT--------- 1693
          ||||||||||||||||||||||||||||||||
Db   2506 CCTGCCCCGGAGCCCTTGCGGTGCTGCACTTTCCTCTTGGTCAGCGACTCCTTCCGGGAGT 2565

Qy   1694 -----TCCTCTGGGGTCCGGACACCCGAGAGGCGGCAGCTGGGAGGTGAACCTGT 1748
               |||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2566 ACTCGGCCCGCCCTGGGGTCCGGACACCCGAGAGGCGGCAGCTGGGAGGTGAACCTGT 2625

Qy   1749 CTTCATCGGACTCTCCCTACCACTACGGAAGGTGACCTACAGCCAGGAGGACGTGGACA 1808
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2626 CTTCATCGGACTCTCCCTACCACTACGGAAGGTGACCTACAGCCAGGAGGACGTGGACA 2685

Qy   1809 AGTGCTGTGCACCTGACACATTACAATGTCTGCAACAACCAGGAGCAGCTGCTGGAGCTC 1868
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2686 AGTGCTGTGCACCTGACACATTACAATGTCTGCAACAACCAGGAGCAGCTGCTGGAGCTC 2745

Qy   1869 TGCGCCAGGCAGTGCAGCGGAGGCGGCGAGGCGGCCCCACTGATGGCCGGGCCCCTGC 1928
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2746 TGCGCCAGGCAGTGCAGCGGAGGCGGCGAGGCGGCCCCACTGATGGCCGGGCCCCTGC 2805

Qy   1929 CACCCCTAACTCTCATTCATTCCCTGCTGAGTTGCAGGTGGGAACTGTCATCACGC 1988
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2806 CACCCCTAACTCTCATTCATTCCCTGCTGAGTTGCAGGTGGGAACTGTCATCACGC 2865

Qy   1989 AGTGCTTCAGAGCCTGGGGCTTCAGGCTCCAGGGTCCAGGGCTGGGA 2048
          ||||||||||||||||||||||||||||||||||||||||||||||
Db   2866 AGTGCTTCAGAGCCTGGGGCTTCAGGCTCCAGGGTCCAGGGCTGGGA 2925

Qy   2049 GCTCCCTTGCGCCTCAGAGTTTGCAGTGGGTAAGGAGGCCAAGCCATTTGTGTAATC 2108
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2926 GCTCCCTTGCGCCTCAGAGTTTGCAGTGGGTAAGGAGGCCAAGCCATTTGTGTAATC 2985

Qy   2109 ACCCAAAACCCCCCGGCCTGTGCCTTGCCTTTTCCCTTCTGCGCCTTCGCTACCTTGAGTAGTTGGAGC 2168
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2986 ACCCAAAACCCCCCGGCCTGTGCCTTGCCTTTTCCCTTCTGCGCCTTCGCTACCTTGAGTAGTTGGAGC 3045

Qy   2169 ACTTGATACATCACAGACTCATACAAAAAAAAAAAAAAAAAA 2204
          ||||||||||||||||||||||||||||||||||||||||
Db   3046 ACTTGATACATCACAGACTCATACAAAAAAAAAAAAAAAAAA 3081

RESULT 4
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Db  2506  CCUGCCCCGGAGCCCGUGCGGUGCUGCACCACCCGCACUUCCUCGGUGUCAGCGACUCCUCCGGGAGU  2565
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Qy  1694  ----TCCUCUGGGUCCGCGCACACCCGAGGAGGCCGGCAGCCAGCAGCCAGGUGGGGAGGUGAACCUGU  1748

Db  2566  ACUCGGGCCCCUGGGGUCCGGCGGACACCCGAGGAGGCCGGCAGCCAGCAGCCAGGUGGGGAGGUGAACCUGU  2625
                 |::||||:||||||||||| :|||||||::::||||||
Qy  1749  CUUCAUCGGACUCUCCCUACCACUACACGAAGGUGACCUGACCUGGACA  1808

Db  1809  AGUCGCUGCACUGACATATTACAAATGTCTGCAACAACCAGGAGCAGCAGCAGCAGCCAGGCUC  1868
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Qy  2626  CUUCAUCGGACUCUCCCUACCACUACACGAAGGUGACCUGACCUGGACA  2685

Qy  2686  AGCUGCUGCACCUGACACAUCAAUGUCUGCAACACACCAGGAGCAGCAGCAGCUGGAGGGUC  2745

Qy  1869  UGGCCCAGCAGUGCAGCGGAGGGGCGCAGCGCAGGCCCCACUGAUGGCCGGGCCCCUGC  1928

Db  2746  UGGCCCAGCCAGCCAGUGCAGCGGCGGAGGCGCAGCGCAGGCCCCACUGAUGGCCGGGCCCCUGC  2805

Db  1929  CACCCCUAACUCUCAUUCCCUGGCUGCUGCACUGUCCCAGGGCUGAGGGCUGGGA  1988

Qy  2806  CACCCCUACUCUCAUCUCCUGGCUGCUGCACUGUCCCAGGGGCUGAGGGGCUGGGA  2865

Qy  1989  AGUGCUUCAGAGCCUCAGGUGCCACUGGGUAAGGAGGCCAAGCCCAUUGUGUAAUC  2048

Db  2866  AGUGCUUCAGAGCCUCGGGCUCAGGUUGCAGUUGCAGUGCCAAGCCCAUUGUGUAAUC  2925

Qy  2049  GCUCCCUGCGCCUCAGCAGUUUGCAGUGGGUAAGGAGGCCAAGCCCCAUUUGUGUAAUC  2108

Db  2926  GCUCCCUUGCGCCUCAGCAGUUGCAGUUGCAGUGGGGUAAGGAGGCCAAGCCCAUUUUGUGUAAUC  2985

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Qy  2169  ACUUGAUCAUCACAGACUCAUCACAAAAAAAAAA  2204
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Db  3046  ACUUGAUCAUCACAGACUCAUCACAAAAAAAAAA  3081
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Qy  1426  UCUCCUACAUCACCGGGGCUCCACCUGGGCCUUGGCCAACCUUUAUGAGGACC  1485

Qy  642   CAGAGUGGUCUCAGAAGGACCUGGCAGGGCCCACUGAGUUGCUGAAGACCCAGGUGACCA  701
                 ||||:::|||:||||||||||||||||||
Db  1486  CAGAGUGGUUCUCAGAAGGACCUGGCAGGGCCGCCACUGAGUUGCUGAAGACCCAGGUGACCA  1545

Db  702   AGAACAAGCUGGGUGGUGUGCUGGCCCCCAGCCAGCCUGCAGCCGCAGCGGUCAGCCUGCGCCG  761
                 ||||||:::|||||||||||||||||||||
Qy  1546  AGAACAAGCUGGGUGGUGUGCUGGCCCCCAGCCAGCCUGCAGCCGCAGCGGUCAGCCUGCGCCG  1605

Db  762   AGCGUGCCCGUUGGGCUACCCAAGCUGCUUCACCAAGUCUUCACCAACCUGUGGGCCCUCAUCAACGAGG  821
                 ||||::::|||||||||||||||||||||||||
Qy  1606  AGCGUGCCCGUUGGGCUACCCAAGCUGCUUCACCAAGUCUUCACCAACCUGUGGGCCCUCAUCAACGAGG  1665

Qy  822   CGCUGCUGCAUGAUGAGCCCCAUGAUCAACAAGCUCUCAGAUCAACACCAACAGGCCCUGAGUC  881
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Db  1666  CGCUGCUGCAUGAUGAGCCCCAUGAUCACCUCAACACCAACAGGCCCUGAGUC  1725

Db  882   AUGGCCAGAACCCUGCCCAUCUACUGUGCCCUCAACACCAAAGGCCAGAGCCUGACCA  941
                 |::::||||||||:::|||||:::||||||||||||||||
Qy  1726  AUGGCCAGAACCCUCGCAUCUACUGUGCCCUCAACACCAAAGGCCAGAGCCUGACCA  1785

Qy  942   CUUUUGAAUUUGGGGAGUGGUGCGAGUUCUCCCUACGAGGUCGGCUUCCCCAAGUACG  1001
                 |:::||||||||:::||||||||||||||
Db  1786  CUUUUGAAUUUGGGGAGUGGUGCGAGUUCUCUUUGGCUCCGAGUCUUUGGGGAGUUCCCCAAGUACG  1845

Db  1002  GGGCCUUCAUCCCCUUUGGCUCCGAGUUCUUUUUUGGGGGCAGCUGAUGGAAGA  1061
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Qy  1846  GGGCCUUCAUCCCCUUCGAGCUCUUUUGGCUCCGAGUUCUUUUUAUGGGGGCAGCUGAUGAAGA  1905

Qy  1062  GGCUUCCUGAGUCCGCAUCUGCUUCUUAGAAGGUAUCUGGAGCAAACUGUAUGCAGCCA  1121
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Db  1906  GGCUUCCUGAGUCCGCAUCUGAGUCCUUUAGAAGAAUCUGGAGCAAACUGUAUGCAGCCA  1965

Db  1122  ACCUCCAGGACAGCAGCUUAUACUGGGCCUCAGAGCCCAGUUCUGGGACCGCUGGGUCA  1181
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Qy  1966  ACCUCCAGGACAGCAGCUUAUACUGGGCCUCAGAGCCCAGUUCUGGGACCGCUGGGGUCA  2025

Qy  1182  GGAACCAGGCCAACCUGGACAAGGAGCAGUCCCUUCUGAAGAUAGAAGAACCACCCU  1241
                 |||||||||||||||||||||||:::||:||||||||
Db  2026  GGAACCAGGCCAACCUGGACAAGGAGCAGUCCCCUUCUGAAGAUAGAAGAACCACCCU  2085

Db  1242  CAACAGCCGGCAGAAUAGCUGAGUUUUUCACCGAUCUUCUGACGUGGGGUCCACUGGCCC  1301
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Qy  2086  CAACAGCCGGCAGAUAUGGCUGAGUUUUUCACCGAUCUUCUGACGUGGGGCUUCCACUGGCCC  2145

Qy  1302  AGGCCACACAUAAUUUCCUGCGUGCCCCAUUCCAUUUCCACAAAGACUACUUUCAGCAUCCUC  1361
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Db  2146  AGGCCACACAUAAUUUCCUGCGUGCCCCAUUUCCACAAAGACUACUUUCAGCAUCCUC  2205

Qy  1362  ACUUCUCCACAUGGAAAGCUACCACUCUGGAUGGGGCUCCCCAACCAGCUGACACCCCUCGG  1421
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Db  2206  ACUUCUCCACAUGGAAAGCUACCACUCUGGAUGGGGCUCCCCAACCAGCUGACACCCCUCGG  2265

Qy  1422  AGCCCCACCUGUGCCUGCUGCGUGAUGUUGGCUACCUCAUCAAUACCAGCUGCUGCCCUCC  1481
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Db  2266  AGCCCCACCUGUGCCCUGUGCUGCGGUGAUGUGGCUACCUCAUCCAUCAAUACCAGCUGCUGCCCUCCC  2325

Db  1482  TGCAGCCCACCUCGGACGUGGACCUGGACUACACACCUCAACCUGCACGGAGCCU  1541
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Qy  1542  TCCAGCAGUUGCAGCUCUCGGGCCUGGGCCGGUUCUGCCAGGAGACCAGGAGGGGAUCCUUCCCACCCA  1601

Qy  1602  TCTCGCCCAGCCCCGAAGAGCUCCAGCCUGGGAGUGCCACACCUUCUCGACCCCA  1661
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Db  2386  UCCAGCAGUUGCAGCUCCUCCGGCCGGAUCCCGUUCUGCCACCACCUUCUCCGACACCCCA  2445

Db  2446  UCUCCGCCCAGCCCCGAAGAGCAGCAGCUCCAGCGUGCCACCUCCACCUUCUCCGACCCCA  2505

Qy  1662  CCUGUGCCCGGAGCCCGCCCUGCUGCUGCACUUU--------------  1693
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; FILING DATE:    19-MAR-1997
; ATTORNEY/AGENT INFORMATION:
;   NAME:  Gaylo, Paul J.
;   REGISTRATION NUMBER:  36,808
; REFERENCE/DOCKET NUMBER: X-10610
; TELECOMMUNICATION INFORMATION:
;   TELEPHONE:  (317) 276-0756
;   TELEFAX:   (317) 276-3861
INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
;   LENGTH:  3085 base pairs
;   TYPE:  nucleic acid
;   STRANDEDNESS:  single
;   TOPOLOGY:  linear
; MOLECULE TYPE:  cDNA
; FEATURE:
;   NAME/KEY:  CDS
;   LOCATION:  48..2786
US-09-498-809-2

Query Match    82.4%;   Score 1816.8;   DB 3;   Length 3085;
Best Local Similarity  98.2%;   Pred. No. 0;
Matches 1861;   Conservative   0;   Mismatches   2;   Indels   33;   Gaps   1;
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Qy    342  GACTGAGGGAGGTGGCCGTGCGACTGGCTTCGGGCCCTGTGCCAGAGGAGCAGGCCTTCC    401
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Db   1186  GACTGAGGGAGGTGGCCGTGCGACTGGCTTCGGGCCCTGTGCCAGAGGAGCAGGCCTTCC   1245

Qy   1906  GGCTTCCTGAGTCCGCATCTGCTTCTTAGAGAGTATCTGGAGCAACCTGTATGCAGCCA   1965
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Db    402  TGAGCAGGAGGAAGCAGCAGGTGGTGCGCAGGCAGGCCCTGAGGCAGGCCCTGAGTGATGAG    461
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Db   1246  TGAGCAGGAGGAAGCAGCAGGTGGTGCGCAGGCAGGCCCTGAGGCAGGCCCTGAGTGATGAG   1305

Qy   1122  ACCTCCAGGACAGCTTATACTGGGCCACCAGTTCTTGGGACCGCTGGGTCA   1181
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Db   1966  ACCTCCAGGACAGCTTATACTGGGCCACCAGTTCTTGGGACCGCTGGGTCA   2025

Qy    462  ACCTGCAGGAGGATGAGATCCCAGTGGTAGCTATTATGGCCACTGGTGGTGGATCCGGG    521
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Db   1306  ACCTGCAGGAGGATGAGATCCCAGTGGTAGCTATTATGGCCACTGGTGGTGGATCCGGG   1365

Qy   1182  GGAACCAGGCCAACCTGGACAAGAGCAGCAGTCCCCCTTCTGAAGATAGAGAAGAACCACCCT   1241
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Db   2026  GGAACCAGGCCAACCTGGACAAGAGCAGCAGTCCCCCTTCTGAAGATAGAGAAGAACCACCCT   2085

Qy    522  CAATGACTTCCCTGTATGGGCAGCTGGCTGGCCTGAAGGAGCTGGGCTTCTTTGGATTGCG    581
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Db   1366  CAATGACTTCCCTGTATGGGCAGCTGGCTGGCCTGAAGGAGCTGGGCTTCTTTGGATTGCG   1425

Qy   1242  CAACAGCCGCAGAATAGCTGAGTTTTCACCGATCTTCTGACGTGGCGTCCACTGGCCC   1301
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Db   2086  CAACAGCCGCAGAATAGCTGAGTTTTCACCGATCTTCTGACGTGGCGTCCACTGGCCC   2145

Qy    582  TCTCCTACATCACCGGGGCCTTGGGCCTTCGGGCCTTCCAACCTTTATGAGACC    641
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Db   1426  TCTCCTACATCACCGGGGCCTTGGGCCTTCGGGCCTTCCAACCTTTATGAGACC   1485

Qy   1302  AGGCCACACATAATTTCCTGCGTGGCCTCCATTTCCACAAAGACTACTTTCAGCATCCTC   1361
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Db   2146  AGGCCACACATAATTTCCTGCGTGGCCTCCATTTCCACAAAGACTACTTTCAGCATCCTC   2205

Qy    642  CAGAGTGGTCTCAGAAGGACCTGAGTTGCTGAAGACCCAGGTGACCA    701
           |||||||||||||||||||||||||||||||||||||||||||||||
Db   1486  CAGAGTGGTCTCAGAAGGACCTGAGTTGCTGAAGACCCAGGTGACCA   1545

Qy   1362  ACTTCTCCACCATGGAAAGCTACCACTCTGGATGGGCTACCTCATCAATACCAGTCGCCTGCCCTCC   1421
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Db   2206  ACTTCTCCACCATGGAAAGCTACCACTCTGGATGGGCTACCTCATCAATACCAGTCGCCTGCCCTCC   2265

Qy    702  AGAACAAGCTGGGTGTGTGCTGGCCCCCAGCCAGCTGCGCAGCCGGTACCGGACGCTGGCCG    761
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1546  AGAACAAGCTGGGTGTGTGCTGGCCCCCAGCCAGCTGCGCAGCCGGTACCGGACGCTGGCCG   1605

Qy   1422  AGCCCCACCTGTGCCTGCTGATGTTGGCTACCTCATCATACCAGCTGCCTGCCCCTCC   1481
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2266  AGCCCCACCTGTGCCTGCTGATGTTGGCTACCTCATCATACCAGCTGCCTGCCCCTCC   2325

Qy    762  AGCGGTGCCCGCTTGGGCTGACCTGCTTCACCAACTGCTGCTTCACCAACCTGTGGGCCCTCATCAACGAGG    821
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1606  AGCGGTGCCCGCTTGGGCTGACCTGCTTCACCAACTGCTGCTTCACCAACCTGTGGGCCCTCATCAACGAGG   1665

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Db   2326  TGCAGCCCACTCGGGACGTGACCTCATCCTGCTCATTGGACTACACACCTCCACGGAGCCT   2385

Qy    822  CGCTGCTGCGATGATGAGCCCATGATCAGAAGCTCTCAACAACTGCTGCTGCAGGAGCCCGAGTC    881
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Db   1666  CGCTGCTGCGATGATGAGCCCATGATCAGAAGCTCTCAACAACTGCTGCTGCAGGAGCCCGAGTC   1725

Qy   1542  TCCAGCAGTTGCAGCTCCTGGGCCGGTTCTGCGCCAGGAGCAGGGATCCCGTTCCCACCCA   1601
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Db   2386  TCCAGCAGTTGCAGCTCCTGGGCCGGTTCTGCGCCAGGAGCAGGGATCCCGTTCCCACCCA   2445

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Db   1726  ATGGCCAGAACCCTCTGCCCATCATCAGTCTGCCCTCAACAACTACTGCCCTCAACACCAAAGGGCAGAGCCTGACCA   1785

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Db   2446  TCTCGCCCAGCCCCGAAGAGCAGCTCCAGCCTGGGAGTGCCACACCTTCTCCGACCCCA   2505

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Qy   1002  GGGCCCTTCATCCCCTCTGAGTCTTTTGGGCTCCGAGTTCTTTATGGGCAGCTGATGAAGA   1061
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Db   1846  GGGCCCTTCATCCCCTCTGAGTCTTTTGGGCTCCGAGTTCTTTATGGGCAGCTGATGAAGA   1905

Qy   1694  -----TCTCTGGGTCCGGCGGACACCCGAGGAGGCGGCGACTCCTTCCGGGAGGTGAACCTGT   1748
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Db   2566  ACTCGGCCCCTGGGTCCGGCGGACACCCGAGGAGGCGGCGACTCCTTCCGGGAGGTGAACCTGT   2625

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Db   2109  ACCCAAAACCCCCGGCCTGTTCCCTTCTGCGTCACTTGAGTTCGCGCTACCTTGAGTAGTTCGAGC   2168

Qy   1749  CTTCATCGGACTCTCCACTACACCAGGACGTGACTCACGCAGCGAGGAGACGTGACA   1808
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Db   2626  CTTCATCGGACTCTCCCTACCACTACACGAAGTGACTCACGCAGCGAGGAGACGTGACA   2685

Qy   1809  AGTGCTGCACCTGACACATTACAATGTCTGCAACAACCAGGAGCAGCTGCTGGAGGCTC   1868
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Db   2686  AGTGCTGCACCTGACACATTACAATGTCTGCAACAACCAGGAGCAGCTGCTGGAGGCTC   2745

Qy   1869  TGCGCCAGGCAGTGCAGCGGAGCGGCGGAGCGGCGGCGGCCCAGGCCCCACTGATGGCCGGGGCCCCTGC   1928
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Db   2746  TGCGCCAGGCAGTGCAGCGGAGCGGCGGAGCGGCGGCGGCCCAGGCCCCACTGATGGCCGGGGCCCCTGC   2805

Qy   1929  CACCCCTAACTCATTCATTCCCTGCGCTGAGTTGCAGGTGGCAACTGTCATCACGC   1988
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Db   2806  CACCCCTAACTCATTCATTCCCTGCGCTGAGTTGCAGGTGGCAACTGTCATCACGC   2865

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Db   2866  AGTGCTTCAGAGCCTGGGCTCAGGTGCACTGTCCCAGGGCTCGAGGGCTGGGA   2925

Qy   2049  GCTCCCTGCCCTCAGCAGTTGCAGTGGGTAAGGAGGCCAAGCCCATTTGTGTAATC   2108
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Db  2986  ACCCAAAACCCCCGGCCTGTGCCGTGTTTCCCTTCTGCGCTACCTTGAGTAGTTGGAGC  3045

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RESULT 6

US-09-498-809-4
; Sequence 4, Application US/09498809
; Patent No. 6242206
; GENERAL INFORMATION:
;   APPLICANT: Chiou, Xue-Chiou C.
;   APPLICANT: Kramer, Ruth M.
;   APPLICANT: Pickard, Richard T.
;   APPLICANT: Sharp, John D.
;   APPLICANT: Strifler, Beth A.
;   TITLE OF INVENTION: HUMAN PHOSPHOLIPASE A2 AND RELATED
;   TITLE OF INVENTION: NUCLEIC ACID COMPOUNDS
;   NUMBER OF SEQUENCES: 4
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE: Eli Lilly and Company
;   STREET: Lilly Corporate Center
;   CITY: Indianapolis
;   STATE: Indiana
;   COUNTRY: United States of America
;   ZIP: 46285
;   COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: PatentIn Release #1.0, Version #1.30
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/09/498,809
;   FILING DATE:
;   CLASSIFICATION:
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: 08/827,208
;   FILING DATE:
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: US 60/041,264
;   FILING DATE: 19-MAR-1997
;   ATTORNEY/AGENT INFORMATION:
;   NAME: Gaylo, Paul J.
;   REGISTRATION NUMBER: 36,808
;   REFERENCE/DOCKET NUMBER: X-10610
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE: (317) 276-0756
;   TELEFAX: (317) 276-3861
; INFORMATION FOR SEQ ID NO: 4:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH: 3085 base pairs
;   TYPE: nucleic acid
;   STRANDEDNESS: single
;   TOPOLOGY: linear
;   MOLECULE TYPE: mRNA

US-09-498-809-4

Query Match   82.4%; Score 1816.8; DB 3; Length 3085;
Best Local Similarity   78.9%; Pred No. 0;
Matches 1496; Conservative 365; Mismatches 2; Indels 33; Gaps 1;
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Qy   342  GACTGAGGAGGAGCTGGCCGTGCGACGTCGGCCTTCGGGCCCTGTGCAGGAGGAGGCCTTCC  401
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Qy   402  TGAGGAGGAAGCAGGAGGACCAGGAGGCCGCGGCCCTGAGGAGGAGCAGCCTGCCCTGATGAG  461
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Db  1246  UGAGGAGGAAGCAGGAGGAUGAGGAUCCCCAGUUGUAGUCCCAGUGCUGGGGGCGGGGAUUGGAG  1305

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Db  1366  CAAUGACUUCCCUGUAUGGGCAGCUGCUGGCAGGAGCUGGGGCCUGGCCUCGGCCUCUUUGGAUUGCG  1425

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Db  1426  UCUCCUACAUCACCGGGCCUUCGGGCUCCACCUGGCCUCCACCUGGCCUCCUGCCAACCUUUAUGAGGACC  1485

Qy   642  CAGAGTGTCTCAGAACGACTTGGCAGGGCCCACTGAGTTGCTGAAGACCCAGTGACCA  701
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Db  1486  CAGAGUGGUCCUCAGAAGACUGGCAGGGCCCACUGAGUUGCUGAAGACCCAGUGACCA  1545

Qy   702  AGAACAAGCTGGGTGTGCTGGCCCCAGCCAGTGCGAGCGGTACCGGCAGGAGGCTGGCCG   761
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Db  1606  AGCGUGCCGCCUGGCUACCAAGCUGCUUCACCAACCUGUGGGCCCUCAUCAACGAGG  1665

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Db  1666  CGCUGCUGCCAUGAUGAGCCCCAUGAUCACAAGUCUCAGAUCAACAAGCUGCCCUGAGUC  1725

Qy   882  ATGGCCAGAACCCTCTGCCCATCTACTGTCCCTCACACACTGTCCCATCTACTGTCCCTGACCA   941
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Db  1726  AUGGCCAGAACCCCUGCCCUCUCCCCAGUUCUUAUGGGGCAGCUGAUGAAGA  1785

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Db  1786  CUUUUGAAUUUGGGGAGUGGUGCGAGUUCUCUUCCCUAGGUUCUUCCCAAGUAGU  1845

Qy  1002  GGGCCTTCATCCCTCTGAGCTCTTTGGCTCCGGAGTTCTTTATGGGGCAGCTGATGAAGA  1061
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Db  1846  GGGCCUUCAUCCCUCCCCUGAGCUCUUGGCUCCGGAGUUCUUCCCUGAAGAUAGGGGCAGAUGAUGAAGA  1905

Qy  1062  GGCTTCCTGAGTCCCGCATCTGCTTCTTAGAAAGGTATCTGTATGCAGCCA  1121
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Db  1906  GGCUUCCUGAGUCCCGCAUCUGCUUCUUUGAAAGGUAUCUGGAGCAACCUGUAUGCAGCCA  1965

Qy  1122  ACCTCCAGGACAGCTTATACTGGGCTCAGAGCCAGTTCTGGACACCGCTGGGTCA  1181
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Db  2026  GGAACCAGGCCAACCUGGACAAGAGGAGCAGGUCCCCUUCUCGAAGAUAGAAGAACCACCCU  2085

Qy  1242  CAACAGCCGCAGAATAGCTGAGTTTTTCACCGATCTTCTGAGTCGGTGGCGTCCACTGGCCC  1301
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Db  2146  AGGCCACAUAAUUUCCUGGUGUGGCCUUCAGUUCCACAUUUCCACAAACAGACUACAUUUCCACAUUUUCAGCAUCCUC  2205

Qy  1362  ACTTCTCCACATGGAAAGCTACCACTCTGATGGGCTCCCAACCAGCTGACACCCTCGG  1421
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;  ATTORNEY/AGENT INFORMATION:
;    NAME:  Brown, Scott A.
;    REGISTRATION NUMBER:  32,724
;    REFERENCE/DOCKET NUMBER:  GI5289
;  TELECOMMUNICATION INFORMATION:
;    TELEPHONE:   (617) 498-8224
;    TELEFAX:     (617) 876-5851
; INFORMATION FOR SEQ ID NO: 3:
;   SEQUENCE CHARACTERISTICS:
;    LENGTH:  2699 base pairs
;    TYPE:  nucleic acid
;    STRANDEDNESS:  double
;    TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
US-09-460-145-3

Query Match          82.0%;    Score 1806.2;   DB 3;   Length 2699;
Best Local Similarity  98.1%;    Pred. No. 0;
Matches 1851;    Conservative  0;   Mismatches  3;   Indels  33;   Gaps  1;

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Db    869 TGAGCAGGAGGAAGCAGAGGTGGTGGCCGCCTGAGGGCCTGCAGCTGGATGAGGAG  928

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Db   1169 AGAACAAGCTGGGTGTGCTGGCCCCAGCAGCTGCAGCGGTACCGGCGAGGAGCTGGGCG  1228

Qy    762 AGCGTGCCCGCTTGGGCTACCAGCTGCTTCCACCTGTGGGCCCTCATCAACGAGG  821
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Db   1289 CGCTGCTGCATGATGAGCCCCATGATCACAAGCTCTCAGATCACCAACGGAGGCCCTGAGTC  1348

Qy    882 ATGGCCAGAACCCTCGCCCATCTACTGTGCCCTACACCAAAGGGCAGAGCCTGACCA  941
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Qy    942 CTTTTGAATTTGGGAGTGGTGCGAGTTCTCCCCAGAGGTGGTTCGCTTCCCCAAGTACG  1001
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Db   1409 CTTTTGAATTTGGGAGTGGTGCGAGTTCTCTCCCCAGAGGTGGTTCGCTTCCCCAAGTACG  1468

Qy   1002 GGGGCCTTCATCCCCTGAGTCTTTGGCTCCGAGTTCTTTATGGGGCAGTCTTATGGGGGACAGTCTTATGGGGACAACCTGTATGCAGCA  1061
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Db   1469 GGGGCCTTCATCCCCTGAGTCTTTGGCTCCGAGTTCTTTATGGGGCAGTCTTATGGGGACAACCTGTATGCAGCA  1528

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Db   1529 GGCTTCCTGAGTCCCGCATCTGCTTCTTAGAAGGTATCTGAGCAACCTGTATGCAGCCA  1588

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Qy   1602 TCTCGCCCAGCCCCGAAGAGCAGCTTCCAGCCTCCGGGAGTGCCACACCTTCTCCGACCCCA  1661
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Db   2446 UCUCGCCCCAGCCCCGAAGAGCAGCAGCAGCCUCCGGGAGUGCCAGCCCACCUUCUCCGACCCCA  2505

Qy   1662 CCTGCCCCGGAGCCCCTGCGGTGCTGCACTTT------  1693
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Db   2506 CCUGCCCCGGAGCCCCUGCGGUGCUGCACUUUCCUCUGGGUCAGCGGACGCCUUCCUGGGGAGU  2565

Qy   1694 ------TCCTTGGGGTCCGCGGACACCCGAGGAGGCGGCCAGCTGGGAGGTGAACCTGT  1748
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Db   2566 ACUCGGCCCCUGGGGUCCGCGGACACCCGAGGAGGCGGCCAGCUGGGAGGUGAACCUGU  2625

Qy   1749 CTTCATCGGACTCTCCCTACCACTACACGAAGGTGACCTACAGCCAGGAGGACGTGGACA  1808
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Db   2626 CUUCAUCGGACUCUCCCUACCACUACACGAAGGUGACCUACAGCCAGGAGGACGUGGACA  2685

Qy   1809 AGCTGCTGCACCTGACACATTACAATGTCTGCAACAACCAGGAGCAGCTGCTGCTGAGGGCTC  1868
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Db   2686 AGCUGCUGCACCUGACACAUUACAAUGUCUGCAACAACCAGGAGCAGCUGCUGCUGAGGGCUC  2745

Qy   1869 TGGGCCAGGCAGTGCAGCGGAGGCGGCAGCGCGCAGGCCCCACTGATGGCCGGGGCCCCTGC  1928
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Qy   1929 CACCCCTAACTCTCATTCCTGCTGCTGAGTTGCAGGTTGGGAACTGTCATCACGC  1988
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Qy   1989 AGTGCTTCAGAGCCTCGGGCTCAGGTGGCACTGTCCCAGGGTCCAGGCTGAGGGCTGGGA  2048
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Db   2866 AGUGCUUCAGAGCCUCGGGCUCAGGUGGCACUGUCCCAGGGUCCAGGCUGAGGGCUGGGA  2925

Qy   2049 GCTCCCTTGCGCCTCAGCAGTTTGCAGTGGGGTAAGGAGGCCAAGCCCATTGTGTAATC  2108
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Db   2926 GCUCCCUUGCGCCUCAGCAGUUUGCAGUGGGGUAAGGAGGCCAAGCCCAUUGUGUAAUC  2985

Qy   2109 ACCCAAAACCCCCGGCCTGTGCCTGCTTTCCCTTCTGCGCTACCTTGAGTAGTTGGAGC  2168
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Db   2986 ACCCAAAACCCCCGGCCUGUGCCUGCUUUCCCUUCUGCGCUACCUUGAGUAGUUGGAGC  3045

Qy   2169 ACTTGATACATCACAGACTCATACACAAAAAAAAAAA  2204
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Db   3046 ACUGAUACAUCACAGACUCAUACACAAAAAAAAAAA  3081
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RESULT 7
US-09-460-145-3
;  Sequence 3, Application US/09460145
;  Patent No. 6287838
;  GENERAL INFORMATION:
;    APPLICANT:  Kriz, Ron
;    APPLICANT:  Song, Chuanzheng
;    TITLE OF INVENTION:  CYTOSOLIC PHOSPHOLIPASE A2-BETA ENZYMES
;    NUMBER OF SEQUENCES:  9
;    CORRESPONDENCE ADDRESS:
;     ADDRESSEE:  Genetics Institute, Inc.
;     STREET:  87 CambridgePark Drive
;     CITY:  Cambridge
;     STATE:  MA
;     COUNTRY:  USA
;     ZIP:  02140
;    COMPUTER READABLE FORM:
;     MEDIUM TYPE:  Floppy disk
;     COMPUTER:  IBM PC compatible
;     OPERATING SYSTEM:  PC-DOS/MS-DOS
;     SOFTWARE:  Patentin Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;     APPLICATION NUMBER:  US/09/460,145
;     FILING DATE:
;    CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;     APPLICATION NUMBER:  08/788,975
;     FILING DATE:
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Db        2669 ACTTGATACATCACAGACTCATACAAA 2695

RESULT 8
US-09-895-547-3
; Sequence 3, Application US/09895547
; Patent No. 6482625
; GENERAL INFORMATION:
;   APPLICANT: Kriz, Ron
;            Song, Chuanzheng
;   TITLE OF INVENTION: CYTOSOLIC PHOSPHOLIPASE A2-BETA ENZYMES
;   NUMBER OF SEQUENCES: 9
;   CORRESPONDENCE ADDRESS:
;     ADDRESSEE: Genetics Institute, Inc.
;     STREET: 87 CambridgePark Drive
;     CITY: Cambridge
;     STATE: MA
;     COUNTRY: USA
;     ZIP: 02140
;   COMPUTER READABLE FORM:
;     MEDIUM TYPE: Floppy disk
;     COMPUTER: IBM PC compatible
;     OPERATING SYSTEM: PC-DOS/MS-DOS
;     SOFTWARE: PatentIn Release #1.0, Version #1.30
;   CURRENT APPLICATION DATA:
;     APPLICATION NUMBER: US/09/895,547
;     FILING DATE: 29-Jun-2001
;     CLASSIFICATION: <Unknown>
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER: 09/460,145
;     FILING DATE: <Unknown>
;   ATTORNEY/AGENT INFORMATION:
;     NAME: Brown, Scott A.
;     REGISTRATION NUMBER: 32,724
;     REFERENCE/DOCKET NUMBER: GI5289
;   TELECOMMUNICATION INFORMATION:
;     TELEPHONE: (617) 498-8224
;     TELEFAX: (617) 876-5851
; INFORMATION FOR SEQ ID NO: 3:
;   SEQUENCE CHARACTERISTICS:
;     LENGTH: 2699 base pairs
;     TYPE: nucleic acid
;     STRANDEDNESS: double
;     TOPOLOGY: linear
;   MOLECULE TYPE: cDNA
;   SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-09-895-547-3

Query Match             82.0%;  Score 1806.2;  DB 4;  Length 2699;
Best Local Similarity   98.1%;  Pred. No. 0;
Matches 1851;   Conservative   0; Mismatches   3;  Indels  33;  Gaps   1;
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(Sequence alignment between Query (Qy) and Database (Db) follows, numbered base positions)

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Qy  702 AGAACAAGCTGGGGTGTGCTGCGGCCCCCAGCTGCAGCGGGTACCGGCAGGAGCTGGCCG 761
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Db 1169 AGAACAAGGTGGGTGTGCTGCGGCCCCCAGCTGCAGCGGGTACCGGCAGGAGCTGGCCG 1228
Qy  762 AGCGGTGCCCGCTTGGGCTACCCAGCTGCTTCACCAGCTGCTTCATCAACGAGG 821
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Db 1229 AGCGGTGCCCGCTTGGGCTACCCAGCTGCTTCACCAGCTGCTTCATCAACGAGG 1288
Qy  822 CGCTGCTGCATGATGAGCCCCATGATCACAAGCTCTCAGATCAACGAGGCCCTGAGTC 881
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Db 1289 CGCTGCTGCATGATGAGCCCCATGATCACAAGCTCTCAGATCAACGAGGCCCTGAGTC 1348
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Db 1529 GGCTTCCTGAGTCCCGCATCTCGTTCGTTCTTAGAAGGTATCTGGAGCAACCTGTATGCAGCCA 1588
Qy 1122 ACCTCCAGGACAGCAGCTTATACTGGGACAAGGAGCAGTCCCCCTTCTCCCTTCTGAAGATAGAAGAACCACCCT 1241
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Db 1649 ACCTCCAGGACAGCAGCTTATACTGGGACAAGGAGCAGTCCCCCTTCTCCCTTCTGAAGATAGAAGAACCACCCT 1708
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Db 1769 AGGCCACCACATAATTTCCTGGCCTCCATTTCCACAAAGACTACTTTCAGCATCCTC 1828
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Db 1829 ACTTCTCCACATGGGAAAGCTACCACTCTGGATGGGCTCCCCAACCAGTCGACACCCTCGG 1888
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Db 1949 TGCAGCCACTCGGGACGTGACCTGACCTCATCCTGTCATTGGACTACAACCTCCACGGAGCCT 2008
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Db 2009 TCCAGCAGTTGCAGCTTCCTGGGCGTTCTGCAGGAGCAGGGGGATCCCGGTTCCCACCCA 2068
Qy 1602 TCTCGCCCCAGCCCCGAGAGAGCAGCTCCAGCCTCGGGAGTGCCACACCTTCTCCGACCCCA 1661
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Db 2069 TCTCGCCCCAGCCCCGAGAGAGCAGCTCCAGCCTCGGGAGTGCCACACCTTCTCCGACCCCA 2128
Qy 1662 CCTGCCCCGGAGCCCCTGCCGGTGGTCTGCACTTT------ 1693
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Db 2129 CCTGCCCCGGAGCCCCTGCCGGTGCTGCACTTTCCTTCTGGTCAGCGACTCCTTCCGGGAGT 2188
Qy 1694 ----TCCTCTGGGGTCCGCGGCGGACACCCGAGGAGGCGGCAGCTGGGGAGGTGAACCTGT 1748
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Db 2189 ACTCGGCCCCTGGGGTCCGGCGGACACCCGAGGAGGCGGCAGCTGGGGAGGTGAACCTGT 2248
Qy 1749 CTTCATCGGACTCTCCCTACCACTACACGAAGGTGACCTACAGCGAGGACGTGGACA 1808
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Db 2249 CTTCATCGGACTCTCCCTACCACTACACGAAGGTGACCTACAGCGAGGACGTGGACA 2308
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Db 2309 AGCTGCTGCACCTGACACATTACAAATGTCTGCAACAACCAGGAGCAGCTGCTGGGAGCTC 2368
Qy 1869 TGCGGCCAGGGAGTGCAGCGGAGGGCGGCAGCCCCACTGATGGCCGGGCCCCTGC 1928
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Db 2369 TGCGGCCAGGCAGTGCGACGGAGGGCGGCAGCCCCACTGATGGCCGGGCCCCTGC 2428
Qy 1929 CACCCCTAACTCTCATTCATTCCCTGCTGCTGAGTTGCAGGTGCAGGTGGAACTGTCATCACGC 1988
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Db 2429 CACCCCTAACTCTCATTCATTCCCTGCTGCTGAGTTGCAGGTGCAGGTGGAACTGTCATCACGC 2488
Qy 1989 AGTGCTTCAGAGCCTCGGGCTCAGGTGGCACTGTCCCAGGTCCAGGGCTGGGA 2048
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Db 2489 AGTGCTTCAGAGCCTCGGGCTCAGGTGGCACTGTCCCAGGTCCAGGGCTGGGA 2548
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Qy 2109 ACCCAAAACCCCCGGCCTGTGCCTGTTTTCCCTTCGCGCTACCTTGAGTAGTTGGAGC 2168
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Db 2669 ACTTGATACATCACAGACTCATACAAA 2695
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RESULT 9
US-09-460-145-1
; Sequence 1, Application US/09460145
; Patent No. 6287838
; GENERAL INFORMATION:
; APPLICANT: Kriz, Ron
; APPLICANT: Song, Chuanzheng
; TITLE OF INVENTION: CYTOSOLIC PHOSPHOLIPASE A2-BETA ENZYMES
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
;   ADDRESSEE: Genetics Institute, Inc.
;   STREET: 87 CambridgePark Drive
;   CITY: Cambridge
;   STATE: MA
;   COUNTRY: USA
;   ZIP: 02140
; COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/09/460,145
;   FILING DATE:
;   CLASSIFICATION:
; PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: 08/788,975
;   FILING DATE:
; ATTORNEY/AGENT INFORMATION:
;   NAME: Brown, Scott A.
;   REGISTRATION NUMBER: 32,724
;   REFERENCE/DOCKET NUMBER: GI5289
; TELECOMMUNICATION INFORMATION:
;   TELEPHONE: (617) 498-8224
;   TELEFAX: (617) 876-5851
; INFORMATION FOR SEQ ID NO: 1:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH: 4183 base pairs

us-09-830-321a-5.rni

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;   TYPE: nucleic acid
;   STRANDEDNESS: double
;   TOPOLOGY: linear
;   MOLECULE TYPE: cDNA
US-09-460-145-1

Query Match        82.0%;    Score 1806.2;   DB 3;   Length 4183;
Best Local Similarity  98.1%;  Pred. No. 0;
Matches 1851;   Conservative 0;   Mismatches 0;   Indels 33;   Gaps 3;
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Qy   402  TGAGCAGGAGGAAGCAGGTGGTGGCGCGGCCTTGAGGCAGGCCCTGCAGCTGGATGGAG    461
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Db  2353  TGAGCAGGAGGAAGCAGGTGGTGGCGCGGCCTTGAGGCAGGCCCTGCAGCTGGATGGAG   2412

Qy   462  ACCTGCGAGGAGGATGAGATCCCAGTGTAGCTATTATGGCCACTGGTGTGTGGGATCCGGG   521
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Db  2473  CAATGACTTCCCTGTATGGGACTGGCTGGCTGAAGGAGCTGGGCCTCTTGGATTGCG     2532

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Db  2593  CAGAGTGGTCTCAGAAGACCTGCAGGCCCACTGAGTTGCTGAAGACACCAGTGACCA     2652

Qy   702  AGAACAAGCTGGGTGTGCTGCCCCCAGCCAGCTGCAGCGGTACGGCAGGAGCTGGCCG     761
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Db  2653  AGAACAAGCTGGGTGTGCTGCCCCCAGCCAGCTGCAGCGGTACGGCAGGAGCTGGCCG    2712

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Db  2713  AGGGTGCCCGCTTGGGCTACCCAAGCTGCTTCACCAACCTGGGCCCTCATCAACGAGG   2772

Qy   822  CGCTGCTGCATGATGAGCCCCATGATCAACAAGCTCTCAGATCAACGGGACCCTGAGTC    881
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Qy  1002  GGGGCCTTCATCCCCTGAGCTCTTTTGGCTCCGAGTTCTTTGGCTCCGAGTTCTTATGGGG  1061
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Db  3013  GGCTTCCTGAGTCCCGACATCCGCATCTGCTTCTTCTTAGAAGTATCTGGAGCAACCTGTA  3072

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Db  3133  GGAACCAGGCCAACCTGGACAAGGAGCAGTTCCCCCTTTCTGAAGATAGAAGAACCACCCT  3192

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Db  3193  CAACAGCCGGCAGGATAGCTGAGTTTTTCACCGATCTTCTGACGTGGCGTTCCACTGGCCC  3252

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Db  3253  AGGCCACACATAATTCCTGCGTGGCCTCCATTCCACAAAGACTACTTTCAGCATCCTC  3312

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Qy  1422  AGCCCCACCTGCTGCCGTGCTGGACGTGTTGGCTACCTCATCATAATACCAGCTG     1481
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Qy  1482  TGCAGCCCACTCGGGACGTGGACCTGATCCTCGTCATTGGACTACAACCTCCACGGAGCCT  1541
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Db  3553  TCTCGCCCAGCCCCGAAGAGCAGCTCCAGCCTCGGGAGTGCCACACCTTCTCCGACCCCA  3612

Qy  1662  CCTGCCCCGGAGCCCCTGCGGCCCTGCGGTCACTTT-------------------    1693
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Qy  1694  -----TCCTCTGGGGTCCGGCGACACCCCGGACACCCCGGACGCGGCTGAACCTGT   1748
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Db  3673  ACTCGTCCTCTGGGGTCCGGCGACACCCCGGACACCCCGGACGCGGCTGAACCTGT  3732

Qy  1749  CTTCATCGGACTCTCCCTACCAGCCAGCGAAGGTGACCTACAGCCAGGACGTGACA   1808
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Db  3733  CTTCATCGGACTCTCCCTACCAGCCAGCGAAGGTGACCTACAGCCAGGACGTGACA  3792

Qy  1809  AGCTGCTGCACCTGACACATTACAATGTCTGCAACAACAGGAGCAGCTGCTGGAGCTC   1868
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Db  3793  AGCTGCTGCACCTGACACATTACAATGTCTGCAACAACAGGAGCAGCTGCTGGAGCTC  3852

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Db  3853  TGCGCCAGGCAGTGCAGCGGAGGCGGCGAGTGCAGCGCCCACTGATGGCCGGGGGCCCTGC  3912

Qy  1929  CACCCTAACTCTCATTCATTCCTGGCTGCTGAGTTGCAGTGCACTGTCATCACGC     1988
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Qy  1989  AGTGCTTCAGAGCCTCGGGCTTCGAGGCCACTGTCCCAGGGTAAGGAGCTGTGGGA    2048
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Db  3973  AGTGCTTCAGAGCCTCGGGCTTCGAGGCCACTGTCCCAGGGTAAGGAGCTGTGGGA   4032

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Qy  2109  ACCCAAAACCCCCGGCCTGTGCCTGTTTCCCTTCGCGTACCTTGGAGC    2168
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RESULT 10

US-09-895-547-1
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; Sequence 1, Application US/0995547
; Patent No. 6482625
;   GENERAL INFORMATION:
;   APPLICANT: Kriz, Ron
;              Song, Chuanzheng
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;;   TITLE OF INVENTION: CYTOSOLIC PHOSPHOLIPASE A2-BETA ENZYMES
;;   NUMBER OF SEQUENCES: 9
;;   CORRESPONDENCE ADDRESS:
;;     ADDRESSEE: Genetics Institute, Inc.
;;     STREET: 87 CambridgePark Drive
;;     CITY: Cambridge
;;     STATE: MA
;;     COUNTRY: USA
;;     ZIP: 02140
;;   COMPUTER READABLE FORM:
;;     MEDIUM TYPE: Floppy disk
;;     COMPUTER: IBM PC compatible
;;     OPERATING SYSTEM: PC-DOS/MS-DOS
;;     SOFTWARE: PatentIn Release #1.0, Version #1.30
;;   CURRENT APPLICATION DATA:
;;     APPLICATION NUMBER: US/09/895,547
;;     FILING DATE: 29-Jun-2001
;;     CLASSIFICATION: <Unknown>
;;   PRIOR APPLICATION DATA:
;;     APPLICATION NUMBER: 09/460,145
;;     FILING DATE: <Unknown>
;;   ATTORNEY/AGENT INFORMATION:
;;     NAME: Brown, Scott A.
;;     REGISTRATION NUMBER: 32,724
;;     REFERENCE/DOCKET NUMBER: GI5289
;;   TELECOMMUNICATION INFORMATION:
;;     TELEPHONE: (617) 498-8224
;;     TELEFAX: (617) 876-5851
;;   INFORMATION FOR SEQ ID NO: 1:
;;     SEQUENCE CHARACTERISTICS:
;;       LENGTH: 4183 base pairs
;;       TYPE: nucleic acid
;;       STRANDEDNESS: double
;;       TOPOLOGY: linear
;;     MOLECULE TYPE: cDNA
;;     SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-895-547-1
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Query Match   82.0%; Score 1806.2; DB 4; Length 4183;
Best Local Similarity 98.1%; Pred. No. 0;
Matches 1851; Conservative   0; Mismatches   0; Indels 33; Gaps   1;

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Qy    462 ACCTGCAGGAGGAGGATGAGATCCCAGTGTAGTCATTATGGCCACTGGTGGTGGGATCCGGG    521
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Qy    582 TCTCCTACATCACCGGGGCCTTCGGGTCCACCTGGGCCTTGGCCAACCTTTATGAGGACC    641
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Qy    822 CGCTGCTGCGATGATGAGCCCATGATCACAAGCTCTCAGATCAACGGAGGCCCTGAGTC    881
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Qy   1122 ACCTCCAGGACAGCTTATACTGGGCTCAGAGCACCCAGTGCTCTGGGACCGGCTGGGTCA    1181
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Db   3073 ACCTCCAGGACAGCTTATACTGGGCTCAGAGCCAGCTGCTGGGACCGGCTGGGTCA   3132

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Qy   1362 ACTTCTCCACATGGAAAGCTACCACTCTGGATGGGCTCCCCAACCAGCTGACACCCTCG    1421
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Qy   1422 AGCCCCACCTGTGCCTGCTGGATGTTGGCTACCTCATCAATACCAGCTGCCTGCCCTC    1481
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Qy   1602 TCTCGCCCAGCCCGAGAGCAGCTCCAGCCTCGGGAGGTGCCACACCTTCTCCGACCCCA    1661
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Qy   1662 CCTGCCCCGGAGCCCCTGCCGGTGCTGCACTTT--------------------    1693
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Qy   1694 -----TCCTCTGGGGGTCCGGCGGACACCCGGACACCCGAGGAGTGAACCTGT    1748
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Db   3673 ACTCGGCCCCTGGGGTCCGGCGGACACCCGGACACCCGAGGAGTGAACCTGT   3732

Qy   1749 CTTCATCGGACTTCCCTACCACTACACGAAGGTGACCTACAGCGCAGGAGACGTGACA    1808
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Db   3733 CTTCATCGGACTTCCCTACCACTACACGAAGGTGACCTACAGCGCAGGAGACGTGACA   3792

Qy   1809 AGCGTGCTGCACCTGACGCTTGTCGCAACATTACAAATGCTGCAACAACCAGGAGCAGCTGCTGGAGGCTC    1868
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Qy    1869 TGCGCCAGGCAGTGCAGCGAGGCCGCGAGGCCGGCAGGCCCCACTGATGGCCCGGGGCCCCTGC 1928
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Db    3853 TGCGCCAGGCAGTGCAGCGAGGCCGCGAGGCCGGCAGGCCCCACTGATGGCCCGGGGCCCCTGC 3912

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RESULT 11
US-09-148-545-86
; Sequence 86, Application US/09148545
; Patent No. 6590075
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 70 Human Secreted Proteins
; FILE REFERENCE: PZ001P1
; CURRENT APPLICATION NUMBER: US/09/148,545
; CURRENT FILING DATE: 1998-09-04
; EARLIER APPLICATION NUMBER: PCT/US98/04482
; EARLIER FILING DATE: 1998-03-06
; EARLIER APPLICATION NUMBER: 60/040,162
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/040,333
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; EARLIER APPLICATION NUMBER: 60/043,315
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/048,974
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/056,886
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,877
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,889
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; EARLIER APPLICATION NUMBER: 60/056,888
; EARLIER FILING DATE: 1997-08-22

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; EARLIER APPLICATION NUMBER: 60/057,650
; EARLIER FILING DATE: 1997-09-05
; EARLIER APPLICATION NUMBER: 60/056,884
; EARLIER FILING DATE: 1997-08-22
; NUMBER OF SEQ ID NOS: 280
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 86
; LENGTH: 1925

Query Match          81.2%;  Score 1788.8;  DB 4;  Length 1925;
Best Local Similarity   97.9%;  Pred. No. 0;
Matches 1844;  Conservative  1;  Mismatches  4;  Indels  34;  Gaps  2;

Qy   347 AGGGAGGCTGCCGTGCGACTGGGCTTCGGCGCCCGTG-CAGAGGAGCAGGCCTTCCTGAG 405
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Qy   586 CTACATCACCGGGGCCTCGGCTCACCTGGGCCTTGGCCAACCTTTATGAGGACCCCAGA 645
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Db   606 TGAATTTGGGAGTGTGCGAGTTCTCTCCCTACGAGGTATCTGGAGCAACCTGTATGCAGC 665

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RESULT 12
US-09-148-545-21
; Sequence 21, Application US/09148545
; Patent No. 6590075

GENERAL INFORMATION:
;   APPLICANT: Rosen et al.
;   TITLE OF INVENTION: 70 Human Secreted Proteins
;   FILE REFERENCE: PZ001P1
;   CURRENT APPLICATION NUMBER: US/09/148,545
;   CURRENT FILING DATE: 1998-09-04
;   EARLIER APPLICATION NUMBER: PCT/US98/04482
;   EARLIER FILING DATE: 1998-03-06
;   EARLIER APPLICATION NUMBER: 60/040,162
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;   EARLIER APPLICATION NUMBER: 60/040,333
;   EARLIER FILING DATE: 1997-03-07
;   EARLIER APPLICATION NUMBER: 60/038,621
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; EARLIER FILING DATE: 1997-09-05
; EARLIER APPLICATION NUMBER: 60/056,884
; EARLIER FILING DATE: 1997-08-22
; NUMBER OF SEQ ID NOS: 280
; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 21
; LENGTH: 1926

Query Match   80.7%;   Score 1777.8;   DB 4;   Length 1926;
Best Local Similarity 97.9%;   Pred. No. 0;
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Qy   347 AGGGAGCTGGCCGTGCGACTGGGCTTCGGCGCCGTCGTG-CAGAGGAGCAGGCCTTCCTGAG 405
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RESULT 13

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EARLIER FILING DATE: 1997-08-22

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; EARLIER APPLICATION NUMBER: 60/056,881
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; EARLIER FILING DATE: 1997-08-22
; NUMBER OF SEQ ID NOS: 280
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 87
; LENGTH: 1818

Query Match             76.1%;  Score 1676.6;  DB 4;  Length 1818;
Best Local Similarity   97.4%;  Pred. No. 0;  Matches  7;  Indels  36;  Gaps  3;
Matches 1745;  Conservative  3;  Mismatches  3;
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(DNA sequence alignment data)

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; Patent No. 6025178
; GENERAL INFORMATION:
;   APPLICANT: Chiou, Xue-Chiou C.
;   APPLICANT: Kramer, Ruth M.
;   APPLICANT: Pickard, Richard T.
;   APPLICANT: Sharp, John D.
;   APPLICANT: Strifler, Beth A.
;   TITLE OF INVENTION: HUMAN PHOSPHOLIPASE A2 AND RELATED
;   TITLE OF INVENTION: NUCLEIC ACID COMPOUNDS
;   NUMBER OF SEQUENCES: 4
;   CORRESPONDENCE ADDRESS:
;     ADDRESSEE: Eli Lilly and Company
;     STREET: Lilly Corporate Center
;     CITY: Indianapolis
;     STATE: Indiana
;     COUNTRY: United States of America
;     ZIP: 46285
;   COMPUTER READABLE FORM:
;     MEDIUM TYPE: Floppy disk
;     COMPUTER: IBM PC compatible
;     OPERATING SYSTEM: PC-DOS/MS-DOS
;     SOFTWARE: PatentIn Release #1.0, Version #1.30
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;     APPLICATION NUMBER: US/08/827,208
;     FILING DATE: 28-MAR-1997
;     CLASSIFICATION: 435
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER: US 60/014,608
;     FILING DATE: 29-MAR-1996
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER: US 60/041,264
;     FILING DATE: 19-MAR-1997
;   ATTORNEY/AGENT INFORMATION:
;     NAME: Gaylo, Paul J.
;     REGISTRATION NUMBER: 36,808
;   REFERENCE/DOCKET NUMBER: X-10610
;   TELECOMMUNICATION INFORMATION:
;     TELEPHONE: (317) 276-0756
;     TELEFAX: (317) 276-3861
; INFORMATION FOR SEQ ID NO: 1:
;   SEQUENCE CHARACTERISTICS:
;     LENGTH: 8517 base pairs
;     TYPE: nucleic acid
;     STRANDEDNESS: single
;     TOPOLOGY: linear
;   MOLECULE TYPE: DNA (genomic)
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US-09-500-358-1

Query Match             63.9%;  Score 1408.6;  DB 3;  Length 8517;
Best Local Similarity   79.3%;  Pred. No. 0;
Matches 1957; Conservative 0; Mismatches 4; Indels 506; Gaps 4;

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Qy   1211 GTCCCCCCTTCTGAAGATAGAAGAACCACCACCGGACAGCAGCGGCAGAAATAGCTGAGTTTTC 1270
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Search completed: October 7, 2004, 18:59:56
Job time : 208.207 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: October 7, 2004, 16:44:09 ; Search time 1131.17 Seconds
(without alignments)
9877.707 Million cell updates/sec

Title: US-09-830-321A-5
Perfect score: 2204
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Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 3340653 seqs, 253478454 residues

Total number of hits satisfying chosen parameters: 6681306

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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SUMMARIES

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

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2	1806.2	82.0	4183	15	US-10-266-388-1	Sequence 1, Appli	
3	1788.8	81.2	1925	9	US-09-981-876-86	Sequence 86, Appl	
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5	1777.8	80.7	1926	10	US-09-981-876-21	Sequence 21, Appl	
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7	1676.6	76.1	1818	9	US-09-981-876-87	Sequence 87, Appl	
8	1676.6	76.1	1818	10	US-09-148-545-87	Sequence 87, Appl	
c 9	602	27.3	3197	13	US-10-332-426-14	Sequence 14, Appl	
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11	439	19.9	494	10	US-09-918-995-32564	Sequence 32564, A	
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ALIGNMENTS

RESULT 1
US-10-266-388-3
; Sequence 3, Application US/10266388
Publication No. US20030124702A1
GENERAL INFORMATION:
APPLICANT: Kriz, Ron
Song, Chuanzheng
TITLE OF INVENTION: CYTOSOLIC PHOSPHOLIPASE A2-BTA ENZYMES
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genetics Institute, Inc.
STREET: 87 CambridgePark Drive
CITY: Cambridge
STATE: MA
COUNTRY: USA
ZIP: 02140
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/266,388
FILING DATE: 07-Oct-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/895,547
FILING DATE: 29-Jun-2001
APPLICATION NUMBER: 09/460,145
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Brown, Scott A.
REGISTRATION NUMBER: 32,724
REFERENCE/DOCKET NUMBER: GI5289
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 498-8224
TELEFAX: (617) 876-5851

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; INFORMATION FOR SEQ ID NO: 3:
;   SEQUENCE CHARACTERISTICS:
;     LENGTH: 2699 base pairs
;     TYPE: nucleic acid
;     STRANDEDNESS: double
;     TOPOLOGY: linear
;   MOLECULE TYPE: cDNA
;   SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-10-266-388-3

Query Match        82.0%;   Score 1806.2;   DB 15;   Length 2699;
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Qy   1809 AGTGCTGCACCTGACACATTACAAATGCTGCAACACCAGGAGCAGCTGCTGCTGGAGGCTC 1868
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Db   2309 AGTGCTGCACCTGACACATTACAAATGCTGCAACAACCAGGAGCAGCTGCTGCTGGAGGCTC 2368

Qy   1869 TGCGGCCAGGCAGTCGAGTGCGAGCGGAGGCGGCAGCGGCAGCGGCCCCACTGATGGCCGGGGCCCCTGC 1928
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Db   2369 TGCGGCCAGGCAGTCGAGTGCGAGCGGAGGCGGCAGCGGCAGCGGCCCCACTGATGCCGGGGCCCCTGC 2428

Qy   1929 CACCCCTAACTCTCATTCATTCCCTGCTCAGGTGGGAGTTGCAGGTGGGAACTGTCATCACGC 1988
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2429 CACCCCTAACTCTCATTCATTCCCTGCTCAGGTGGGAGTTGCAGGTGGGAACTGTCATCACGC 2488

Qy   1989 AGTGCTTCAGAGCCTCGGGCTCCGGGCTCCAGGGTCCCAGGGCTCCAGGCTGGGA 2048
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Db   2489 AGTGCTTCAGAGCCTCGGGCTCCGGGCTCCAGGGTCCCAGGGCTCCAGGCTGGGA 2548

Qy   2049 GCTCCCTTGCGCTCGCAGTTGCAGTGGGTAAGGAGGCCAAGCCCATTGTGTAATC 2108
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Db   2549 GCTCCCTTGCGCTCGCAGTTGCAGTGGGTAAGGAGGCCAAGCCCATTGTGTAATC 2608

Qy   2109 ACCCAAAACCCCCGGCCCTGTGCCTGTTTCCCTTGCGCTACCTTGAGTAGTTGGAGC 2168
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Db   2609 ACCCAAAACCCCCGGCCCTGTGCCTGTTTCCCTTGCGCTACCTTGAGTAGTTGGAGC 2668

Qy   2169 ACTTGATACATCACAGACTCATCACAAA 2195
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RESULT 2
US-10-266-388-1
; Sequence 1, Application US/10266388
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; Publication No. US20030124702A1
  GENERAL INFORMATION:
    APPLICANT: Kriz, Ron
             Song, Chuanzheng
    TITLE OF INVENTION: CYTOSOLIC PHOSPHOLIPASE A2-BETA ENZYMES
    NUMBER OF SEQUENCES: 9
    CORRESPONDENCE ADDRESS:
      ADDRESSEE: Genetics Institute, Inc.
      STREET: 87 CambridgePark Drive
      CITY: Cambridge
      STATE: MA
      COUNTRY: USA
      ZIP: 02140
    COMPUTER READABLE FORM:
      MEDIUM TYPE: Floppy disk
      COMPUTER: IBM PC compatible
      OPERATING SYSTEM: PC-DOS/MS-DOS
      SOFTWARE: PatentIn Release #1.0, Version #1.30
    CURRENT APPLICATION DATA:
      APPLICATION NUMBER: US/10/266,388
      FILING DATE: 07-Oct-2002
      CLASSIFICATION: <Unknown>
    PRIOR APPLICATION DATA:
      APPLICATION NUMBER: US/09/895,547
      FILING DATE: 29-Jun-2001
      APPLICATION NUMBER: 09/460,145
      FILING DATE: <Unknown>
    ATTORNEY/AGENT INFORMATION:
      NAME: Brown, Scott A.
      REGISTRATION NUMBER: 32,724
      REFERENCE/DOCKET NUMBER: GI5289
    TELECOMMUNICATION INFORMATION:
      TELEPHONE: (617) 498-8224
      TELEFAX: (617) 876-5851
  INFORMATION FOR SEQ ID NO: 1:
    SEQUENCE CHARACTERISTICS:
      LENGTH: 4183 base pairs
      TYPE: nucleic acid
      STRANDEDNESS: double
      TOPOLOGY: linear
    MOLECULE TYPE: cDNA
    SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-10-266-388-1
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Query Match       82.0%;   Score 1806.2;   DB 15;   Length 4183;
Best Local Similarity  98.1%;   Pred. No. 0;
Matches 1851;   Conservative  0;   Mismatches  3;   Indels 33;   Gaps  1;
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Qy    342 GACTGAGGAGGAGCTGCCGTGCCGACTGGGCTTCGGCGCCTTCGGAGGAGGAGGAGGAGCCTTCC 401
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Db   2293 GACTGAGGAGGAGCTGCCGTGCCGACTGGGCTTCGGCGCCTTCGGAGGAGGAGGAGGAGGAGGAGCCTTC 2352

Qy    402 TGAGCAGGAGGAAGCAGGTGGTGCCGCGCGCCCGGAGGAGGAGGAGCCGCAGCTGCAGCTGGATGGAG 461
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2353 TGAGCAGGAGGAAGCAGGTGGTGCCGCGCGCCCGGAGGAGGAGGAGCCTGCAGCTGCAGCTGGATGGAG 2412

Qy    462 ACCTGCAGGAGGATGAGATCCCAGTGTAGTAGCTATTATGGCCACTGGTGGGGGATCCGG 521
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2413 ACCTGCAGGAGGATGAGATCCCAGTGTAGTAGCTATTATGGCCACTGGTGGGTGGGGATCCGG 2472

Qy    522 CAATGACTTCCCTGTATGGCCAGCTGGCTCGGGCTCCACCTGGGCCTTGGGCCTTGGGCCTTGGATTGCG 581
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Db   2473 CAATGACTTCCCTGTATGGCCAGCTGGCTCGGGCTCCACCTGGGCCTTGGGCCTTGGGCCTTGGATTGCG 2532

Qy    582 TCTCCTACATCACCGGGGGCTCCACCTGGGCTCCAACCTTTATGAGGACC 641
          ||||||||||||||||||||||||||||||||||||||||||||||
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Qy    642 CAGAGTGGTCTCAGAAGGACCTGCAGGGCCCACTGAGTTGCTGAAGACCCAGCTGACCA 701
          |||||||||||||||||||||||||||||||||||||||||||||||||
Db   2593 CAGAGTGGTCTCAGAAGGACCTGCAGGGCCCACTGAGTTGCTGAAGACCCAGCTGACCA 2652

Qy    702 AGAACAAGCTGGGTGTGCTGCCCCCAGCTGCAGCTGCAGGCCGGTACCGGCAGGAGAGCTGGCCG 761
          ||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2653 AGAACAAGCTGGGTGTGCTGCCCCCAGCTGCAGCTGCAGGCCGGTACCGGCAGGAGAGCTGGCCG 2712

Qy    762 AGCGGTGCCGCTTGGGCTACCCAAGCTGCTTCACCAAGCTGTGGGCCCTCATCAACGAGG 821
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Db   2713 AGCGGTGCCGCTTGGGCTACCCAAGCTGTTCACCAAGCTGTGGGCCCTCATCAACGAGG 2772

Qy    822 CGCTGCTGCATGATGAGCCCATGATCACAAGCTCTCAGATCAACAACGGGAGGCCCTGAGTC 881
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2773 CGCTGCTGCATGATGAGCCCATGATCACAAGCTCTCAGATCAACAACGGGAGGCCCTGAGTC 2832

Qy    882 ATGGCCAGAACCCTGCCCATCTACTGTGCCCTCAACACCAAAGGGCAGAGCTGACCA 941
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Db   2833 ATGGCCAGAACCCTGCCCATCTACTGTGCCCTCAACACCAAAGGGCAGAGCCTGACCA 2892

Qy    942 CTTTTGAATTGGGAGTGGTGGCGAGTTCTCCCTAGGAGGTCGGCTTCCCCAAGTACG 1001
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Db   2893 CTTTTGAATTGGGAGTGGTGCCGAGTTCTCCCTAGGAGGTCGGCTTCCCCAAGTACG 2952

Qy   1002 GGGCCTTCATCCCCTGAGCTCTTTGGCTCCGAGTTCTTTATGGGGCAGCTGATGAAGA 1061
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Db   2953 GGGCCTTCATCCCCTGAGCTCTTTGGCTCCGAGTTCTTTATGGGGCAGCTGATGAAGA 3012

Qy   1062 GGCTTCCTGAGTCCGCATCTGCTTCTTAGAAGTATCTGGAGCAACCTGTATGCAGCCA 1121
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Db   3013 GGCTTCCTGAGTCCGCATCTGCTTCTTAGAAGTATCTGGAGCAACCTGTATGCAGCCA 3072

Qy   1122 ACCTTCCAGACAGCTTATACTGGGCTTCGGACTTCTCGGACCGCGTGGGTCA 1181
          ||||||||||||||||||||||||||||||||||||||||||||||||
Db   3073 ACCTTCCAGACAGCTTATACTGGGCTTCGGACTTCTCGGACCGCGTGGGTCA 3132

Qy   1182 GGAACCAGGCCAACCTGGACAAGGAGCAGGTCCCCCTTCGAAGATAGAAGAACCACCCT 1241
          |||||||||||||||||||||||||||||||||||||||||||||||||
Db   3133 GGAACCAGGCCAACCTGGACAAGGAGCAGGTCCCCCTTCGAAGATAGAAGAACCACCCT 3192

Qy   1242 CAACAGCCGGCAGAATAGCTGAGTTTTTCACCGATCTTCTGACGTGGCGTCCACTGGCCC 1301
          |||||||||||||||||||||||||||||||||||||||||||||||||
Db   3193 CAACAGCCGGCAGAATAGCTGAGTTTTTCACCGATCTTCTGACGTGGCGTCCACTGGCCC 3252

Qy   1302 AGCCCACACATAATTTCCTGCGTGGCCTCCATTTCCACAAAGACTACTTTCAGCATCCTC 1361
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Db   3253 AGCCCACACATAATTTCCTGCGTGGCCTCCATTTCCACAAAGACTACTTTCAGCATCCTC 3312

Qy   1362 ACTTCTCCACATGGAAAGCTACCACCTCTGATGGGCTCCCAACCAGCTGACACCCTCGG 1421
          |||||||||||||||||||||||||||||||||||||||||||||||||
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Qy   1422 AGCCCCACCTGTGCCTGTGCCTGCTACCTCATCAATCAATACCAGCTGCCCCTCC 1481
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Db   3373 AGCCCCACCTGTGCCTGTGCCTGCTACCTCATCAATCAATACCAGCTGCCCCTCC 3432

Qy   1482 TGCAGCCACTCGGGACGTGACCTGTCCATCCCGTTCCCAGGAGACGGGGATCCGG 1541
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Db   3433 TGCAGCCACTCGGGACGTGACCTGTCCATCCTGTTCCCAGGAGACGGGGATCCGG 3492

Qy   1542 TCCAGCAGTTGCAGCTCCTGGGCGCCGTTCCGCCAGGAGGGGATCCGG 1601
          |||||||||||||||||||||||||||||||||||||||
Db   3493 TCCAGCAGTTGCAGCTCCTGGGCGCCGTTCCGCCAGGAGGGGGATCCGG 3552

Qy   1602 TCTCGCCCAGCCCGAAGACAGCTCCGGGAGTGCCACACCTTCTCCGACCCCCA 1661
          |||||||||||||||||||||||||||||||||||||||||||||||||
Db   3553 TCTCGCCCAGCCCGAAGACAGCTCCGGGAGTGCCACACCTTCTCCGACCCCCA 3612

Qy   1662 CCTGCCCCGGAGCCCCGCGTGCACTTT------------ 1693
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Db   3613 CCTGCCCCGGAGCCCCGCGTGCACTTTCCTCCTGGTCAGCGACTCCTTCCGGGAGT 3672

Qy   1694 -----TCCTCTGGGGTCCGCGGGTCCGGCGACACCCGAGGAGGCGGCAGCTGGGAGACCTGT 1748
               ||||||||||||||||||||||||||||||||||||||||||
Db   3673 ACCTCGGCCCCCTGGGGTCCGCGGGTCCGGCGACACCCGAGGAGGCGGCAGCTGGGAACCTGT 3732

Qy   1749 CTTCATCGGACTCTCCCTACCACTACACGAAGTGACCTACGCCAGGAGGACGTGGACA 1808
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Db   3733 CTTCATCGGACTCTCCCTACCACTACACGAAGGTGACCTACAGCCAGGAGGACGTGGACA 3792
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Qy   1809 AGTCGTGCTGCACCTGACACATTACAATGTCTGCAACAACCAGGACGCAGCTGCTGGAGGCTC 1868
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3793 AGTCGTGCTGCACCTGACACATTACAATGTCTGCAACAACCAGGAGCAGCTGCTGGAGGCTC 3852

Qy   1869 TGCGCCAGGCAGTGCAGCGGAGGCGGCAGCGCCCCACTGATGGCCGGGGCCCCTGC 1928
               ||||| |||||||||||||||||||||||||||||||||||||||||||||||||
Db   3853 TGCGCCAGGCAGTGCAGCGCGGAGGCGGCAGCGCCCCACTGATGGCCGGGGCCCCTGC 3912

Qy   1929 CACCCCTAACTCTCATTCATTCCCTGGCTGCGTGAGTTGCAGGTGGGAACTGTCATCACGC 1988
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3913 CACCCCTAACTCTCATTCATTCCCTGGCTGCGTGAGTTGCAGGTGGGAACTGTCATCACGC 3972

Qy   1989 AGTGCTTCAGAGCCTTCGGGCTCAGGTGGCACTGTCCCAGGGGTCCAGGCTGGGA 2048
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Qy   2049 GCTCCCTTGCGCCTCAGCAGTTTGCAGTGGGGTAAGGAGGCCAAGCCCATTTGTGTAATC 2108
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Qy   2109 ACCAAAAACCCCCCGGCCTGTGCCCTTCCCTTCGCTCACTTGAGTAGTTGGAGC 2168
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Db   4093 ACCAAAAACCCCCCGGCCTGTGCCCTGTTTTCCCTTCGCTCACCTTGAGTAGTTGGAGC 4152

Qy   2169 ACTTGATACATCACAGACTCATACAAA 2195
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Db   4153 ACTTGATACATCACAGACTCATACAAA 4179
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RESULT 3
US-09-981-876-86
; Sequence 86, Application US/09981876
; Patent No. US2002016469A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 70 Human Secreted Proteins
; FILE REFERENCE: PZ001P1
; CURRENT APPLICATION NUMBER: US/09/981,876
; CURRENT FILING DATE: 2001-10-19
; PRIOR APPLICATION NUMBER: 09/148,545
; PRIOR FILING DATE: 1998-09-04
; PRIOR APPLICATION NUMBER: 60/040,162
; PRIOR FILING DATE: 1997-03-07
; PRIOR APPLICATION NUMBER: 60/040,333
; PRIOR FILING DATE: 1997-03-07
; PRIOR APPLICATION NUMBER: 60/038,621
; PRIOR FILING DATE: 1997-03-07
; PRIOR APPLICATION NUMBER: 60/040,161
; PRIOR FILING DATE: 1997-03-07
; PRIOR APPLICATION NUMBER: 60/040,626
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; PRIOR APPLICATION NUMBER: 60/040,163
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; PRIOR FILING DATE: 1997-05-23
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; PRIOR FILING DATE: 1997-05-23
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; PRIOR APPLICATION NUMBER: 60/043,580
; PRIOR FILING DATE: 1997-04-11
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; PRIOR APPLICATION NUMBER: 60/043,314
; PRIOR FILING DATE: 1997-04-11
; PRIOR APPLICATION NUMBER: 60/043,569
; PRIOR FILING DATE: 1997-04-11
; PRIOR APPLICATION NUMBER: 60/043,311
; PRIOR FILING DATE: 1997-04-11
; PRIOR APPLICATION NUMBER: 60/043,671
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; PRIOR FILING DATE: 1997-04-11
; PRIOR APPLICATION NUMBER: 60/043,315
; PRIOR FILING DATE: 1997-04-11
; PRIOR APPLICATION NUMBER: 60/048,974
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/056,886
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 60/056,877
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 60/056,889
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 60/056,893
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 60/056,630
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 60/056,878
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 60/056,662
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 60/056,872
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 60/056,882
; PRIOR FILING DATE: 1997-08-22

PRIOR FILING DATE: 1997-08-22
PRIOR APPLICATION NUMBER: 60/056,887
PRIOR FILING DATE: 1997-08-22
PRIOR APPLICATION NUMBER: 60/056,908
PRIOR FILING DATE: 1997-08-22
PRIOR APPLICATION NUMBER: 60/048,964
PRIOR FILING DATE: 1997-06-06
PRIOR APPLICATION NUMBER: 60/057,650
PRIOR FILING DATE: 1997-09-05
PRIOR APPLICATION NUMBER: 60/056,884
PRIOR FILING DATE: 1997-08-22
NUMBER OF SEQ ID NOS: 280
SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 86
LENGTH: 1925

Query Match   81.2%; Score 1788.8; DB 9; Length 1925;
Best Local Similarity   97.9%; Pred. No. 0;
Matches 1844; Conservative   1; Mismatches   1; Indels   34; Gaps   2;

Qy   347 AGGGAGCTGCCCGTTGCGACTGGGCTTCGGCCCCTGTG-CAGAGGAGCAGGCCTTCCTGAG 405
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Db   6 AGGGAGCTGCCCGTTGCGACTGGGCTTCGGCGCCCCTGTGCCAGAGGAGCAGGCCTTCCTGAG 65

Qy   406 CAGGAGGAAGCAGTGGTGGTGCCGCGGCCTTGAGGCAGGCCCTGCAGCTGGATGGAGACCT 465
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Db   66 CAGGAGGAAGCAGTGGTGGTGCCGCGGCCTTGAGGCAGGCCCTGCAGCTGGATGGAGACCT 125

Qy   466 GCAGGAGGATGAGATCCCAGTGGTAGCTATTATTGGCGGTGGTGTGGGATCCGGGCAAT 525
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Db   126 GCAGGAGGATGAGATCCCAGTGGTAGCTATTATTGGCGGTGGTGTGGGATCCGGGCAAT 185

Qy   526 GACTTCCCTGTATGGGCAGCTGGCTGGCCTGAAGGAGCTGGGCCTCTTGGATTGCGTCTC 585
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||:||||
Db   186 GACTTCCCTGTATGGGCAGCTGGCTGGCCTGAAGGAGCTGGGCCTCTTGGATTGCKTCTC 245

Qy   586 CTACATCACCGGGGCCTTCGGGCTCCACCTGGGCTCCACCTTTATGAGACCCAGA 645
          |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   246 CTACATCACCGGGGCCTTCGGGCTCCACCTGGGCTCCACCTTTATAAGGACCCAGA 305

Qy   646 GTGGTCTCAGAGGACCTGGCAGGGGCCCACCAGTGGCTGGAGACCAGTGACCAAGAA 705
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   306 GTGGTCTCAGAGGACCTGGCAGGGGCCCACCAGTGGCTGGAGACCAGTGACCAAGAA 365

Qy   706 CAAGCTGGGTGTGCTGGCGCCCCAGCCAGCTGCAGCGGTACCGCAGGAGCTGCCGCAGCG 765
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Db   366 CAAGCTGGGTGTGCTGGCGCCCCAGCCAGCTGCAGCGGTACCGCAGGAGCTGCCGCAGCG 425

Qy   766 TGCCCGCTTGGGCTACCCAAGCTGCTTCACCAACCTGTGGGCCCTCATCAACGAGGGGCT 825
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Db   426 TGCCCGCTTGGGCTACCCAAGCTGCTTCACCAACCTGTGGGCCCTCATCAACGAGGGGCT 485

Qy   826 GCTGCATGATGAGCCCATGATCACAAGCTCTCAGATCAACACCAAAGGCAGAGCCTGAGTCATGG 885
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Db   486 GCTGCATGATGAGCCCATGATCACAAGCTCTCAGATCAACACCAAAGGCAGAGCCCTGAGTCATGG 545

Qy   886 CCAGAACCCCTGCCCATCACTACTGTCCCTCAACACCAAAGGCAGAGCCTGACCACTTT 945
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   546 CCAGAACCCCTGCCCATCACTACTGTCCCTCAACACCAAAGGCAGAGCCTGACCACTTT 605

Qy   946 TGAATTTGGGGAGTCGTGCGAGTTCTTCGGCTCCGAGTTCTTTATGGGCAGCTGATGAAGAGGCT 1005
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Db   606 TGAATTTGGGGAGTCGTGCGAGTTCTTCGGCTCCGAGTTCTTTATGGGCAGCTGATGAAGAGGC 665

Qy   1006 CTTCATCCCCTCGATGCTCTTTGGCTCCGAGTTCTTTATGGGCAACCTGTATGCAGCCAACCT 1065
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Db   666 CTTCATCCCCTCGATGCTCTTTGGCTCCGAGTTCTTTATGGGCAGCTGATGAAGAGGCT 725

Qy   1066 TCCTGAGTCCCGCATCTGCTTCTTAGAAGGTATCTGGAGCAACCTGTATGCAGCCAACCT 1125
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Db   726 TCCTGAGTCCCGCATCTGCTTCTTAGAAGGTATCTGGAGCAACCTGTATGCAGCCAACCT 785

Qy   1126 CCAGGACAGCTTATACTGGGCCTCAGAGCCCAGCCAGTTCTTCGGGACCGGTCAGGAA 1185
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||

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Fri Oct 8 10:22:37 2004

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Db   786 CCAGGACAGCTTATACTGGGCTCAGAGCCCAGCCAGTTCTGGGACCGCTGGGTCAGGAA 845

Qy  1186 CCAGGCCAACCTGACAAGGAGCAGTGCCCCTTCTGAAGATAGAAGAACCACCCTCAAC 1245
         ||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   846 CCAGGCCAACCTGACAAGGAGCAGTGCCCCTTCTGAAGATAGAAGAACCACCCTCAAC 905

Qy  1246 AGCCGGCAGAATAGCTGAGTTTTCACCGATCTTCTGACGTGGCGTCCACTGGCCCAGGC 1305
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Qy  1306 CACACATAATTTCCTGCGTGGCCTCCATTTCCACAAAGACTACTTTCAGCATCCTCACTT 1365
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; SOFTWARE: PatentIn Ver. 2.0
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; SEQ ID NO 86
; LENGTH: 1925

Query Match   81.2%;   Score 1788.8;   DB 10;   Length 1925;
Best Local Similarity   97.9%;   Pred. No. 0;
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; Patent No. US2002016465A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 70 Human Secreted Proteins
; FILE REFERENCE: P2001P1
; CURRENT APPLICATION NUMBER: US/09/981,876
; CURRENT FILING DATE: 2001-10-19
; PRIOR APPLICATION NUMBER: 09/148,545
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;    PRIOR APPLICATION NUMBER: 60/057,650
;    PRIOR FILING DATE: 1997-09-05
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;    PRIOR FILING DATE: 1997-08-22
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;    SOFTWARE: PatentIn Ver. 2.0
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; SEQ ID NO 21
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Query Match         80.7%;   Score 1777.8;   DB 9;   Length 1926;
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Matches 1844;   Conservative    1;   Mismatches    1;   Indels   35;   Gaps    3;

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Qy   1006 CTTCATCCCCTGAGCTCTTGGCTCGGAGTTCTTTAGGGGC 1065
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Qy   1066 TCCTGAGTCCGGCATCTGGTTCTTAGAAGGTATCTGAGAA 1125
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Qy   1933 CCTAACTCTCATTCATTCCTGCGTCTGGTTGCAGTTGCAG 1992
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RESULT 6
US-09-148-545-21
; Sequence 21, Application US/0914854S
; Publication No. US20030027132A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 70 Human Secreted Proteins
; FILE REFERENCE: PZ001P1
; CURRENT APPLICATION NUMBER: US/09/148,545
; CURRENT FILING DATE: 1998-09-04
; EARLIER APPLICATION NUMBER: PCT/US98/04482
; EARLIER FILING DATE: 1998-03-06
; EARLIER APPLICATION NUMBER: 60/040,162
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/040,333
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Qy  406 CAGGAGGAAGCAGGTGGTGCCGCGGCCCTTGAGGCAGGCCCTGCAGCTGGATGGAGACCT 465
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Db  126 GCAGGAGGATGAGATCCCAGTGGTAGCTAGTTATATGGCCACTGGTGGTGGGATCCGGGGCAAT 185

Qy  526 GACTTCCCTGTATGGGCCAGCTGGCTGGCCTGAAGGAGCTGGGCCTCTTGGATTGCGTCTC 585
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Db  186 GACTTCCCTGTATGGGCCAGCTGGCTGGCCTGAAGGAGCTGGGCCTCTTGGATTGCKTCTC 245

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Qy   1753  ATCGGACTCTCCTACCACTACACGAGAGGTGACCTACAGCCAGGAGACGTGACAAGCT 1812
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Db   1446  ATCGGACTCTCCTACCACTACACGAGAGGTGACCTACAGCCAGGAGACGTGACAAGCT 1505

Qy   1813  GCTGCACCTGACACATTACAATGTCTGCAACAACCAGGAGCAGCTGCTGGAGGCTCTGCG 1872
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Db   1506  GCTGCACCTGACACATTACAATGTCTGCAACAACCAGGAGCAGCTGCTGGAGGCTCTGCG 1565

Qy   1873  CCAGGCAGTGCAGCGGAGGCGGCAGCGCGCAGCCCCACTGATGGCCGGGGCCCCTGCCACC 1932
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Db   1566  CCAGGCAGTGCAGCGGAGGCGGCAGCGCGCAGCCCCACTGATGGCCGGGGCCCCTGCCACC 1625

Qy   1933  CCTAACTTCTCATTCATTCCCTGGCTGCTGAGTTGCAGGTGGGAACTGTCATCACGCAGTG 1992
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Db   1626  CCTAACTCTCATTCATTCCCTGGCTGCTGAGTTGCAGGTGGGAACTGTCATCACGCAGTG 1685

Qy   1993  CTT-CAGAGCCTCGGGCTCAGGTGGCACTGTCCCAGGGTCAGGCTGAGGGCTGGGAGCT 2051
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Db   1686  CTTNCAGAGCCTCGGGCTCAGGTGGCACTGTCCCAGGGTCAGGCTGAGGGCTGGGAGCT 1745

Qy   2052  CCCTTGCGCCTCAGCAGTTTGCAGTGGGGTAAGGAGGCCAAGCCCATTTGTGTAATCACC 2111
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Qy   2112  CAAAACCCCCGGCCTGGCCTGTGCCTGTGCCTGTTTCCCTTCTGCGCCTACCTTGGAGCACT 2171
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Qy   2172  TGATACATCACAGACTCATACAAA 2195
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Db   1866  TGATCATCACAGACTCATACAAA 1889
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RESULT 7
US-09-981-876-87/c
; Sequence 87, Application US/09981876
; Patent No. US2002016469A1
; GENERAL INFORMATION:
;   APPLICANT: Rosen et al.
;   TITLE OF INVENTION: 70 Human Secreted Proteins
;   FILE REFERENCE: PZ001P1
;   CURRENT APPLICATION NUMBER: US/09/981,876
;   CURRENT FILING DATE: 2001-10-19
;   PRIOR APPLICATION NUMBER: 09/148,545
;   PRIOR FILING DATE: 1998-09-04

;   PRIOR APPLICATION NUMBER: 60/040,162
;   PRIOR FILING DATE: 1997-03-07
;   PRIOR APPLICATION NUMBER: 60/040,333
;   PRIOR FILING DATE: 1997-03-07
;   PRIOR APPLICATION NUMBER: 60/038,621
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;   PRIOR APPLICATION NUMBER: 60/043,674

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;   PRIOR FILING DATE: 1997-08-22
;   NUMBER OF SEQ ID NOS.: 280
;   SOFTWARE: PatentIn Ver. 2.0
;   SEQ ID NO 87
;   LENGTH: 1818

Query Match             76.1%;  Score 1676.6;  DB 9;  Length 1818;
Best Local Similarity   97.4%;  Pred. No. 0;
Matches 1745;   Conservative    3;  Mismatches    3;  Indels   36;  Gaps  3;

Qy    450 AGCTGGATGGAGACCTGCAGGAGGATGAGATCCCAGTGTAGCTATTATGGCCACTGGTG 509
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Qy    510 GTGGGATCCGGCAATGACTTCCCTGTATGGGCAGCTGGCCTGAA--GGAGCTGGG 567
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Qy    628 CCTTTATGAGAGACCAGAGTCGTCTCAGAAGGACACCTGGCAGGGCCCACTGAGTTGCTGAA 687
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Qy    688 GACCCAGGTGACCAAGAACAAGCTGGGTGCGTGCTGGGTCGCAGCCAGCTGGGTACCG 747
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Qy    748 GCAGGAGCTGGCCCGAGCGTGCCCGCCTTGGGTCACCCAAGCTGCTTCACCAACCTGTCGGGC 807
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Db   1518 GCAGGAGCTGGCCCGAGCGTGCCCGCCTTGGGCTACCCAAGCTGCTTCACCAACCTGTGGGGC 1459
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;   PRIOR APPLICATION NUMBER: 60/056,845
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;   PRIOR APPLICATION NUMBER: 60/057,761
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;   PRIOR APPLICATION NUMBER: 60/047,599
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;   PRIOR APPLICATION NUMBER: 60/047,588
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;   PRIOR APPLICATION NUMBER: 60/047,585
;   PRIOR FILING DATE: 1997-05-23
;   PRIOR APPLICATION NUMBER: 60/047,586
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;   PRIOR APPLICATION NUMBER: 60/047,590
;   PRIOR FILING DATE: 1997-05-23
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Qy  1915 GCCGGGGCCCCTGCCACCCTAACTCTCATTCATTCCTCGGCTGCTGAGTTGCAGGTGGG   1974
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Db   318 GCCGGGGCCCCTGCCACCCTAACTCTCATTCATTCCTCGGCTGCTGAGTTGCAGGTGGG    259

Qy  1975 AACTGTCATCACGCAGTGCTT-CAGAGCCTCGGGCTCAGGTGGCACTGTCCCAGGGTCCA  2033
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Db   258 AACTGTCATCACGCAGTGCTTNCAGAGCCTCGGGCTCAGGTGGCACTGTCCCAGGGTCCA   199

Qy  2034 GGCTGAGGGCTGGGAGCTCCCTTGCGCCTCAGCAGTTGCGAGTGGGTAAGGAGGCCAAG   2093
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Qy  2094 CCCATTTGTGTAATCACCCAAAACCCCCGGCCTGTGCCTGTTTCCCTTCTGCGCTACC    2153
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Db   138 CCCATTTGTGTAATCACCCAAAACCCCCGGCCTGTGCCTGTTTCCCTTCTGCGCTACC     79

Qy  2154 TTGAGTAGTTGGAGCACTTGATACATCACAGACTCATACAAAAAAAAAAA            2204
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Db    78 TTGAGTAGTTGGAGCACTTGATACATYACAGACTCATAMAAAAAAAAAAA             28
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RESULT 8
US-09-148-545-87/c
; Sequence 87, Application US/09148545
; Publication No. US2003027132A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 70 Human Secreted Proteins
; FILE REFERENCE: PZ001P1
; CURRENT APPLICATION NUMBER: US/09/148,545
; CURRENT FILING DATE: 1998-09-04
; EARLIER APPLICATION NUMBER: PCT/US98/04482
; EARLIER FILING DATE: 1998-03-06
; EARLIER APPLICATION NUMBER: 60/040,162
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/040,333
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; EARLIER APPLICATION NUMBER: 60/038,621
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; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,597
; EARLIER FILING DATE: 1997-05-23
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Qy  1228 AGAAGAACCACCCTCAACAGCCCGCAGAATAGCTGAGTTTTTCACCGATCTTCTGACGTG 1287
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Qy  1288 GCGTCCACTGGCCCAGGCCACACATAATTTCCTGCGTGCCTCCATTTCCACAAAGACTA  1347
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Qy  1348 CTTTCAGCATCCTCACTTCTCCACATGGAAAGTACCACTCTGGATGGGCTCCCCAACCA  1407
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Qy  1408 GCTGACACCCTCGGAGCCCCACCTGTCCTGCTGGATGTTGGCTACCTCATCAATACCAG  1467
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; EARLIER FILING DATE: 1997-09-05
; EARLIER APPLICATION NUMBER: 60/056,884
; EARLIER FILING DATE: 1997-08-22
; NUMBER OF SEQ ID NOS: 280
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Query Match   76.1%; Score 1676.6; DB 10; Length 1818;
Best Local Similarity 97.4%; Pred. No. 0;
Matches 1745; Conservative 3; Mismatches 7; Indels 36; Gaps 3;

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; Sequence 14, Application US/10332426
; Publication No. US2004029136A1
; GENERAL INFORMATION:

; APPLICANT: INCYTE GENOMICS, INC.; TANG, Y. Tom;
; APPLICANT: AZIMZAI, Yalda; DAS, Debopriya;
; APPLICANT: THORNTON, Michael; LU, Dyung Aina M.;
; APPLICANT: TRIBOULEY, Catherine M.; YUE, Henry;
; APPLICANT: GANDHI, Ameena R.; CHAWLA, Narinder K.;
; APPLICANT: KHAN, Farrah A.; LU, Yan;
; APPLICANT: YAO, Monique G.; HAFALIA, April J. A.;
; APPLICANT: ELLIOTT, Vicki S.; ARVIZU, Chandra S.;

APPLICANT: LAL, Preeti; RAMKUMAR, Jayalaxmi;
APPLICANT: NGUYEN, Danniel B.; BAUGHN, Mariah R.
TITLE OF INVENTION: LIPID METABOLISM MOLECULES
FILE REFERENCE: PI-0152 USN
CURRENT APPLICATION NUMBER: US/10/332,426
CURRENT FILING DATE: 2003-01-06
PRIOR APPLICATION NUMBER: US 60/216,803
PRIOR FILING DATE: 2000-07-07
PRIOR APPLICATION NUMBER: US 60/216,801
PRIOR FILING DATE: 2000-07-07
PRIOR APPLICATION NUMBER: US 60/218,233
PRIOR FILING DATE: 2000-07-14
PRIOR APPLICATION NUMBER: US 60/220,046
PRIOR FILING DATE: 2000-07-21
PRIOR APPLICATION NUMBER: US 60/220,739
PRIOR FILING DATE: 2000-07-26
PRIOR APPLICATION NUMBER: US 60/222,824
PRIOR FILING DATE: 2000-08-04
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SOFTWARE: PERL Program
SEQ ID NO 14
LENGTH: 3197
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NAME/KEY: misc_feature
OTHER INFORMATION: Incyte ID No. US20040029136A1 7477093CB1
US-10-332-426-14

Query Match 27.3%;   Score 602; DB 13; Length 3197;
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Db 2918 CCTACACCCGTGCCAACATGACCTACCACACGAAGAGCCTACCACGACCTTTG 2977

Qy 1824 CACATTACAATGTCTGCAACAACCAGCCCCATGAGCCCATGATCACAAAGC 1883
           |||||||| ||||||||||||||||||||| ||| ||| ||||||||||
Db 2978 GTGACTACAACGTGCGACCACCAGCCAGCTGCCATCCTGCAGGGTGATGATCAGAAGC 3037

Qy 1884 AGCGGGAGG 1891
           || |||||
Db 3038 AGCACCGG 3045

RESULT 10
US-10-103-313-127
; Sequence 127, Application US/10103313
; Publication No. US20030082758A1
; GENERAL INFORMATION:
;   APPLICANT: Rosen et al.
;   TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
;   FILE REFERENCE: PJ207C1
;   CURRENT APPLICATION NUMBER: US/10/103,313
;   CURRENT FILING DATE: 2002-03-12
;   NUMBER OF SEQ ID NOS: 653
;   Prior Application removed - See File Wrapper or Palm
;   SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 127
;   LENGTH: 1915
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-103-313-127

Query Match   22.0%;   Score 483.8; DB 15; Length 1915;
Best Local Similarity   98.4%;   Pred. No. 3.8e-120;
Matches 499;   Conservative   0; Mismatches   7; Indels   1; Gaps   1;

Qy   1698 CTGGGGTCCGGCGGACACCCGAGGAGGCGGCAGCTGGGGAGGTGAACCTGTCTTCATCGG 1757
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1396 CAGGGGTTCCGGCGGACACCCGAGGAGGCGGCAGCTGGGGAGGTGAACCTGTCTTCATCGG 1455

Qy   1758 ACTCTCCCTACCACTACACGAGAAGGTGACCTACAGCCAGGAGGACGTGGACAAGCTGCTGC 1817
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1456 ACTCTCCCTACCACTACACGAGAAGGTGACCTACAGCCAGGAGGACGTGGACAAGCTGCTGC 1515

Qy   1818 ACCTGACACATTACAATGTCTGCAACAACCAGGAGCAGCTGCTGCTGCGCCAGG 1877
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1516 ACCTGACACATTACAATGTCTGCAACAACCAGGAGCAGCTGCTGCTGCGCCAGG 1575

Qy   1878 CAGTGCAGCGGAGCGGCAGCCGAGGCCCACTGATGCGCGGGCCCCTGCCACCCCTAA 1937
          ||||||||||||||||||||||||||||| |||||||||||||||||||||||||||
Db   1576 CAGGGCAGCGGAGCGGCGAAGCCCAGGGCCCACTGATGCGCGGGCCCCTGCCACCCCTAA 1635

Qy   1938 CTCTCATTCATTCCCTGGCTGCGAGTTGCAGTTGGGAACTGTCATCACGCAGTGCTTCA 1997
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1636 CTCTCATTCATTCCCTGGCTGTGTGAGTTGCAGTTGGGAACTGTCATCACGCAGTGCTTCA 1695

Qy   1998 GAGCCTCGGGCTCAGGTGGCACTGTCCCAGGGTCGAGGGCTGGAGCTCCCTTG 2057
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1696 GAGCCTCGGGCTCAGGTGGCACTGTCCCAGGGTCGAGGGCTGGAGCTCCCTTG 1755

Qy   2058 CGCCTCAGCAGTTGCAGTGGGTAAGGAGGCCAAGCCCATTTGTAATCACCCAAAAC 2117
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1756 CGCCTCAGCAGTTGCAGTGGGTAAGGAGGCCAAGCCCATTTGTAATCACCCAAAAC 1815

Qy   2118 CCCCCGGCCCTGTGCCCTGTTTTCCCTTCTGCGCTACCTTGAGTAGTTGGAGCACTTGATAC 2177
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1816 CCCCCGGCCCTGTGCCCTGTTTTCCCTTCTGCGCTACCTTGAGTAGTTGGAGCACTTGATAC 1875

Qy   2178 ATCACAGACTCATACAAAAAAAAAAAA 2204
          || ||||||||||||| |||||||||
Db   1876 AT-ACAGACTCATACAACAAAAAAAAAAA 1901

RESULT 11
US-09-918-995-32564
; Sequence 32564, Application US/09918995
; Publication No. US20030073623A1
; GENERAL INFORMATION:
;   APPLICANT: HyseqC, Inc.
;   TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
;   TITLE OF INVENTION: FROM VARIOUS cDNA LIBRARIES
;   FILE REFERENCE: 20411-756
;   CURRENT APPLICATION NUMBER: US/09/918,995
;   CURRENT FILING DATE: 2001-07-30
;   PRIOR APPLICATION NUMBER: US/09/235,076
;   PRIOR FILING DATE: 1999-01-20

; NUMBER OF SEQ ID NOS: 38054
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 32564
;   LENGTH: 494
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)...(494)
;   OTHER INFORMATION: n = A,T,C or G
US-09-918-995-32564

Query Match   19.9%;   Score 439; DB 10; Length 494;
Best Local Similarity   98.4%;   Pred. No. 3.4e-108;
Matches 442;   Conservative   0; Mismatches   7; Indels   0; Gaps   0;

Qy   817 CGAGGCGCGTCGCTGCATGATGAGCCCATGATGACAGCTCTCAGATCAACGGGAGGCCCT 876
          ||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   46 CGNGAANTCCTGCGTGATGATGAGCCCATGATGATCAGATCTCAGATCAACGGGAGGCCCT 105

Qy   877 GAGTCATGGCCAGAACCCTCGCCCATCTACTGTGCCCTCAACACCACCAAAGGCAGAGCTT 936
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   106 GAGTCATGGCCAGAACCCTCGCCCATCTACTGTGCCCTCAACACCACCAAAGGCAGAGCTT 165

Qy   937 GACCACTTTGAATTGGGAGTGGTGTGCGAGTTCTTCTCCTACGAGTCGGCTTCCCAA 996
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   166 GACCACTTTGAATTGGGAGTGGTGTGCGAGTTCTTCTCCTACGAGTCGGCTTCCCAA 225

Qy   997 GTACGGGGGCCTTCATCCCCTCGAGCTCTTTGGCTCCGAGTTCTTTATGGGGCAGCTGAT 1056
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   226 GTACGGGGGCCTTCATCCCCTCGAGCTCTTTGGCTCCGAGTTCTTTATGGGGCAGCTGAT 285

Qy   1057 GAAGAGGCTTCCTGAGTCCCGCATCTGCTTCTTAGAAGGTATCTGGAGCAACCTGTATGC 1116
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   286 GAAGAGGCTTCCTGAGTCCCGCATCTGCTTCTTAGAAGGTATCTGGAGCAACCTGTGTGC 345

Qy   1117 AGCCAACCTCCAGACAGCTTATACTGGGCCTCCAGAGCCCAGAGCCCAGTTCTGGGACCGCTG 1176
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   346 AGCCAACCTCCAGACAGCTTATACTGGGCCTCCAGAGCCCAGAGCCCAGTTCTGGGACCGCTG 405

Qy   1177 GGTCAGGAACCAGGCCAACCTGGACAAGGAGCAGTCCCCTTCTGAAGATAGAAGAACC 1236
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   406 GGTCAGGAACCAGGCCAACCTGGACAAGGAGCAGTCCCCTTCTGAAGATAGAAGAACC 465

Qy   1237 ACCCTCAACAGCCGGCAGAATAGCTGAGT 1265
          |||||||||||||||||||||||||||||
Db   466 ACCCTCAACAGCCGGCAGAGATAGCTGAGT 494

RESULT 12
US-10-467-248-10
; Sequence 10, Application US/10467248
; Publication No. US2004008690SA1
; GENERAL INFORMATION:
;   APPLICANT: DAS, Debopriya; YAO, Monique G.;
;   APPLICANT: ARVIZU, Chandra S.; BAUGHN, Mariah R.;
;   APPLICANT: LU, Yan; HAFALIA, April J.A.;
;   APPLICANT: CHAWLA, Narinder K.; GRIFFIN, Jennifer A.;
;   APPLICANT: LU, Dyung Aina M.; YUE, Henry;
;   APPLICANT: DING, Li; ELLIOTT, Vicki S.;
;   APPLICANT: FORSYTHE, Ian J.; RAMKUMAR, Jayalaxmi;
;   APPLICANT: GANDHI, Ameena R.; ISON, Craig H.;
;   APPLICANT: WARREN, Bridget A.; TANG, Y. Tom;
;   APPLICANT: EMERLING, Brooke M.; HONCHELL, Cynthia D.;
;   APPLICANT: LYNE, Michael; BARROSO, Ines
;   TITLE OF INVENTION: LIPID-ASSOCIATED MOLECULES
;   FILE REFERENCE: PI-0358 USN
;   CURRENT APPLICATION NUMBER: US/10/467,248
;   CURRENT FILING DATE: 2003-08-06
;   PRIOR APPLICATION NUMBER: PCT/US02/03813
;   PRIOR FILING DATE: 2002-02-06
;   PRIOR APPLICATION NUMBER: US 60/266,910
;   PRIOR FILING DATE: 2001-02-06

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; PRIOR APPLICATION NUMBER: US 60/276,891
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: US 60/276,855
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: US 60/279,760
; PRIOR FILING DATE: 2001-03-28
; PRIOR APPLICATION NUMBER: US 60/283,818
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: US 60/285,405
; PRIOR FILING DATE: 2001-04-20
; NUMBER OF SEQ ID NOS: 18
; SEQ ID NO 10
; LENGTH: 3879
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No: 7472774CB1
US-10-467-248-10
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Query Match         19.5%;    Score 429.6;  DB 17;  Length 3879;
Best Local Similarity 56.2%;  Pred. No. 1.9e-105;
Matches    909;    Conservative    0;    Mismatches    644;    Indels   63;    Gaps   3;
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Qy    353  CTGGCCGTGCGACTGGGCTTCGGGCCCTGTCGCAGAGGAGCAGGCCTTCCTGAGCAGGAGG  412
           ||||||| ||||||||||||||||||||| | |||||||| |||||| |||||||||||||
Db   1681  CTGGACGTGCGCGGCTGGGCTTCAGCCTGTGCCCAGACGCTGGAGTTTCTGCAGAAGCGG  1740

Qy    413  AAGCAGGTGGTGGCCGCCGGCCCTGAGGCAGGCAGCCCTGCGCTCGAGCTGATGAGAGACCTGCAGGAG  472
           |||||||||| |  ||||||||||||| ||| ||||| |||||| |||||||  ||||||| ||| |||
Db   1741  AAGGTCGTGGTGGCCAAGGCCCTGAAGCAGGTGCTGCAGCGCTGGGCCGTTCTGCCAGGAGCAGGGG  1800

Qy    473  GATGAGATCCCAGTGGTAGCTATTATGGCCATCATGCCACTGTGTGTGGGATCCGGGCAATGACTTCC  532
           ||||||| |||||| | ||| ||| |||||||| ||||||||||||  |||||||||||||||||||||
Db   1801  GACGAGGTGCCGCTGATGAGCCATCATGCCACTGTGGGGTGAACAAGATCCATGACCTCC  1860

Qy    533  CTGTATGGGCAGCTGGCTGGCTGGAAGGAGCTGGGCCTCTTGATTGCGTCTCCTACATC  592
           |||||||||||||||||| |||||||||||||||||||||||||||||||||||||||||
Db   1861  ATGTATGCTGCCACCTGCTGGGGCTGCAGAAGCTGAACCTCTGGACTGTGCCAGCTACATC  1920

Qy    593  ACGGGGGCCTCGGGGCTCGGGCCTTGGCCAACCTTTATGAGAGCCAGAGTGGTCT  652
           ||||||||||||||||||||||||||||||||||||||| |||||||||||||||
Db   1921  ACTGGTCTATCAGGGGCCACCTGACCATGCTACCTTGTACCGTGACTGGTTCC  1980

Qy    653  CAGAAGGACCTGCAGGGCCGCAGGGCCCACTGAGTTGCTGAAGACCCAGTGACCAAGAACAAGCTG  712
           ||| ||||||||||||| |||||||||||||||||||||||||||||||||||||||||||||
Db   1981  TCCAAAAACTTGGAGCCCCCAGCCAGCTGCAGCGGTACCGGCAGCGAGCCAGGCAGGCGTCGCCCGC  2040

Qy    713  GGTGTGCTTGGCCCCCAGCCAGCTGCAGAAGCTGAACCTTCGACTGTGTCCAGCTACATC  772
           |||||||||||||||||||||||| || ||||||||||||||||| |||||||||||
Db   2041  CCCTCCCTGTTCCCAGAACCAGCTCCGCAAATTCCAGGAGCCCTCATCAACGCTGTCATC  2100

Qy    773  TTGGGCTACCCCAAGCTGCTTCACCAGTCGCTTCACACCTTTACAGACTTCTGGGGCCTCTGAGATCAA  832
           |||||||||||||||||||||||||||| | |||||||||| |||||||||||||||||
Db   2101  GAAGGCTACAGGGTCACCTTCAGTCAGATCACACAGTCTCCAGGCCCTGACTGGCCCTGGGG  2160

Qy    833  GATGAGAAATGAATGAATCGAAACTGTCAAACTGTCAGATCAGATCAGACGTGCTGCTGTCTTGAGCTGAGCTG  892
           ||||| ||||||||||||||||||||| |||
Db   2161  GACGAGAGAAATGAATGAATCAGCCAAGAGGCAGAGCCTGCAACACCAAAGGGCAGACAGACGGGAAC  2220

Qy    893  CCTCTGCCATCTACTGTGCCCTCAACACCAAAGGGCAGAGCCTGACCCACTTTGAATTT  952
           |||||||||||||||||||  ||
Db   2221  CCCCTGCCCATCTA------CCTCACCATCAATGTCAAGGATGATGTAAGGCAACCAGGAT  2274

Qy    953  GGGGAGTGGTGCGAGTTCTCTCCCTACGAGGTCGGTTCCCCAAGTACGGGGCCTTCATC  1012
           ||||| |||||| ||| |||||||||||||||||||||||||||||||||||||||||||
Db   2275  GTCAGATGGTTCGAGTTCTCGAGTTCTTTGGCTCGAGTTCTTTATGGGGCAGCTCTTCAGGGGCAGCTCTTCCTGAGG  2334

Qy   1013  CCCTCTGAGCTCTTTGGCTCGAGTTCTTTATGGGGCAGCTGATGAGAAGAGGCTTCCTGAG  1072
           |||||||||||||||||||||||||||||||||||||| ||||||||||||||||||||
Db   2335  CCCTCCGAGCTCTTCGGCTCCGAGTTCTTCATGGGGCGGCGCTCCGTGGAAGAGATCCCGGAG  2394
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Qy   1073  TCCCGCCATCTGCTTCTTAGAGGTATCTGGAGCAACCTGTATGCAGCGACCTTCCAGGAC  1132
           ||| ||||| || |||| |  ||||| ||||||||| |||||||||||||||||||||||
Db   2395  TCTCGAATCTGCTACATGCTACAGCGCCTGTGGGACCAGCATCTTCCCTGGACCGCTGGGT  2454

Qy   1133  AGCTTATACTGGGCCTCAGAGCCCAGGTTCTGGGACCACCTGGAGGAGTTTTCCACAGGTGGACAAGGGAGAAAGTG  1192
           |||  ||||||||||||||||||||| |||| || |||||||||||
Db   2455  GCCTGGAACCTGTCACCACCTCGGAGGAGTTTTCCACAGGTGGACAAGGGAGAAAGTG  2514

Qy   1193  AACCTGACAAGGAGCAGGTCCCCTTCTGAAGATAGAGAGAACCACCTCAA--------  1244
           |||||| ||||||||||||||||||||||||||
Db   2515  CAGGACATCGAAGACGAGCAGCCGATCCTGCCTGAAATGTGATGCTAACATCCTG  2574

Qy   1245  -----------------CAGCCGGCAGAATAGCTGAGTTTTCACCGATCTTCTGACG  1285
                            ||||||| || || |||||||
Db   2575  GAGACCACGTAGTAGTCCAGGTCATGGCTGTCGTCCAATTCTTTCCGAGAAATCCTTACC  2634

Qy   1286  TGGCGTCCACTGGCCCAGGCCACACATAATTCCTGCGTGGCCTCCATTTCCACAAAGAC  1345
           ||||||||||||||||||||||||| ||||||||||||||||||
Db   2635  CATCGGTCTCTTCGTGTCTGAGTTTCACAACTTCCGTGTCTGGGCTGCAGTCTGCACCACCAAC  2694

Qy   1346  TACTTTCAGCATCCTCACTTCTCCACATGGAAAGCTACCACCTGATGGGCTCCCCAAC  1405
           ||| |||||||||||||||||||  ||||||||||||||||||
Db   2695  TACCTCCAGAATGGCCAGTTCTCTAGGTGGAAAGACACCAGTGCTAGAGTGTTTCCCAAAC  2754

Qy   1406  CAGCTGCACCCCTGGAGCCCCACCTGTGCCTGCTGGACACTGGCACTGCGTTCTTTGTCAACTCC  1465
           |||||||||| ||| |||||||||||||||||||||||||||||||
Db   2755  CAGCTGACCGAGTCGCGAACCACGTGCCTGCTGGACACGTGGACTGACTACTAC  2814

Qy   1466  AGCTGCCTGCCCCTCCTCAGCCTCCTCCGGAGCGCCACTGGACCTGGCTGGACTAC  1525
           ||||||||||||||| |||||||||||||
Db   2815  AGCTACCCGCCCCCTCCTCCAGGCACAGCAGTGCAAAAGCCGATCTCATCACCTCAACTAC  2874

Qy   1526  AACCTCCACGGAGCCTTCAGCAGTGCAGTCGAGCTCTGGGCCGTTCTGCCAGGAGCAGGGG  1585
           |||||||||||||||||||
Db   2875  TGTGCTGGTGGTCCAGACAAAGCCCCTGAGCACAAACAAAACCTGTGATACTGTGCAGAAC  2934

Qy   1586  ATCCCGTTCCC--------------------------ACCCATCTCGCCCAGCCCC  1615
           ||||| |||||
Db   2935  ATCCCCTTCCCCAAATACGAGCTGCCCAGATGAGAAGATCTGAAAATCTCAAGGAATGCTACCTG  2994

Qy   1616  GAAGAGCAGCTCCAGCCTCGGGAGTGCCACACCTTCTCCGAGCCTGCCCCGAGCC  1675
           |||||||||||||||
Db   2995  ATGGAGAACCCCAGGAACCCGATGCCCCATCGTGACTTTCTTCCCACTCATCAATGAC  3054

Qy   1676  CCTGCGGTGCTGCACTTTCCTCTGGGGTCCGGCCGACACCGGACGCGGCAGCTGGG  1735
           |||||||||||||||||||
Db   3055  ACTTTCGAAAATACAACAAGGCACCAGGTGTAGAGCAAGGCAAGAGCTA  3114

Qy   1736  GAGGTGAACCTGTCTTCATCGGACTTCATCCTGGAGAACAACCTACCAGCCAG  1795
           |||||||||||||||||||||||
Db   3115  CAGGTGGACATTTATGTCCCAAAACTCCCTGACACATTACAATGTCAACAACACAGAG  3174

Qy   1796  GAGGACGTGGACAAGCTGCTGCACACTGCACCTACACATTACAATCAATGAC  1855
           |||||||||||||||||||
Db   3175  GCCACCTTTGACAAGCTGGTGAAACTCTCAGAGTATAACATCCTGAGTAGTAATAAGGACACACT  3234

Qy   1856  CTGCTGGAGGCTCTCGGCCAGCGAGTGCGCCAGCCAGTGCAGCGGCTGGAGGCCCAGGGCCCAGAAC  1911
           |||||||||||||||||||
Db   3235  CTCCTCCCGAGGCTCTGCGGCCTCCGGCTCTGCCAGTGCAGTGGAGGAGAAGGAGCGCCTGAAGGGCCAGTG  3290
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RESULT 13
US-10-380-873B-2
; Sequence 2, Application US/10380873B
; Publication No. US20040014089A1
; GENERAL INFORMATION:
; APPLICANT: Hiromasa MIYAJI, et al.
; TITLE OF INVENTION: Polypeptide having phospholipase A2 activity
; FILE REFERENCE: 2139.34
; CURRENT APPLICATION NUMBER: US/10/380,873B
; CURRENT FILING DATE: 2003-07-09
; PRIOR APPLICATION NUMBER: JP 00/146466
; PRIOR FILING DATE: 2000-09-19
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;  PRIOR APPLICATION NUMBER: JP 01/284044
;  PRIOR FILING DATE: 2001-05-16
;  NUMBER OF SEQ ID NOS: 47
;  SOFTWARE: PatentIn Ver. 2.0
;  SEQ ID NO 2
;  LENGTH: 3460
;  TYPE: DNA
;  ORGANISM: Homo sapiens
;  FEATURE:
;  NAME/KEY: CDS
;  LOCATION: (93)..(2639)
US-10-380-873B-2

Query Match     18.1%;   Score 398.2;  DB 16;  Length 3460;
Best Local Similarity  55.2%;   Pred. No. 5.5e-97;
Matches  880;  Conservative  0;  Mismatches 658;  Indels 57;  Gaps  3;

Qy   348 GGGAGCTGCCGTGCGACTGGCGTTCGGCGCCCTGTGCTGCAGGAGGCAGGCCTTCCTGAGCA  407
Db  1021 GGGACCTTAGACCTACGGCCTTGGCTTGCACCTCTCTGACCGGGGAGCAGGAGTTTCTGGACA 1080

Qy   408 GGAGGAAGCAGGTGGTGCCGCGGCCCTGAGCGCCCTGAGCTGGATGGAGACCTGC  467
Db  1081 GGAGGAAGCAGGTCGTGTCCAAGGCCCTGCAGCAAGTGCTGGGATTGAGTGAGGCTCTGG 1140

Qy   468 AGGAGGATGAGATCCCAGTGGTAGCTATTATGGCCACTGGTGTGTGGGATCCGGGCAATGA  527
Db  1141 ACAGTGGCCAGGTGCCTGTAGTGGCTGTGTTGGGTTCCGGGGTGGAACCCGAGCCATGT 1200

Qy   528 CTTCCCTGTATGGCAGTGGCTGGCCTGGAAGAGCTTCTTGGATTGCGTCTCCT  587
Db  1201 CTTCTCTGTACGGCAGCCTGGCAGCCTGGCCTTCTGGCCCTTCTAGACACTGTGACCT 1260

Qy   588 ACATCACCGGGGCCTCGGGCTTCCACCTGGCCCAACCTTTATGAGGACCCAGAGT  647
Db  1261 ACCTGAGTGGGGGTCTCTGGGTTCTCTGGTCATCTGCATTCTCACACTCTACAGGACCCAGCCT 1320

Qy   648 GGTCTCAGAAGGACCTGGCAGGCCCACTGAGTTGCTGAAGACCGGTGACCAAGAACA  707
Db  1321 GGTCCCAGGTGGCCCTTGCAGGGCCCCAGGTTCACGTCTGCAGCAGTA 1380

Qy   708 AGCTGGGTGTGTGGCCCCCAGCTCAGCGTGCACGGGTACCGGCGAGCTGGCCGAGCGTG  767
Db  1381 AGATGGGAGCTTTGTCATCAACGGAGCCGGCTACACTACTACTCAGGAACTGGGGGTCCGGG 1440

Qy   768 CCCGCTTGGGTGGCTACCCAAGCTGCTTCACCAACCTGTGGCCCTCATCAACGAGGCGCTGC  827
Db  1441 AGCGGCAGTGGGCCACAGCGTGTCCATCGAACCTCTGGGGCCCTCCTTGTTGAGTATCTCC 1500

Qy   828 TGCATGATGAGCCCATGATCAACAAGCTCTTCAGATCAACAGCGGGAGGGCCCTGAGTCATGGCC  887
Db  1501 TGTACCAGGAGGAGAACCCTGCCAAGCGTGTCGACCAACAGCAGAGGGGTCCGCCAGGGTC 1560

Qy   888 AGAACCCTCTGCCCATCTACTGTGCCCTCAACACCAAAGGGCAGAGCCTGACCACTTTG  947
Db  1561 AGAACCCTTACCCCATTACACCACGTGTCAACGTC---CGCACCAACTTGAGTGGGGAAG 1617

Qy   948 AATTTTGGGAGTGGTGCAGTTCTCTCCCTACAGAGGTCGCTTCCCCAAGTACGGGGCCTT 1007
Db  1618 ATTTTTGCAGAGTGGTGCAGTTCACGCCCTATGAGGTTGGCTTCCCCAAGTACGGGGCTT 1677

Qy  1008 TCATCCCCCTGAGCTCTTGGCTCCGAGTTCTTTATGGGGCAGCTGATGAAGAGGCTTC 1067
Db  1678 ATGTTCCCACCACGGAGCTCTTCGGCTCAGAACTTCATGGGACGATTGCTGCAGCTCCAGC 1737

Qy  1068 CTGAGTCCCGCATCGTCTTCTTAGAGGTATCTGAGCAACGCTGTATGCACCACCTCC 1127
Db  1738 CTGAACCCGGATCGTTGTTACCTGCAAGGTATGTGGGGCAGCCGCCTTTGCCACCAGCTGG 1797

Qy  1128 AGGACAGCTTATACTGGGCCTCAGAACCGCCGCCTCGGCGTCACCCGAGTGGTACAGAGGCA 1187
Db  1798 ATGAGATCTTCCTAAAGAACCCGCCTCGGCCGCCTCCAGCTTCCTGAGTGGTACACAGAGGGCA 1857
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Qy  1188 AGGCCAACCTGGACAAGGA---------------GCAAGGTCCCCTTCTGAAGATAG 1229
Db  1858 GTGTGAATATCACAGACGACTGCCAGAAGCCTCAGCTGCACAACCCCTCGAGGCTGCGAA 1917

Qy  1230 AAGAACCACCCTCAACAGCCGGAGAATAGCTGAGTTTTCACCGATCTCTGACGTGGC 1289
Db  1918 CGAGGCTCCTCACCCCACAGGGGCCCTTCTCACCAGCTGTGCTGACATATTCACCTCCC 1977

Qy  1290 GTCCACTGGCCCAGGCCACACATAATTCCTGCGTGGCCTCCATTTCCACAAAGACTACT 1349
Db  1978 GCTTCACTTCCGCCCAGAGCTTTAACTTCACCCGGGGTCTCTGCTTGCTTGCACAAGGACTATG 2037

Qy  1350 TTCAGCATCCTCACTTCTCCACATGGAAAGCTACCACTCTGGATGGCTCCCAACCAGC 1409
Db  2038 TGGCTGCAGGGAGTTCGTGCCTGGAAAGACACACACCCCGACGCCTTCCCCAACCAGC 2097

Qy  1410 TGACACCCTCGGAGCCCCACCTGTGCCTGCTGATGTTGGCTACCTACTCATCAATACCAGCT 1469
Db  2098 TCACCCCATGCGGGACTGCCTGTACCTGTGGACGAGCTTTGCCATCAACTCTCCGT 2157

Qy  1470 GCCTGCCCCTTCTGCAGCCCACTCGGGACGTGGACCTCATCCTGTCATTGGACTACAACC 1529
Db  2158 TCCCACTGGCTCTGCCTTCAGAGCAGCAGTGGACCTCATTCTGTCCTTTGACTATTCCT 2217

Qy  1530 TCCACGGAGCCTTCAGCAGTTGCAGTTCTCCTCGGCGTTCTGCCAGGAGCAGGGGATCC 1589
Db  2218 TGGAAGCCCCTTTTGAGGTCTTGAAGATGACAGAGAAGTACTGCCTGGACCGAGAATCC 2277

Qy  1590 CGTTCCCACCCATCTGCCCAGCCCGAAGAGCAGCGTCCAGCCTCGGGAGTGCCACACT 1649
Db  2278 CCTTCCCTAGCATCGAGGTGGGCCCTGAGGAGGTGGAGGAGCCCGTGAGTGCTATCTGT 2337

Qy  1650 TCTTCCGAGCCCCACCTGCCCGAGCCCCCTGCGGTGCTGCACTTTTCCTC------- 1698
Db  2338 TTGCCAAGGCTGAGGAGACCCCCGCTCCCCCATTGTGCTGCACTTGTGCTGCACTGTTAACCGTA 2397

Qy  1699 ---------------TGGGGTCCGGCGACACCCGAGGAGCGGCGAGCTG 1733
Db  2398 CCTTCCGCACACACCTGGCCACTCTCCCTACACCGTGGAGCGGCACAAACAGCTGAGGAGGAAGGCCTTTG 2457

Qy  1734 GGGAGGGTGAACCTGTCTTCATCGGACTCTCCCTACCACTACACGAAGGTGACCTACAGCC 1793
Db  2458 GGGACTTTGTCATCAACAAGGCCAGACACCCCCTATGGCATGATGAACTTCACCTATGAGC 2517

Qy  1794 AGGAGGACGTGGACAAAGCTGCTGCACCATTACAATGTCTGCAACACCAGGAGC 1853
Db  2518 CCCAGGACTTTTATCGGCGTGGTGCCCTCAGTCGATACAACGTCCTGAACAATGTGGAGA 2577

Qy  1854 AGTGCTGGAGGCTGTCGCGCCAGCAGTGCAGCGG 1888
Db  2578 CCTTGAAGTGCGCCCCTCAGCTGCCTGGCTGGACCGG 2612
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US-10-332-426-11
;  Sequence 11, Application US/10332426
;  Publication No. US2004029136A1
;  GENERAL INFORMATION:
;  APPLICANT:  INCYTE GENOMICS, INC.; TANG, Y. Tom;
;  APPLICANT:  AZIMZAI, Yalda; DAS, Debopriya;
;  APPLICANT:  THORNTON, Michael; LU, Dyung Aina M.;
;  APPLICANT:  TRIBOULEY, Catherine M.; YUE, Henry;
;  APPLICANT:  GANDHI, Ameena R.; CHAWLA, Narinder K.;
;  APPLICANT:  KHAN, Farrah A.; LU, Yan;
;  APPLICANT:  YAO, Monique G.; HAFALIA, April J. A.;
;  APPLICANT:  ELLIOTT, Vicki S.; ARVIZU, Chandra S.;
;  APPLICANT:  LAL, Preeti; RAMKUMAR, Jayalaxmi;
;  APPLICANT:  NGUYEN, Danniel B.; BAUGHN, Mariah R.
;  TITLE OF INVENTION: LIPID METABOLISM MOLECULES
;  FILE REFERENCE: PI-0152 USN
;  CURRENT APPLICATION NUMBER: US/10/332,426
;  CURRENT FILING DATE: 2003-01-06
;  PRIOR APPLICATION NUMBER: US 60/216,803
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;   PRIOR FILING DATE: 2000-07-07
;   PRIOR APPLICATION NUMBER: US 60/216,801
;   PRIOR FILING DATE: 2000-07-07
;   PRIOR APPLICATION NUMBER: US 60/218,233
;   PRIOR FILING DATE: 2000-07-14
;   PRIOR APPLICATION NUMBER: US 60/220,046
;   PRIOR FILING DATE: 2000-07-21
;   PRIOR APPLICATION NUMBER: US 60/220,739
;   PRIOR FILING DATE: 2000-07-26
;   PRIOR APPLICATION NUMBER: US 60/222,824
;   PRIOR FILING DATE: 2000-08-04
;   NUMBER OF SEQ ID NOS: 16
;   SOFTWARE: PERL Program
; SEQ ID NO 11
;   LENGTH: 2547
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   OTHER INFORMATION: Incyte ID No. US2004002136A1 1281946CB1
US-10-332-426-11

  Query Match      17.5%;    Score 385.8; DB 13; Length 2547;
  Best Local Similarity   54.7%;    Pred. No. 1.1e-93;
  Matches  873;  Conservative   0;  Mismatches  662;  Indels  60; Gaps   3;
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Qy    348 GGGAGCTGGCCGTGCCACTGGGCTTCCGGCCCTGTGCAGAGGAGCAGGCCTTCCTGAGCA 407
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Db    929 GGGACCTAGACGCCTTGGCTTGACCTCTCTGACGGGGAGCAGGAGTTTCTGACA 988

Qy    408 GGAGGAGGCAGGTGGTGGCCGCGGCCCTGAGCTGAGTCTGAGTGATGGAGACCTGC 467
              |||||||||||||||||  | ||||||||||||||||| ||||||||| |||
Db    989 GGAGGAGGCAGGTGCGTGTCCAAGGCCCTGCAGCAAGTGCTGGGATTGCTGGGATTGAGGGTCTGG 1048

Qy    468 AGGAGGATGAGATCCCAGTGGTAGCTATTATGGCCACTGGTGCGGCAATGA 527
              | |||| |||||||||  |||||| ||  || |||||||||||||||||||||
Db   1049 ACAGTGGCCAGGTGCCTGTAGTGCTGTGTTGGTTCCGGGGGTGGAACCCGAGCCATGT 1108

Qy    528 CTTCCCTGTATGGCCAGCTGGCTGGCTGGCCTGAAGAGGAGCTGGGCCTTGATTGCGTCTTCCT 587
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Db   1109 CTTCTCTGTACGGCAGCCTGGGCGGGGGTTGCAGGAGTCGCAGGAGCTCGGAGGCTCTGTGACCT 1168

Qy    588 ACATCACCGGGGGCCTCGGGCTCACCTGGGCATCCTGGCCCAACCTTTATGAGGACCCAGAGT 647
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Db   1169 ACCTGAGTGGGGTCTCTGGGTCTACCTGGTCATCTCCACACTTCCACCTGGGGACCCAGCCT 1228

Qy    648 GGTCTCAGAAGGACACCTGGCAGGGCCCACTGAGTTGCTGAAGACCCAGGTGACCAAGAACA 707
              |||| |||||| ||| ||||| ||||||| |||  | |||||||||||| |||||| ||||
Db   1229 GGTCCCAGGTGGCTTGCAGGGCCCATTGAGCGTGCCCAGGTCACGTCTGCAGCAGTA 1288

Qy    708 AGCTGGGTGTGCTGGGGCCCCCAGCCAGCTGCGAGGGTACCGGCGCAGGAGCGTG 767
              ||||||||| ||||  ||||| || | |||||  || |||||||||||||||||||
Db   1289 AGATGGGAGCTTTGTCACGGACGCGGCTACAGTACTACACTCAGGAACTGGGGGGTCCGGG 1348

Qy    768 CCCGGCTTGGGCTACCAAGCTGCTTCACCCAAGCTGTCCCTCATCGAGCTGCTCCTGGGTCTCCGGGATCTCC 827
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Db   1349 AGCCAGTGGCCACCAGAGTTGGCTAGTGCTGTGTGTGGCCCTCCTTGTTGAGTATCTCC 1408

Qy    828 TGCATGATGAGCCCATGATCAACAAGCTCTCAGATCAACGAGGAGCCCTGAGTCATGGCC 887
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Db   1409 TGTACCAGGAGGAGAACCCCTGCCAAGCTGCTGCTGCGTCTGACCAACAGAAGGCGGTCCGGCGGGGTC 1468

Qy    888 AGAACCCTGCCATCTACTGTGCCCTCAACACCAAAGGGCAGAGCCTGACCACTTTTG 947
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Db   1469 AAAACCCTTACCCATTA----CACCAGTGTCAACGTCCGACCAACTTGAGTGGGG 1522

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Db   1523 AAGATTTGCATGGTGCGAGTTCACGCGAGTTGGCTTCACGGGGGAGTGATGAAGAGAGCTTC 1582

Qy   1008 TCATCCCCTGAGCTCTTTGGCTCCAGTTCTTTATGGGGCAGCTGATGACTGAAGAAGCTC 1067
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Db   1703 ATGAGATCTTCCTAAAGACCGGCTCGGGCCTCAGCTTGCTGGGGTACAGAGGCA 1762

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Qy   1290 GTCCACTGGCCCAGGCCACCATAATTTCCTGCGTGGCCTCCTCCATCATCAAAGACTACT 1349
Db   1883 GCTTCACTTCCGCCCAGAGCTTTAACTTCACCGGGGTCTCTGCTTGCTGCACAAGGACTATG 1942

Qy   1350 TTCAGCATCCTCACTTCTCCACATGGAAAGTACCACTCTGGATGGGCTCCCAACCAGC 1409
              ||| || ||||  || ||  |||||| ||| ||| ||||| |||||||||||||
Db   1943 TGGCTGGCAGGGAGTTCGTGCCGTGGCCTGGAAAGACACACACCCGGACGCCTTCCCCAACCAGC 2002

Qy   1410 TGACACCCTGGAGCCGTCCATCTCGCCGTGTGCAGCCATTCGCTGCTACCCTCATCAATACCAGCT 1469
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Db   2063 TCCCACTGGCCTGCCTGCTGCCTGCTCAGAGTCCTGGGCCGGTTCTGCAGGAGCAGGGGATCC 2122

Qy   1530 TCCACGGAGCCTTCCAGAGTTGCACGTTCTGCAGCTGCCGGTTCTGGGCCGGTCAGGGGATCC 1589
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Db   2123 TGGAAGCCCCTTTTGAGGTCTTGAAGATGACAGAAGAGTACTGCCTGGACCGGAGAATCC 2182

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Db   2183 CCTTCCCTAGCATCGAGGTGGGCCCTGAGGACGTGGAGCGAGGAGGCCCGTGAGTGCTATCGT 2242

Qy   1650 TCTCCGACCCCACCTGCCCAGAGCCCCGCTCCCCATTGTTGCTGCACTTGTGCACTTCCCCTGTGTTAACCGTA 1698
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Db   2243 TTGCCAAGGCTGAGGACCCCCTGACTTGCTGCCCATTGTGCTGCACTTGTGCACTTCCCCTGTGTTAACCGTA 2302

Qy   1699 ------------------------------TGGGGTCCGGCGGCACCCCAGGAGGAGCGGCAGCTG 1733
Db   2303 CCTTCCGCACACACCTGGCCCCAGGTGTGGAGCGGACCAAACAGCTGAGGAGAGGCCTTTG 2362

Qy   1734 GGGAGGTGAACCTGTTCATCAGCCAGGTGTCACGTCTGCAGCAGTA 1793
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Db   2363 GGGACTTTGTCATCAACAGGCCAGACACCCCCTATGCATGATGAACTTCACCTATGAGC 2422

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US-10-380-873B-39
; Sequence 39, Application US/10380873B
; Publication No. US2004014089A1
; GENERAL INFORMATION:
;   APPLICANT: Hiromasa MIYAJI, et al.
;   TITLE OF INVENTION: Polypeptide having phospholipase A2 activity
;   FILE REFERENCE: 2139.34
;   CURRENT APPLICATION NUMBER: US/10/380,873B
;   CURRENT FILING DATE: 2003-07-09
;   PRIOR APPLICATION NUMBER: JP 00/146466
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;   PRIOR FILING DATE: 2000-09-19
;   PRIOR APPLICATION NUMBER: JP 01/284044
;   PRIOR FILING DATE: 2001-05-16
;   SOFTWARE: PatentIn Ver. 2.0
;   SEQ ID NO 39
;   LENGTH: 2694
;   TYPE: DNA
;   ORGANISM: Mus musculus
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (52)...(2610)
US-10-380-873B-39

Query Match       16.6%;   Score 365;   DB 16;   Length 2694;
Best Local Similarity   54.3%;   Pred. No. 4.7e-88;
Matches  882;   Conservative   0;   Mismatches  665;   Indels   78;   Gaps   4;
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Qy    348 GGGAGCTGGCCGTGCGACTGGCTGGGCTTCGGGCCCTGTGCAGAGGAGCAGGCCTTCCTGAGCA 407
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Db    968 GGGACTTGGACCTGCGCCCTTGGTTTGACCTCTGTGATGGAGCAGGAATTTCTGGACA 1027

Qy    408 GGAGGAAGCAGGTGGTGCCGCCCTTGAGGCAGGCCCTGCAGCTGGATGGAGACCTGC 467
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Db   1028 AGAGGAAGCAGGTGGCGTCCAAGGCCTGCAGCGGGTGATGGGAGTTGAGTGAGGCTCTGC 1087

Qy    468 AGGAGGATGAGATCCCAGTGGTAGTATTATGGCCACTGGTGTGGGGATCGGGCAATGA 527
              || || || ||| | |  |  ||||| |||||| || ||| |||||  |||  |||
Db   1088 ACTGTGACCAGGTACCTGTGGTAGCCGTGTAGGCTCTGTGGGGGTGGAACCAGAGCCATGA 1147

Qy    528 CTTCCCGTGTATGGCAGCTGGCTGGCCTGAAGGAGGGCCTCCTTGGATTGCGTCTCCT 587
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Db   1148 CTTCCCTGTACGGCAGCCTGGGTGGGCTGCAGGAGTCGTCTTCTGATGCCGTGGACCT 1207

Qy    588 ACATCACCGGGGCCTCGGGCTCCACCTGGCCAACCTTTATGGAGGACCCAGAGT 647
              || ||||||||| |||||||||  ||| |||| || |||| || || ||||||
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Qy    648 GGTCTCAGAAGGACCTGGCAGGGCCCACTGAGTTGCTGAAGACCCAGTGACCAAGAACA 707
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Db   1625 ACGTTCCCACGGAACTCTTTGGCTGTCTGAATTCTTCATGGGCGTGCTGCTTGCATTTCTGGC 1684

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Db   1745 ATGAGATCTTCCTGAAGCTGGGAGCTGGGACTGAGCTTTCTGGACTTTCTGGACTGGCACAGGGGGA 1804
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Qy   1188 AGGCCAACCTGGACAA--------------------------GGAGCAGGTCCCCCTTCTGAAGATAG 1229
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Db   1805 GTGTCAGTGTCACAGATGACTGGCCAAAGTACGGAGCAGGACCCCACCACGGCTGCCTA 1864

Qy   1230 AAGAACCACCCTCAACAGCCGCAGAATAGCTGAGTTTTCACCGATCTTCTGACGTGGC 1289
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Qy   1290 GTCCACTGGCCGCCAGGCCACACATAAATTCCTGCGTGCCTCCTCCATTTCCACAAAGACTACT 1349
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Db   1925 GTATTACTTGTGCCCAGACCTTAACTTACCCGAGCTCTGCATGTGACAAAGACTACA 1984

Qy   1350 TTCAGCATCCTCACTTCTCCACATGGAAAGCTAC----------------------CACTC 1388
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Db   2045 CTGATGCCTGTCCCAACCAGTCACACCCATGAAGGAATTTCTGGACA 2104

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Db   2105 GCTTTGCTATCAACTCGCCATTCCACTGTCCTGCAGCCGCAGCCGGTGTGGACCTCA 2164

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Qy   1569 TCTGCCAGAGCAGGGATCCCGTTCCACCCATCTGCTTGGATTGCTGTCTCCT 1628
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Qy   1629 AGCCTCGGGAGTGCCACACCTGGGGGTCCTCCTCCGGACCCAGAGT 1688
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Db   2285 ACCCCGTGAATGCTATCTGTTGTCGTGAGGCAGGAGACCCCTGCTCGCCCATCGTGTCGTGC 2344

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Db   2345 ATTTCCCTCTTGTTGTCAACAGGACCTTTCGCACCTGCCACCTGTCTTCATGGGAACGACACAA 2404

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Db   2405 CAGCTGAGGAGAAGGCCTTCGGGGACTTTATCATCAACGGGCCAGATACTGCCTATGGCA 2464

Qy   1773 ACACGAAGGTGACCTACAGCCAGGAGGACTGTGCACCTGACACTGACCATTACA 1832
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Db   2525 AGTCTTGAACAACAGGAGACTATACGGCCATGCCCCTGCCCCAGCTGCGGCTCGGACCCGGCCGC 2584

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Db   2585 GGCAG 2589
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Search completed: October  7, 2004, 22:41:01
Job time : 1150.17 secs
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OM nucleic - nucleic search, using sw model

            Copyright   GenCore version 5.1.6
                       (c) 1993 - 2004 Compugen Ltd.

Run on:        October 7, 2004, 12:49:19 ; Search time 6234.42 Seconds
                                            (without alignments)
                                       10556.917 Million cell updates/sec

Title:           US-09-830-321A-5
Perfect score:   2204
Sequence:        1 catggttgggggcagaga.........acctatacaaaaaaaaaa 2204

Scoring table:   IDENTITY NUC
                 Gapop 10.0 , Gapext 1.0

Searched:        27513289 seqs, 1493109276 residues

Total number of hits satisfying chosen parameters:       55026578

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :       EST:*
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           19: em_gss_pln:*
           20: em_gss_vrt:*
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           22: em_gss_mam:*
           23: em_gss_mus:*
           24: em_gss_pro:*
           25: em_gss_rod:*
           26: em_gss_phg:*
           27: em_gss_vrl:*
           28: gb_gss1:*
           29: gb_gss2:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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Result        %     Query
No.   Score  Match  Length DB  ID         Description
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  1  1129.8  51.3    4240  11  AK037218   AK037218 Mus muscu
  2   892.8  40.5    1131  12  BM928260   BM928260 AGENCOURT
  3   697    31.6     957  14  CA48226    CA48226 AGENCOURT
  4   677.6  30.7     949  12  BI768993   BI768993 603058145
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      6 615.2  27.9  701  12  BM982475  BM982475 UI-CF-EN1
  c   7 608    27.6  869  14  CD252554  CD252554 AGENCOURT
      8 594    27.0  935  12  BG696408  BG696408 60265950d
      9 574.4  26.1  1149 12  BM906397  BM906397 AGENCOURT
     10 569.8  25.9  653  13  BU742347  BU742347 UI-E-EO1-
  c  11 562    25.5  922  13  BQ887656  BQ887656 AGENCOURT
     12 558.2  25.3  666  10  AW959903  AW959903 EST371974
     13 556.2  25.2  810  14  CA319426  CA319426 UI-M-FW0-
  c  14 514.4  23.3  579  10  BF769253  BF769253 QV3-IT000
  c  15 507.4  23.0  577  14  CB306001  CB306001 UI-CF-EN1
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     21 475.4  21.6  545  14  CD675848  CD675848 fs28h09.y
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     26 417.8  19.0  461  10  BF827819  BF827819 CM4-HN002
     27 412.4  18.7  550  13  BX523358  BX523358 BX523358
  c  28 401.2  18.2  472  14  N71116    N71116 za87h11.s1
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  c  30 373.6  17.0  408   9  AI261401  AI261401 qk08b11.x
     31 366.4  16.6  429  14  W05477    W05477 za87h11.r1
  c  32 357.8  16.2  361  10  BF924507  BF924507 IL2-NT019
     33 357.4  16.2  383   9  AA297121  AA297121 EST112698
     34 355    16.1  406  10  BF856340  BF856340 RC0-FN020
     35 348    15.8  379   9  AA293135  AA293135 zt26e03.r
     36 347.6  15.8  383  10  BF878339  BF878339 CM2-ET012
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     38 332.6  15.1  411  10  BF301381  BF301381 602029836
     39 332.2  15.1  386   9  AA134150  AA134150 zo18a11.r
  c  40 326.8  14.8  337  14  CB321642  CB321642 UI-CF-EN1
  c  41 325    14.7  328  10  BF530010  BF530010 602042432
  c  42 324.8  14.7  573  10  AW130552  AW130552 xf52h09.x
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ALIGNMENTS

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RESULT 1
AK037218
LOCUS       AK037218              4240 bp    mRNA    linear   HTC 19-SEP-2003
DEFINITION  Mus musculus 6 days neonate skin cDNA, RIKEN full-length enriched
            library, clone:A03011C02 product:similar to CYTOSOLIC
            PHOSPHOLIPASE A2 BETA [Homo sapiens], full insert sequence.
ACCESSION   AK037218
VERSION     AK037218.1  GI:26085667
KEYWORDS    HTC; CAP trapper.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1
  AUTHORS   Carninci,P. and Hayashizaki,Y.
  TITLE     High-efficiency full-length cDNA cloning
  JOURNAL   Meth. Enzymol. 303, 19-44 (1999)
   MEDLINE   99279253
   PUBMED   10349636
REFERENCE   2
  AUTHORS   Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K.,
            Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
  TITLE     Normalization and subtraction of cap-trapper-selected cDNAs to
            prepare full-length cDNA libraries for rapid discovery of new genes
  JOURNAL   Genome Res. 10 (10), 1617-1630 (2000)
   MEDLINE   20499374
   PUBMED   11042159
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Matches 1321; Conservative   0; Mismatches 247; Indels  33; Gaps   1;

Qy    334 GGATTACAGACTGAGGGAGCTGGCCGTGCGACTGGGCTTCGGCCCTGTGCCCTGTGCAGAGGAGCA 393
          ||||     |||  ||     |||||||||||  ||  |  |||||| |||||| ||||  |||  |
Db   2270 GGAAGAAGGACCAAAGGAGCTGGCCCTGCGCGGCCTGGGCTGGGCCCTGCCCTGAGGAACA 2329

Qy    394 GGCCTTCCTGAGCAGCAGGAAGCAGGCAGGTGGTGCGCGGCCTTGAGGCAGGCCCTGCAGCT 453
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Qy    454 GGATGGAGACTTGCAGGAGGATGAGATCCCAGTGGTAGCTATTATGCCCACTGGTGGTGG 513
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Qy    514 GATCCCGGCAATGACTTCCCTGTATGGCAGCTGGCCTGGCCGCGGCCTGGCCTCT 573
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Db   2450 GATCCCGGCCATGACGTCTTTGTATGGGCAGCTGCCTGCCTGCAGGAGCTCGGCCTTCT 2509

Qy    574 GGATTGGCTCTCCTACATCACCGGGGCCTTCAGGATCACCTGGGCACTGGCCAACCTTA 633
          |||  | ||||||||| |||| ||||||||||||||||| ||||||||||||||||| ||
Db   2510 CGACTGCATCTCCTATATCACGGGGCTTCAGGATCACCTGGGCACTGGCCAACCTCTA 2569

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Db   2570 TGAGGACCCAGAGTGGTCGCAGAAGGACCTGCAGGGCCCACTGAGGTGCTGAAGACACA 2629

Qy    694 GGTGACCAAGAACAAGCTGGGTGTGCTGCCCCAGCCAGCTGCAGCGGGTACCGGCAGGA 753
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Db   2630 GGTGACAAAGAGCAAGCTGGGTGCTGCCCTAGCCAACTTTGGCGGTACCGGCAAGA 2689

Qy    754 GCTGGCCAGGGTGCCCGCTTGGGCTACCAGCTGCTTCACCAACCTGGGCCCTCAT 813
          |||||| |||||||| || ||||| |||| ||||||||||||||| ||||||||||
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Qy    874 CCTGAGTCATGGCCAGAACCCTCTGCCATCTACTGGCCTCACACCCAAAGGCAGCAG 933
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Qy    934 CCTGACCACTTTGAATTTGGGAGTGGTTGCGAGTTCTCTCCTACGAGGTCGGCTTCCC 993
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Db   2870 CCTGAGTACCTTTGATTTTGGGAGGTGGTGTTGAGTTCTCTCCATATGAAGTCGGCTTCCCC 2929

Qy    994 CAAGTACGGGGCCTTCATCCCCTGAGCTCTTCGGCTCCGAGTTCTCTTTATGGGCAGCGT 1053
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Db   2930 CAAGTATGGAGCCTTCATCTCCTCCGAGTCTTTGGCTCCGAGTTCTTTTATGGGGCGGCT 2989

Qy   1054 GATGAAGAGGCTTCCTGAGTCCGCATCTTCTTAGAAGTGATCTGGAGCAACCTGTA 1113
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Db   2990 GGTGAAGCAGCTCGCAGGTTCCCGGATCCAGCATCGTGAGCATCTGAGCGAATCGTT 3049

Qy   1114 TGCAGCCAACCTCAGGACAGCTTATACTGGGCCTCAGAGGCCAGCAGCCAGGTTCTGGGACCG 1173
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Db   3050 TGCGGCCCAGCCTCCAAGACAGCTTGTTACTGGTCCTCAGAACCCAGCCAGTTCTGGGGACCG 3109

Qy   1174 CTGGGTCAGGAACCTGGACAAGGACCAGCTGCCCTTCTGAGATAGAAGA 1233
          |||||  |  ||  | |  || | |||    |  || |||||| ||  ||
Db   3110 CTGGGGCGCAGGATCAGGCCAACCTGGACAAAGACAGCAGGTCCCCATCTGAAGATAGCAGA 3169

Qy   1234 ACCACCCTCAACAGCCGGCAGAATAGCTGAGTTTTCACCGATCTTCTGACGTGGCCGTCC 1293
          |||||||  ||||  || ||| | |  || |   |||| | | | ||||  | | ||||||
Db   3170 GCCACCCGACAATGGCTGGCAGGATCGGCGAGCTCTTCACTGACCTCCTGACAAAGGCTCC 3229

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Db   3230 CCTCGCCCACGCCACCCCACAACTTCACGCGAGCCTCCATTTCCACAAGACTATTTCCA 3289

Qy   1354 GCATCTCCACTTCTTCTGCCTCGCATGGAAAGCTACCACTCGTCGATGGCCCAACCAGCTGAC 1413
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Db   3290 GAACTCTCCACTTCTTCTGCCTGGAAAAGCTTCCAAACTGACAGCTCCCCAACCAGCTGAC 3349
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REFERENCE   3
AUTHORS   Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P.,
            Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M.,
            Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A.,
            Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K.,
            Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M.,
            Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,K., Matsuura,K., Kawai,J.,
            Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.
TITLE   RIKEN integrated sequence analysis (RISA) system--384-format
            sequencing pipeline with 384 multicapillary sequencer
JOURNAL   Genome Res. 10 (11), 1757-1771 (2000)
MEDLINE   20530913
PUBMED   11076861
REFERENCE   4
AUTHORS   The RIKEN Genome Exploration Research Group Phase II Team and the
            FANTOM Consortium.
TITLE   Functional annotation of a full-length mouse cDNA collection
JOURNAL   Nature 409, 685-690 (2001)
REFERENCE   5
AUTHORS   The FANTOM Consortium and the RIKEN Genome Exploration Research
            Group Phase I & II Team.
TITLE   Analysis of the mouse transcriptome based on functional annotation
            of 60,770 full-length cDNAs
JOURNAL   Nature 420, 563-573 (2002)
REFERENCE   6 (bases 1 to 4240)
AUTHORS   Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Bono,H., Carninci,P.,
            Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hashizume,W.,
            Hayashida,K., Hayatsu,N., Hiraoka,T., Hiramoto,K., Hirozane,T.,
            Hori,F., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Kasukawa,T.,
            Katoh,H., Kawai,J., Kojima,Y., Kondo,S., Konno,H., Kurata,M.,
            Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Murata,M.,
            Nakamura,M., Nishi,K., Nomura,K., Numazaki,R., Ohno,M., Ohsato,N.,
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            Sano,H., Sasaki,D., Shibata,K., Shinagawa,A., Shiraki,T.,
            Sogabe,Y., Tagami,M., Tagawa,A., Takahashi,F., Takaku-Akahira,S.,
            Takeda,Y., Tanaka,T., Tomaru,A., Toya,T., Yasunishi,A.,
            Muramatsu,M. and Hayashizaki,Y.
TITLE   Direct Submission
JOURNAL   Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of
            Physical and Chemical Research (RIKEN), Laboratory for Genome
            Exploration Research Group, RIKEN Genomic Sciences Center (GSC),
            RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,
            Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp,
            URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222,
            Fax:81-45-503-9216)
COMMENT   cDNA library was prepared and sequenced in Mouse Genome
            Encyclopedia Project of Genome Exploration Research Group in Riken
            Genomic Sciences Center and Genome Science Laboratory in RIKEN.
            Division of Experimental Animal Research in Riken contributed to
            prepare mouse tissues.
            Please visit our web site for further details.
            URL:http://genome.gsc.riken.go.jp/
            URL:http://fantom.gsc.riken.go.jp/.
FEATURES   Location/Qualifiers
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                     /organism="Mus musculus"
                     /mol_type="mRNA"
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                     /note="similar to CYTOSOLIC PHOSPHOLIPASE A2 BETA [Homo
                     sapiens] (SPTR|O95712, evidence: FASTY, 70.9%ID,
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ORIGIN

Query Match   51.3%; Score 1129.8; DB 11; Length 4240;
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/note="Organ: brain; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: EcoRV (destroyed); RNA source anonymous pool of 3
fetal brains, female age 20 weeks, female age 24 weeks,
and male age 26 weeks. Library is oligo-dT primed and
directionally cloned (EcoRV site is destroyed upon
cloning). Average insert size 1.7 kb, insert size range
0.7-3.5 kb. Library is normalized and enriched for
full-length clones and was constructed by C. Gruber
(Invitrogen). Research Genetics tracking code 017. Note:
this is a NIH_MGC Library."

ORIGIN

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Query Match      40.5%;   Score 892.8;  DB 12;   Length 1131;
Best Local Similarity  93.4%;   Pred. No. 3.8e-168;
Matches 998;  Conservative  0;  Mismatches  60;  Indels  11;  Gaps  6;

Qy   627 ACCTTTATGAGAGACCCAGAGTGGTCTCAGAGGACCTGGCAGGGCCCACTGAGTTGCTGA  686
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Db    18 ATCTTTATGAGAGACCCAGAGTGGTCTCAGAGGACCTGGCAGGGCCCACTGAGTTGCTGA   77

Qy   687 AGACCCAGGTGACCAAGAACAAGCTGGGTGTGCTGGCCCCCAGCCAGCTGCAGCCGGTACC  746
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy   747 GGCAGGAGCTGGCCGAGCGTGCCGCGCTTGGGCTACCAAGCTGCTTCACCAACCTGTGGG   806
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Db   138 GGCAGGAGCTGGCCGAGCGTGCCGCGCTTGGGCTACCAAGCTGCTTCACCAACCTGTGGG   197

Qy   807 CCCTCATCAACGAGCGCGCTGCTGCAGAACCCTGCCATCTACTGTGCCCTCAACACCAAAG  866
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Qy   867 GGGAGAGCCCTGAGTCATGCCACAGAACCCTCTGCCCATCTACTGTGCCCTCAACACCAAAG  926
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             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   498 ACCTGTATGCAGCAACCTCCAGGACAGCAGCTTATACTGGGCCTCAGGCCTCAGAGCCCAGCCAGTTCT   557

Qy  1167 GGGACCGCTGGGTCAGGAACCAGGCCAACCTGGACAAGAGGAGCAAGAGCAGGTCCCCCTTCTCGAAGA  1226
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Qy  1227 TAGAAGAACCACCCTCAACAGCCGGCAGAATAGCTGAGTTTTTCACGATCTTCTGACGT  1286
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Qy  1287 GGCGTCCACTGGCCCAGGCCACACATAATTTCCTGCGTGCCTCCATTTCCACAAAGACT  1346
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Qy  1347 ACTTTCAGCATCCCACTTCTCCACATGGAAAGCTACCACTCTGATGGCGTCCCCAACC  1406
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Qy  1407 AGCTGACACCCCTGGAGCCCCGAGCCCTGTGCCTCGTGGATGTTGGCTACCTCATCAATACCA  1466
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Qy  1467 GCTGCTGCCTGCCCCCTCCTGCAGCCCCTGCAGCCGGGACGTGGACC-TCATCCTGTCATTGGACTAC  1525
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RESULT 2
BM928260
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LOCUS       BM928260                1131 bp    mRNA    linear   EST 12-MAR-2002
DEFINITION  AGENCOURT_6699873 NIH_MGC_121 Homo sapiens cDNA clone IMAGE:5770097
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ACCESSION   BM928260
VERSION     BM928260.1  GI:19378639
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1131)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Life Technologies, Inc.
            cDNA Library Preparation: Life Technologies, Inc.
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Agencourt Bioscience Corporation
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM12832  row: j  column: 18
            High quality sequence stop: 629.
FEATURES             Location/Qualifiers
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Db  3350 ACCCTGAGCCCCACCTGCTGCCTCGTGGATGTTGGCTATCTCATCAATACTAGCTGCCC  3409

Qy  1474 GCCCCTCCTGCAGCCCACTGGGACGTGGACCTCATCCTGTCATTGGACTACACCTCCA  1533
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Db   151  TGAGCAGGAGGAAGCAGGTGTGGCGCGGCCTTGAGGCAGGCCCTGCAGCTGGACGGAG  210
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Qy   462  ACCTGCAGGAGGATGAGATCCCAGTGGTAGCTATTATGGGCCACTGGTGGTGGGATCCGGG  521
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Db   211  ACCTGCAGGAGGATGAGATCCCAGTGGTAGCTATTATGGGCCACTGGTGGTGGGATCCGGG  270

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Qy   762  AGCGTGCCGCCTTGGCTACCCAAGCTGCTTCACCACCGTGGCCCTCATCAACGAGG  821
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   511  AGCGTGCCGCCTTGGCTACCCAAGCTGCTTCACCACCGTGGCCCTCATCAACGAGG  570

Qy   822  CGGTGCTGCATGATGAGCCCATGATCATCACAAGCTCTCAGATCAACGGAGGCCCTGAGTC  881
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   571  CGTTGCTGCATGATGAGCCCATGATCATCACAAGCTCTCAGATCAACGGAGGCCCTGAGTC  630

Qy   882  ATGGCCAGAACCCTCTGCCATCTACTGTGCCCTCAACACCAAAGGGCAGAGAGCCTGACCA  941
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   631  ATGGCCAGAACCCTCTGCCATCTACTGTGCCCTCAACACCAAAGGGCAGAGAGCCTGACCA  690

Qy   942  CTTTTGAATTTGGGGAGTGGTGCGGAGTTCTCTCCCTACGAGGTCGGCTTCCCCAAGTACG  1001
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   691  CTTTTGAATTTGGGGAGTGGTGCGGAGTTCTCTCCCTACCAGGCCGGCTTCCCCAAGTACG  750

Qy   1002 GGGCCTTCATCCCCCTGAGCTCTTTGGCTCCGAGTTC-TTTATGGGGCCAGCTGATGAAG  1060
          |||||||||||||||||||||||||||||||||||| |||||||||||||||||||||
Db   751  GGGCCTTCCTCCCCCTGAGCTCTTTGGCTCCGAGTTCTTTTATGGGGCAACTGATGAAA  810

Qy   1061 AGGCTTCCTGAGTCCCGCATCTGCTTCTT  1089
          ||||||||||||||||||||||||||||
Db   811  AAGGCTTCCTGGATTCCCCCATTCTGCCCT  839
```

```
RESULT 4
BI768993
LOCUS       BI768993                  949 bp    mRNA      linear   EST 25-SEP-2001
DEFINITION  603058145F1 NIH_MGC_122 Homo sapiens cDNA clone IMAGE:5207531 5',
            mRNA sequence.
ACCESSION   BI768993
VERSION     BI768993.1  GI:15760571
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 949)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Life Technologies, Inc.
            cDNA Library Preparation: Life Technologies, Inc.
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Incyte Genomics, Inc.
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM11520  row: j  column: 12
```

```
Db   858  GCTGCCTGCCCCCTGCTGCCAGCCCACTCGGGACGTGGACCTTCATCTGNNCATTGGACTAC  917
          |||||||||||||||||||||||||||||||||||||||||||  |||||||||
Qy   1526 AACCTCCACGGAGCCAGCCTTCCAGCAGTTGCAGCT--CCTGGGCCGGTTC--TGCCAGGAGCA  1581
          ||||| ||||  |||| | ||||| |  ||| ||  ||  | |||| |
Db   918  AACCTTCACGGAACCNTCCAGCAGTTGCAGTTGCAGTTCAGTTCCTTGGGCCGGTTCCTGCCCCCGGAGCC  977

Qy   1582 GGGGA--TCCCGTTCCCACCCATCTCG--CCCAGCCCCGAAGAGACAGCTCCAGCCTC---G  1635
          ||||   |||  ||||||||||||| |   || ||| ||||||||||||||||| |
Db   978  GGGGAATCCCGTTCCCCACCCATTTCGCCCCAGCCCCAAAGAGACGGTTTTCGGCCCTGGG  1037

Qy   1636 GGAGTGCCACACCTTCTCCGACCCCACTGCCCCGAGCCCCTGCGGTG  1684
          |||||||||| |||||||||||||||||||||||||||||||||
Db   1038 GAAGGCCCACACCCTTTTTGGACCCCACTGCCCACCTGCCCGGAAACCCCCTGGG  1086
```

```
RESULT 3
CA488226
LOCUS       CA488226                  957 bp    mRNA      linear   EST 14-NOV-2002
DEFINITION  AGENCOURT_10807975 MAPcL Homo sapiens cDNA clone IMAGE:6719969 5',
            mRNA sequence.
ACCESSION   CA488226
VERSION     CA488226.1  GI:24949530
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 957)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Kristi A. Egland, Ira Pastan
            cDNA Library Preparation: Invitrogen Corp
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Agencourt Bioscience Corporation
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM14278  row: l  column: 17
            High quality sequence stop: 611.
FEATURES             Location/Qualifiers
     source          1..957
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:6719969"
                     /cell_line="ZR-75-1, MCF7, SK-BR-3, MDA-MB-231,
                     hTERT-HME1, LNCaP"
                     /lab_host="EMDH10B"
                     /clone_lib="MAPcL"
                     /note="Vector: pCMV-SPORT6; Site_1: EcoRV; Site_2: Not I;
                     Subtracted with brain, liver, lung, kidney and muscle.
                     Directionally cloned. Priming method: oligo-dT. Average
                     insert size: 1800 bp. Library amplification: 26,000 fold.
                     Kristi A. Egland, James J. Vincent, Robert Strausberg,
                     Bungkook Lee & Ira Pastan: Discovery of new breast
                     cancer genes encoding membrane and secreted proteins.
                     Manuscript submitted."
ORIGIN
Query Match          31.6%;  Score 697;  DB 14;  Length 957;
Best Local Similarity 96.5%;  Pred. No. 5.9e-129;
Matches  723;  Conservative  0;  Mismatches  25;  Indels  1;  Gaps  1;
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```
Qy   342  GACTGAGGGAGCTGCCGTGCGACTGGGCTTCGGGCCCTGTGCAGAGGAGGAGGCCTTCC  401
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   91   GACTGAGGGAGCTGGCCGTGCGACTGGGCTTCGGGCCCTGTGCAGAGGAGGAGGCCTTCC  150

Qy   402  TGAGCAGGAGGAAGCAGGTGGTGGCGCGGCCTTGGCGGCCCTGAGGCAGGCCCTGCAGCTGGATGAG  461
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
```

```
Qy   1711 GACA--CCGGAGGAGGCGGCAGCTGGGAGGTGAACCTGT--CTTCATCGGACTCTCCCTA 1767
          ||||  ||||||||||||||||||||||||||||||||||  ||||||||||||||||||
Db    720 GACACCCCGGAGGAGGCGGCAGCTGGGAGGTGAACCTGTTCTTCATCGGACTCTCCCTA 779

Qy   1768 CCACTACACG-AAGGTGACCTACAGCCAGGAGG--ACGTGACACAAGCTGTGCACCTGA 1823
          ||||||||| ||||||||||||||||||||||| ||||||||||||||||||||||||
Db    780 CCACTACACGAAATGTGACTTACAGCCAGGAGGAACCGTGGGACCAAGCTGTGCACTGAA 839

Qy   1824 CACATTACAATGTCTGCAACAACAGGAGACAGCTGCTCGGAGGCTCTGCGCCAGGCAGTGC 1883
          |||||||| |||||||  ||||||||||||| ||||| |||  ||||||||| |||||||
Db    840 CACATTACAAATGTCTGCAAAACCA-GAGCAAGTGTTAAGGCTCTG-GCCAGGCAGTGC 897

Qy   1884 AGCGGAGGCGGCAGCGGCAGCGCCCCACTGATGGCCGGGGCC 1923
          |||||||||||||||||||  |||||| |||||||||||||
Db    898 AGGGAAGGCGAACCG---AGGCCCCTTGATGGCCGGGGCCC 934
```

RESULT 5
BU68449/c

LOCUS   BU68449   759 bp   mRNA   linear   EST 07-OCT-2002
DEFINITION   UI-CF-EC1-aea-j-17-0-UI.s1 UI-CF-EC1 Homo sapiens cDNA clone
             UI-CF-EC1-aea-j-17-0-UI 3', mRNA sequence.
ACCESSION   BU68449
VERSION   BU68449.1 GI:23454244
KEYWORDS   EST.
SOURCE   Homo sapiens (human)
  ORGANISM   Homo sapiens
             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
             Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 759)
  AUTHORS   Bonaldo,M.F., Lennon,G. and Soares,M.B.
  TITLE   Normalization and subtraction: two approaches to facilitate gene
             discovery
  JOURNAL   Genome Res. 6 (9), 791-806 (1996)
   MEDLINE   97044477
   PUBMED   8889548
COMMENT   Contact: McCray, PB
             McCray Lab
             University of Iowa
             2024 University of Iowa Med Labs, Iowa City, IA 52242, USA
             Tel: 319 356 4866
             Fax: 319 356 7171
             Email: paul-mccray@uiowa.edu
             Tissue Procurement: Dr. M. J. Welsh, University of Iowa
             cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
             cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
             DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
             Clone Distribution: Researchers may obtain clones from Research
             Genetics (www.resgen.com) or from Open Biosystems
             (www.openbiosystems.com).
             Seq primer: M13 FORWARD
             POLYA=Yes.
FEATURES   Location/Qualifiers
     source   1..759
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="UI-CF-EC1-aea-j-17-0-UI"
                     /tissue_type="Lung"
                     /dev_stage="Adult and Fetal"
                     /lab_host="DH10B (Life Technologies) (T1 phage resistant)"
                     /clone_lib="UI-CF-EC1"
                     /note="Organ: Lung; Vector: pT7T3-Pac (Pharmacia) with a
                     modified polylinker; Site_1: EcoR I; Site_2: Not I;
                     UI-CF-EC1 is a normalized cDNA library containing the
                     following tissue(s): Normal lung from adult and from fetal
                     day 64, day 87, week 19 and week 42. The library was
                     constructed according to Bonaldo, Lennon and Soares,
                     Genome Research, 6:791-806, 1996. First strand cDNA
                     synthesis was primed with an oligo-dT primer containing a
                     Not I site. Double stranded cDNA was ligated to an EcoR I
                     adaptor, digested with Not I, and cloned directionally
                     into pT7T3-Pac vector. The oligonucleotide used to prime
```

FEATURES      High quality sequence stop: 900.
     source          Location/Qualifiers
                     1..949
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:5207531"
                     /lab_host="DH10B"
                     /clone_lib="NIH_MGC 122"
                     /note="Organ: pooled lung and spleen; Vector: pCMV-SPORT6;
                     Site_1: NotI; Site_2: EcoRV (destroyed); RNA source
                     anonymous pool of 24 week female lung, 16 week female
                     spleen, and 20-22 week male spleens. Library is oligo-dT
                     primed and directionally cloned (EcoRV site is destroyed
                     upon cloning). Average insert size 1.4 kb, insert size
                     range 1-3 kb.Library is normalized and enriched for
                     full-length clones and was constructed by C. Gruber
                     (Invitrogen). Research Genetics tracking code 026. Note:
                     this is a NIH_MGC Library."

ORIGIN

Query Match    30.7%;   Score 677.6;   DB 12;   Length 949;
Best Local Similarity   90.4%;   Pred. No. 4.5e-125;
Matches  850;  Conservative  0;  Mismatches  44;  Indels  46;  Gaps  10;

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Qy   1024 CTTTGGCTCCGAGTTCTTTATGGGGCAGCTGATGAAGAGGCTTCCTGAGTCCCGCATCTG 1083
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 CTTTGGCTCCGAGTTCTTTAATGGGGCAGCTGATGAAGAGGCTTCCTGAGTCCCGCATCTG 60

Qy   1084 CTTCTTAGAAGGTATCTGGAGACAACCTGTATGCAGCCAACCTCCAGGACAGCTTATATCTG 1143
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 CTTCTTAGAAGGTATCGGAGACAACCTGTATGCAGCCAACCTCCAGGACAGCTTATATCTG 120

Qy   1144 GGCCTCAGAGCCCAGCCAGTTCTGGGACCGCTGGGTCAGGAACCAGGCCAACCTGGACAA 1203
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 GGCCTCAGAGCCCAGCCAGTTCTGGGACCGCTGGGTCAGGAACCAGGCCAACCTGGACAA 180

Qy   1204 GGAGCAGGTCCCCCTTCTGAAGATAGAAGAACCACCCTCAACAGCGCCGGCAGAATAGCTGA 1263
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 GGAGCAGGTCCCCCTTCTGAAGATAGAAGAACCACCCTCAACAGCCCGGCAGGATAGCTGA 240

Qy   1264 GTTTTTCACCGATCTTCTGACGTGGCGTCCACTGGCCCAGGCCACACATAATTTCCTGCCG 1323
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 GTTTTTCACCGATCTTCTGACGTGGCGTCCACTGGCCCAGGCCACACATAATTTCCTGCCG 300

Qy   1324 TGGCCTCCATTTCCACAAAGACTACTTTCAGCATCCTCACTTCTCCACATGGAAAGCTAC 1383
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 TGGCCTCCATTTCCACAAAGACTACTTTCAGCATCCTCACTTCTCCACATGGAAAGCTAC 360

Qy   1384 CACTCTGGATGGGCTCCCCAACCAGCTGACACCCTGGAGCCCCACCTGTGCCTGCTGGA 1443
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 CACTCTGGATGGGCTCCCCAACCAGCTGACACCCTGGAGCCCCACCTGTGCCTGCTGGA 420

Qy   1444 TGTTGGCTACCTCATCAATACCAGTGCTGCCTGCCCCTCCTGGGAGCCCACTCGGGACGTGGA 1503
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421 TGTTGGCTACCTCATCAATCACCAGTGCCCTGCCCCTCCTGCCAGCCCACTCGGGACGTGGA 480

Qy   1504 CCTCATCCTGTCATTGGACTACAACCTCACGGAGAGCCTTCCAGCAGTTGCAGCTCCTGGG 1563
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    481 CCTCATCCTGTCATTGGACTACAACCTCACGGAGAGCCTTCCAGCAGTTGCAGCTCCTGGG 540

Qy   1564 CCGGTTCTGCCAGGAGCAGGAGCAGGGGATCCCGTTCCCCATCTCGCCCAGCCCCGAAGAGCA 1623
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    541 CCGGTTCTGCCAGGAGCAGGAGCAGGGGATCCCGTTCCCCATCTCGCCCAG-CCCGAAGAGCA 599

Qy   1624 GCTCCAGCCTC-GGGAGTGCCACACTTCTCCGACCCGCCCCCGGAGCCCCTGCCG 1682
          ||||||||||| ||||||||||||||||||||||||||||||||||||||||||
Db    600 GCTCCAGCCTCGGGGAGTGCCACACCTTCTCCGACCCCACCCGCCCCCGGAGCCCCTGCCG 659

Qy   1683 TGCTGCACTTTC-----------------CTCTGGGGTCCGGCG 1710
          ||||||||||| |||||||||||||
Db    660 TGCTGCACTTTCCTCTGGTCAGCGGACTCCCTCCGGGAGTACTCGGCCCTGGGTCCGGCG 719
```

VERSION   BM718675.1 GI:19037020
KEYWORDS   EST.
SOURCE   Homo sapiens (human)
ORGANISM   Homo sapiens
             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
             Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 647)
AUTHORS   Bonaldo,M.F., Lennon,G. and Soares,M.B.
TITLE   Normalization and subtraction: two approaches to facilitate gene
             discovery
JOURNAL   Genome Res. 6 (9), 791-806 (1996)
MEDLINE   97044477
PUBMED   8889548
COMMENT   Contact: Soares, MB
             Coordinated Laboratory for Computational Genomics
             University of Iowa
             375 Newton Road, 4156 MEBRF, Iowa City, IA 52242, USA
             Tel: 319 335 8250
             Fax: 319 335 9565
             Email: bento-soares@uiowa.edu
             Tissue Procurement: Dr. Gregg Hageman
             cDNA Library preparation: Dr. M. Bento Soares, Univeristy of Iowa
             cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
             DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
             Clone Distribution: Researchers may obtain clones from Research
             Genetics (www.resgen.com).
             Seq primer: M13 Reverse.
FEATURES   Location/Qualifiers
     source   1..647
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="UI-E-EO1-ajc-i-21-0-UI"
                     /tissue_type="fetal eye"
                     /dev_stage="fetal"
                     /lab_host="DH10B (Life Technologies) (T1 phage resistant)"
                     /clone_lib="UI-E-EO1"
                     /note="Organ: eye; Vector: pT7T3-Pac (Pharmacia) with a
                     modified polylinker; Site_1: EcoR I; Site_2: Not I;
                     UI-E-EO1 is a normalized cDNA library containing the
                     following tissue(s): fetal eye. The library was
                     constructed according to Bonaldo, Lennon and Soares,
                     Genome Research, 6:791-806, 1996. First strand cDNA
                     synthesis was primed with an oligo-dT primer containing a
                     Not I site. Double stranded cDNA was ligated to an EcoR I
                     adaptor, digested with Not I, and cloned directionally
                     into pT7T3-Pac vector. The oligonucleotide used to prime
                     the synthesis of first-strand cDNA contains a library tag
                     sequence that is located between the Not I site and the
                     (dT)18 tail. The sequence tag for this library is
                     CGCTATACC. This library was created for the program, Gene
                     Discovery in the Visual System, supported by National Eye
                     Institute (NEI)."
ORIGIN

Query Match   28.7%;   Score 633.2; DB 12; Length 647;
Best Local Similarity   99.4%;   Pred. No. 3.5e-116;
Matches   635;   Conservative   0;   Mismatches   4;   Indels   0; Gaps   0;

Qy   470 GAGGATGAGATCCCAGTGCGTAGTCATTATGGCCACTGGTGCGTGGGATCCGGCCAATGACT 529
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 GAGGATGAGATCCCAGTGCGTAGTCATTATGGCCACTGGTGCGTGGGATCCGGCCAATGACT   60

Qy   530 TCCCTGTATGGGCAGCTGGCTGGCCTGAAGGAGCTGGGCCTTCTTGGATTGCGTCTCCTAC 589
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 TCCCTGTATGGGCAGCTGGCTGGCCTGAAGGAGCTGGGCCTTCTTGGATTGCGTCTCCTAC 120

Qy   590 ATCACCCGGGCCTCGGGCTCCAACCTTTATGAGGACCCCAGAGTGG 649
           |||||||||||||||||||||||||||||||||||||||||||||
Db   121 ATCACCCGGGCCTCGGGCTCCAACCTTTATGAGGACCCCAGAGTGG 180

Qy   650 TCTCAGAAGGACCTGCAGGGCCCACTGAGTTGCTAGACCAGTGACCAAGAACAAG 709
           ||||||||||||||||||||||||||||||||||||||||||

RESULT 6
BM718675
LOCUS   BM718675   647 bp   mRNA   linear   EST 01-MAR-2002
DEFINITION UI-E-EO1-ajc-i-21-0-UI.r1 UI-E-EO1 Homo sapiens cDNA clone
            UI-E-EO1-ajc-i-21-0-UI 5', mRNA sequence.
ACCESSION   BM718675

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the synthesis of first-strand cDNA contains a library tag
sequence that is located between the Not I site and the
(dT)18 tail. The sequence tag for this library is
AAGTGCTTAC.
TAG_TISSUE=Normal Lung Epithelial Cells Tissue nos 369-371
and 380-383
TAG_LIB=UI-CF-EC1
TAG_SEQ=AAGTGCTTAC"

ORIGIN

Query Match   30.0%;   Score 661.4; DB 13; Length 759;
Best Local Similarity   94.2%;   Pred. No. 7.9e-122;
Matches   711;   Conservative   0;   Mismatches   11;   Indels   33; Gaps   1;

Qy   1483 GCAGCCCACTCGGGACGTGGACCTCATCCTGTCATTGGACTACAACCTCCACGGAGGCCTT 1542
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   759 GCAGCCCACTCGGGACGTGGACCTCATCCTGTCATTGGACTACAACCTCCACGGAGGCCTT 700

Qy   1543 CCAGCAGTTGCAGCTCCTGGGCCGGTTCTGCGAGAGCAGGGGATCCGTTCCCACCCAT 1602
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   699 CCAGCAGTTGCAGCTCCTGGGCCGGTTTGCCAGGAGCAGGGGATCCGTTCCCACCCAT 640

Qy   1603 CTCGCCCCAGCCCGGAAGAGCAGCTCCAGCCTCGGGAGTGCCACACCTTCTCCGACCCCAC 1662
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   639 CTCGCCCCAGCCCGGAAGAGCAGCTCCAGCCTCGGGAGTGCCACACCTTCTCCGACCCCAC 580

Qy   1663 CTGCCCCCGGAGCCCCTGCGGTGCTGCACTTT------------------- 1693
           ||||||||||||||||||||||||||||||||
Db   579 CTGCCCCGGAGCCCCTGCGGTGCTGCACTTTCCTCTGGTCAGCGACTCCTTCCGGGAGTA 520

Qy   1694 ---TCCTCTGGGGTCCGGCGGACACCCGGACAGGAGGCCGGCAGCTGGGGAGGTGAACCTGTC 1749
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   519 CTCGGCCCTGGGGTCCGGGACACCCGGGAGACACCCGAGAGGAGGCCGGCAGCTGGGGAGGTGAACCTGTC 460

Qy   1750 TTCATCGGACTCTCCCTACCACTACACAGAAGTGACCTACAGCAGAGGACGTGGACAA 1809
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   459 TTCATCGGACTCTCCCTACCACTACACAGAAGTGACCTACAGCAGAGGACCAGGGACAA 400

Qy   1810 GCTGCTGCACTGACACATTACAATGTCTGCAACAACCAGGAGCGCTGCTGAGGGTCT 1869
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   399 GCTGCTGCACTGACACATTACAATGTCTGCAACAACCAGGAGCGCTGCTGAGGGTCT 340

Qy   1870 GGGCCAGGCAGTGCAGCGAGGCGGAGGCGGCAGCGCCCACTGAGTGCCGGGGCCCCTGCC 1929
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   339 GGGCCAGGCAGTGCAGCGAGGCGGAGGCGGCAGCGCCCACTGAGTGCCGGGGCCCCTGCC 280

Qy   1930 ACCCCTAACTCTCATTCATTCCCTGGCTGCTGAGTTGCAGGTGGGAACTGTCATCACGCA 1989
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   279 ACCCCTAACTCTCATTCATTCCCTGGCTGCTGAGTTGCAGGTGGGAACTGTCATCACGCA 220

Qy   1990 GTGCTTCAGAGCCTCGGGCTCAGGTGGCACTGCTCCCAGGGTCCCAGGGCTCAGGGCTGGGAG 2049
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   219 GTGCTTCAGAGCCTCGGGCTCAGGTGGCACGGTCCCAGGGTCCCAGGGCTCAGGGCTGGGAG 160

Qy   2050 CTCCCTTGCGCCTCAGCAGTTGCAGTGGGGTAAGGAGGCCAAGCCCATTTGTGTAATCA 2109
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   159 CTCCCTTGCGCCTCAGCAGTTGCAGTGGGGGGTAAGGAGGCCAAGCCCATTTGTGTAATCA 100

Qy   2110 CCCAAAACCCCCGGCCCGGCCTGTGTTTCCCTTCTGCGCTACCTTGAGTAGTTGGAGCA 2169
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   99 CCCAAAACCCCCGGCCCGGCCTGTGCCTGTTTCCCTTCTGCGCTACCTTGAGTAGTTGGAGCA   40

Qy   2170 CTTGATACATCACAGACTCATACAAAAAAAAAAAAA 2204
           |||||||||||||||||||||||||||
Db   39 CTTGATACATCACAGACTCATACAAAAAAAAAAAAA   5

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Db   181 TCTCAGAAGGACCTGGCAGGGCCCACTGAGTTGCTGAAGACCCAGTGACCAAGAACAAG 240

Qy   710 CTGGGTGTGCTGGGCCCCAGCCAGCTGCAGCGGTACCGGCAGGAGCGTGGCCGAGCGTGCC 769
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241 CTGGGTGTGCTGGGCCCCAGCCAGCTGCAGCCGCAGCGGTACCGGCAGGAGCGTGGCCGAGCGTGCC 300

Qy   770 CGCTTGGGCTACCCAAGCTGCTTCACCAAACCTGTGGGCCCTCATCAACGAGGGCTGCTG 829
         ||||||||||||||||||||||||||||||||||| ||||||||||||||||||||
Db   301 CGCTTGGGCTACCCAAGCTGCTTCACCAAACCTGTGGGCCCTCATCAATGAGGGCTGCTG 360

Qy   830 CATGATGAGCCCCATGATCACAAGCTCTCAGATCAACGGGAGGCCCTGAGTCATGGCCAG 889
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   361 CATGATGAGCCCCATGATCACAAGCTCTCAGATCAACGGGAGGCCCTGAGTCATGGCCAG 420

Qy   890 AACCCTCTGCCCATCTACTGTGCCTCAACACCAAAGGGCAGAGCTGCCACTTTTGAA 949
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   421 AACCCTCTGCCCATCTACTGTGCCCTCAACACCAAAGGGCAGAGCCTGACCACTTTTGAA 480

Qy   950 TTTGGGGAGTGGTGTGCGAGTTCTCTCCTACGAGGTCGGCTTCCCCAAGTACGGGGGCCTTC 1009
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   481 TTTGGGGAGTGGTGTGCGAGTTCTCTCCTACGAGGTCGGCTTCCCCAAGTACGGGGGCCTTC 540

Qy  1010 ATCCCCCCTGAGCTCTTTGGCTCCGAGTTCTTTATGGGGCAGCTGATGAAGAGAGGCTTCCT 1069
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   541 ATCCCCCCTGAGCTCTTTGGCTCCGAGTTCTTTATGGGGCAGCTGATGAAGAGAGGCTTCCT 600

Qy  1070 GAGTCCCGCATCTGCTTCTTAGAAGGTATCTGAGCAAC 1108
         |||||||||||||||||||||||||||||||||
Db   601 GAGTCTCGCATCGCATTCTTCTTANAAGGTATCTGAGCACC 639
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RESULT 7
BM982475/c
LOCUS       BM982475            701 bp    mRNA        linear   EST 21-FEB-2003
DEFINITION  UI-CF-EN1-acq-e-01-0-UI.s1 UI-CF-EN1 Homo sapiens cDNA clone
            UI-CF-EN1-acq-e-01-0-UI 3', mRNA sequence.
ACCESSION   BM982475
VERSION     BM982475.1  GI:19606011
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 701)
  AUTHORS   Bonaldo,M.F., Lennon,G. and Soares,M.B.
  TITLE     Normalization and subtraction: two approaches to facilitate gene
            discovery
  JOURNAL   Genome Res. 6 (9), 791-806 (1996)
   MEDLINE   97044477
   PUBMED    8889548
COMMENT     Contact: McCray, PB
            McCray Lab
            University of Iowa
            2024 University of Iowa Med Labs, Iowa City, IA 52242, USA
            Tel: 319 356 4866
            Fax: 319 356 7171
            Email: paul-mccray@uiowa.edu
            Tissue Procurement: Dr. M. J. Welsh, University of Iowa
            cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
            cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
            DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
            Clone Distribution: Researchers may obtain clones from Research
            Genetics (www.resgen.com) or from Open Biosystems
            (www.openbiosystems.com).
            Seq primer: M13 FORWARD
            POLYA=Yes.
FEATURES             Location/Qualifiers
     source          1..701
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="UI-CF-EN1-acq-e-01-0-UI"
                     /tissue_type="Primary Lung Cystic Fibrosis Epithelial
```

```
                     Cells"
                     /dev_stage="Adult"
                     /lab_host="DH10B (life Technologies) (T1 phage resistant)"
                     /clone_lib="UI-CF-EN1"
                     /note="Organ: Lung; Vector: pT7T3-Pac (Pharmacia) with a
                     modified polylinker; Site_1: EcoR I; Site_2: Not I;
                     UI-CF-EN1 is a normalized cDNA library containing the
                     following tissue(s): Primary Lung Cystic Fibrosis
                     Epithelial Cells. The library was constructed according to
                     Bonaldo, Lennon and Soares, Genome Research, 6:791-806,
                     1996. First strand cDNA synthesis was primed with an
                     oligo-dT primer containing a Not I site. Double stranded
                     cDNA was ligated to an EcoR I adaptor, digested with Not
                     I, and cloned directionally into pT7T3-Pac vector. The
                     oligonucleotide used to prime the synthesis of
                     first-strand cDNA contains a library tag sequence that is
                     located between the Not I site and the (dT)18 tail. The
                     sequence tag for this library is CTGCTCAGGT.
                     TAG TISSUE=Human Lung Epithelial Cell Lines untreated LPS
                     6hr_to LPS 24h
                     TAG_LIB=UI-CF-EN1
                     TAG_SEQ=CTGCTCAGGT"
ORIGIN

Query Match             27.9%;  Score 615.2;  DB 12;  Length 701;
Best Local Similarity   94.7%;  Pred. No. 1.4e-112;
Matches   660;  Conservative    0;  Mismatches    0;  Indels    4;  Gaps   1;
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Qy  1541 TTCCAGCAGTTGCAGCTCCTGGCCCGGTTCTGCCAGGAGCAGGAGGGGGATCCCGTTCCGACCC 1600
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   701 TTCCAGCAGTTGCAGCTCCTGGCCCGGTTNTGCCAGGAGCAGGAGGGGGATCCCGTTCCGACCC 642

Qy  1601 ATCTCGCCCAGCCCCGAAGAGCAGCTCCAGCTCTGGGAGTGCCACACCTTCTCCGACCC 1660
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   641 ATCTCGCCCAGCCCCGAAGAGCAGCTCCAGCTCTGGGAGTGCCACACCTTCTCCGACCC 582

Qy  1661 ACCTGCCCCGGAGCCCCTGCGGTGCTGCACTTT----------------------- 1693
         ||||||||||||||||||||||||||||||||||
Db   581 ACCTGCCCCGGAGCCCCTGCGGTGCTGCACTTTCCTCTGGTCAGCGACTCCTTCCGGGAG 522

Qy  1694 ------TCCTCTGGGGTCCGGCGGACACCCGAGGAGGCGGCAGCTGGGGAGGTGAACCTG 1747
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   521 TACTCGGCCCCTGGGGTCCGGCGGACACCCGAGGAGGCGGCAGCTGGGGAGGTGAACCTG 462

Qy  1748 TCTTCATCGGACTCTCCCTACCACTACAGAGGTGACCTACAGCCAGGAGGACGTGGAC 1807
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   461 TCTTCATCGGACTCTCCCTACCACTACAGAGGTGACCTACAGCCAGGAGGACGTGGAC 402

Qy  1808 AAGCTGCTGCACCTGACACATTACAATGTCTGCAACAACCAGGAGCAGCTGCTGGAGGCT 1867
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   401 AAGCTGCTGCACCTGACACATTACAATGTCTGCAACAACCAGGAGCAGCTGCTGGAGGCT 342

Qy  1868 CTGCGCCAGGCAGTGCAGCGGCGGCAGGCGGCAGGCGCCCACTGATGCCGGGGCCCCTG 1927
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   341 CTGCGCCAGGCAGTGCAGCGGCGGCAGGCGGCAGGCGCCCACTGATGCCGGGGCCCCTG 282

Qy  1928 CCACCCCTAACTCTCATTCATTCCCTGGCTGCAGTTGCAGTGGGAACTGTCATCACG 1987
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   281 CCACCCCTAACTCTCATTCATTCCCTGGCTGCAGTTGCAGTGGGAACTGTCATCACG 222

Qy  1988 CAGTGCTTCAGAGCCTCGGGCTCAGGTGGCACTGTCCCAGGGTCCGAGGGCTGGG 2047
         |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   221 CAGTGCTTCAGAGCCTCGGGCTCAGGTGGCACGGTGCCAGGGTCCGAGGGCTGGG 162

Qy  2048 AGCTCCCTTGCGCCTTCAGCAGTTGCAGTGGGGTAAGGAGGCCAAGCCCATTGTGTAAT 2107
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   161 AGCTCCCTTGCGCCTTCAGCAGTTGCAGTGGGGTAAGGAGGCCAAGCCCATTGTGTAAT 102

Qy  2108 CACCCAAAACCCCCCGCCTGCCTGTTTTCCCTTCGCCTACCTTGAGTAGTTGGAG 2167
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   101 CACCCAAAACCCCCCGCCTGCCTGTTTTTCCCTTCGCCTACCTTGAGTAGTTGGAG 42

Qy  2168 CACTTGATACATCACAGACTCATACAAAAAAAAAAA 2204
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Db    41 CACTTGATACATCACAGACTTCATCACAAAAAAAAAAAA 5
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RESULT 8
CD252554
LOCUS      CD252554                 869 bp    mRNA    linear   EST 22-MAY-2003
DEFINITION AGENCOURT_14161855 NIH_MGC_181 Homo sapiens cDNA clone
           IMAGE:30374934 5', mRNA sequence.
ACCESSION  CD252554
VERSION    CD252554.1  GI:31013020
KEYWORDS   EST.
SOURCE     Homo sapiens (human)
  ORGANISM Homo sapiens
           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
           Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE  1 (bases 1 to 869)
AUTHORS    NIH-MGC http://mgc.nci.nih.gov/.
TITLE      National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL    Unpublished (1999)
COMMENT    Contact: Daniela S. Gerhard, Ph.D.
           Office of Cancer Genomics
           National Cancer Institute / NIH
           Bldg. 31 Rm10A07 Bethesda, MD 20892
           Email: cgapbs-r@mail.nih.gov
           Tissue Procurement: Dr. Michael Brownstein
           cDNA Library Preparation: Invitrogen Corp
           cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
           DNA Sequencing by: Agencourt Bioscience Corporation
           Clone distribution: MGC clone distribution information can be
           found through the I.M.A.G.E. Consortium/LLNL at:
           http://image.llnl.gov
           Plate: NDAM435  row: c  column: 07
           High quality sequence start: 6
           High quality sequence stop: 549.
FEATURES             Location/Qualifiers
     source          1..869
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:30374934"
                     /tissue_type="White Matter"
                     /dev_stage="Unknown"
                     /lab_host="DH10B-Ton A ( T1 and T5 phage resistances)"
                     /clone_lib="NIH_MGC_181"
                     /note="Vector: pCMV-SPORT6.1; Site_1: NotI; Site_2: EcoRV
                     (destroyed); Library is oligo-dT primed and directionally
                     cloned (EcoRV site is destroyed upon cloning). Average
                     insert size 1.42 kb. Library was constructed by
                     (Invitrogen). Note: this is a NIH_MGC Library."
ORIGIN
Query Match        27.6%;  Score 608;  DB 14;  Length 869;
Best Local Similarity  99.0%;  Pred. No. 3.8e-111;
Matches  622;  Conservative  0;  Mismatches  5;  Indels  1;  Gaps  1;

Qy   879 GTCATGGCCAGAACCCTGCCCATCTACTACTGTGCCTCAACACCAAAGGGCAGAGCCTGA 938
         ||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||
Db     5 GTCATGGCCAGAACCCTGCCCC-TCTACTGTGCCTCAACACCAAAGGGCAGAGCCTGA 63

Qy   939 CCACTTTTGAATTTGGGGAGTGGTGCGAGTTCTCTCCCTACGAGGTCGGCTTCCCCAAGT 998
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    64 CCACTTTTGAATTTGGGGAGTGGTGCGAGTTCTCTCCCTACGAGGTCGGCTTCCCCAAGT 123

Qy   999 ACGGGGCCTTCATCCCCTCTGAGCTTTTGGCTCCGAGTTCTTTATGGGGCAGCTGATGA 1058
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   124 ACGGGGCCTTCATCCCCTCTGAGCTTTTGGCTCCGAGTTCTTTATGGGGCAGCTGATGA 183

Qy  1059 AGAGGCTTCCTGAGTCCCGCATCTGCTTCTTAGAAGGTATCTGAGCAACCTGTATGCAG 1118
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   184 AGAGGCTTCCTGAGTCCCGCATCTGCTTCTTAGAAGGTATCTGAGCAACCTGTATGCAG 243

Qy  1119 CCAACCTCCAGGACAGCTTATACTGGGCCTCAGAGCCCAGCCAGTTCTGGGACCGCTGGG 1178
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Db   244 CCAACCTCCAGGACAGCAGTTATACTGGGCCTCAGAGCCCAGCCAGTTCTGGGACCGCTGGG 303
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Qy  1179 TCAGGAACCAGGCCAACCTGGACAAGGAGCAGTCCCCCTTCTGAAGATAGAAGAACCAC 1238
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   304 TCAGGAACCAGGCCAACCTGGACAAGGAGCAGTCCCCCTTCTGAAGATAGAAGAACCAC 363

Qy  1239 CCTCAACAGCCGCCAGAATAGCTGAGTTTTTCACCGATCTTCTGACGTGGCGTCCACTGG 1298
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   364 CCTCAACAGCCGCCAGAATAGCTGAGTTTTTCACCGATCTTCTGACGTGGCGTCCACTGG 423

Qy  1299 CCCAGGCCACACATAATTTCCTGCGTGGCCTCCATTTCCACAAAGACTACTTTCAGCATC 1358
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   424 CCCAGGCCACACATAATTTCCTGCGTGGCCTCCATTTCCACAAAGACTACTTTCAGCATC 483

Qy  1359 CTCACTTCTCCACATGGAAAGCTACCACTCTGGATGGGCTCCCAACCAGTCAGCCACCCT 1418
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   484 CTCACTTCTCCACATGGAAAGCTACCACTCTGGATGGGCTCCCAACCAGTCAGCCACCCT 543

Qy  1419 CGGAGCCCCACCTGCCTGCTGGAGGTGGCTACCTCATCAATCACCAGTGCCTGCCCCC 1478
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   544 CGGAGCCCCACCTGCCTGCTGGAGGTGGCTACCTCATCAATCACCAGTGCCTGCCCCC 603

Qy  1479 TCCTGCAGCCCACTCGGGACGTGACCT 1506
         |||||||||||| ||||||||
Db   604 TCCTGCAACCCACTCAGGAAGTGAAACT 631
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RESULT 9
BG696408
LOCUS      BG696408                 935 bp    mRNA    linear   EST 07-MAY-2001
DEFINITION 602659504F1 NCI_CGAP_Skn3 Homo sapiens cDNA clone IMAGE:4802713 5',
           mRNA sequence.
ACCESSION  BG696408
VERSION    BG696408.1  GI:13961522
KEYWORDS   EST.
SOURCE     Homo sapiens (human)
  ORGANISM Homo sapiens
           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
           Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE  1 (bases 1 to 935)
AUTHORS    NIH-MGC http://mgc.nci.nih.gov/.
TITLE      National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL    Unpublished (1999)
COMMENT    Contact: Robert Strausberg, Ph.D.
           Email: cgapbs-r@mail.nih.gov
           Tissue Procurement: James Cleaver, M.D.
           cDNA Library Preparation: Life Technologies, Inc.
           cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA
           Sequencing by: Incyte Genomics, Inc
           Clone distribution: MGC clone distribution information can be
           found through the I.M.A.G.E. Consortium/LLNL at:
           http://image.llnl.gov
           Plate: LLAM10697 row: g  column: 02
           High quality sequence stop: 707.
FEATURES             Location/Qualifiers
     source          1..935
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:4802713"
                     /lab_host="DH10B (T1 phage-resistant)"
                     /clone_lib="NCI_CGAP_Skn3"
                     /note="Organ: skin; Vector: pCMV-SPORT6; Site_1: NotI;
                     Site_2: SalI; Cloned unidirectionally. Primer: oligo dT.
                     Average insert size 1.5kb. Library constructed by Life
                     Technologies. Note: this is a NCI_CGAP Library."
ORIGIN
Query Match        27.0%;  Score 594;  DB 12;  Length 935;
Best Local Similarity  86.8%;  Pred. No. 2.4e-108;
Matches 799;  Conservative  0;  Mismatches  65;  Indels  56;  Gaps  11;
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SOURCE   Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 1149)
AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
TITLE   National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL   Unpublished (1999)
COMMENT   Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Invitrogen
            cDNA Library Preparation: Life Technologies, Inc.
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Agencourt Bioscience Corporation
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAMI2364   row: i   column: 09
            High quality sequence stop: 568.
FEATURES   Location/Qualifiers
     source   1..1149
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:5590352"
                     /lab_host="DH10B"
                     /clone_lib="NIH_MGC_125"
                     /note="Organ: ovary (pool of 3); Vector: pCMV-SPORT6;
                     Site 1: EcoRV (destroyed); Site 2: NotI; RNA source pool
                     of three ovaries, from females ranging in age from 38 to
                     49 yo. Library is oligo-dT primed and directionally cloned
                     (EcoRV site is destroyed upon cloning). Average insert
                     size 2.1 kb, insert size range 1-3.5 kb. Library is
                     normalized and enriched for full-length clones and was
                     constructed by C. Gruber (Invitrogen). Research Genetics
                     tracking code 036."

ORIGIN

Query Match   26.1%; Score 574.4; DB 12; Length 1149;
Best Local Similarity   92.0%; Pred. No. 2e-104;
Matches 653; Conservative   0; Mismatches 21; Indels 36; Gaps 3;

Qy   1492 TCGGGAGTGGACCTCATCCTGTCATTGGACTACAACCTCCACGGAGCCTTCCAGCAGTT 1551
          ||||||||||||||||||||||||| |||||||||||||||||||||||||||||||||
Db   11 TCGGGAGTGGACCTCATCCTGTCATTGGACTACAACCTCCACGGAGCCTTCCAGCAGTT 70

Qy   1552 GCAGCTCCTGGGCCGGTTCTGCCAGGAGCAGGGGATCCGGTTCCCACCCATCTCGCCCAG 1611
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   71 GCAGCTCCTGGGCCGGTTCTGCCAGGAGCAGGGGATCCGGTTCCCACCCATCTCGCCCAG 130

Qy   1612 CCCCGAAGAGCAGCTCCAGCCTCGGGAGTGCCACACCTTCTCCGACCCCACCTGCCCCGG 1671
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   131 CCCCGAAGAGCAGCTCCAGCCTCGGGAGTGCCACACCTTCTCCGACCCCACCTGCCCCGG 190

Qy   1672 AGCCCCTGCGGTGCTGCACTTT----------------------------TCCTC 1698
          |||||||||||||||||||||| |||||
Db   191 AGCCCCTGCGGTGCTGCACTTTCCTCTGGTCAGGACTCCTTCCGGGAGTACTCGGCCCC 250

Qy   1699 TGGGGTCCGGCGGACACCCGAGGAGGCGGCAGCTGGGGAGGT 1758
          ||||||||||||||||||||||||||||||||||||| |||||
Db   251 TGGGGTCCGGCGGACACCCGAGGAGGCGGCAGCTGGGGAGTGAACCTGTCTTCATCGGA 310

Qy   1759 CTCTCCCTACCACTACAGAGAAGTGACCTACAGCAGAGCAGTGCTGCA 1818
          |||||||||||||||||||||||||||||||||||||||||||||||
Db   311 CTCTCCCTACCACTACAGAGAAGTGACCTACAGCAGAGCAGTGCTGCA 370

Qy   1819 CCTGACACATTACAATGTCTGCAACAACAGCGGCTCTGGCCAGGC 1878
          |||||||||||||||||||||||||||||||||||||||||||||
Db   371 CCTGACACATTACAATGTCTGCAACAACAGCGGCTCTGGAGGCTCTGGCCAGGC 430

Qy   1879 AGTGCAGCGGAGCGGAGCGGCAGCGCGCAGCCCCTGCCACCCCTAAC 1938
          |||||||||||||||||||||||||||||||||||||||||||||||
Db   431 AGTGCAGCGGAGCGGAGCGGCAGCGCGCAGCCCCTGCCACCCCTAAC 490

Qy   1062 GGCTTCCTGAGTCCGCATCTGCTTCTTAGAAGGTATCTGGAGCAACCTGTATCGCAGCCA 1121
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 GGCTTCCTGAGTCCGCATCTGCTTCTTAGAAGGTATCTGGAGCAACCTGTATGCAGCCA 60

Qy   1122 ACCTCCAGGACAGCAGCTTATACTGGGCCTCAGAGCCCAGCCCAGTTCTGGGACCGCTGGGTCA 1181
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 ACCTCCAGGACAGCAGCTTATACTGGGCCTCAGAGCCCAGCCCAGTTCTGGGACCGCTGGGTCA 120

Qy   1182 GGAACCAGGCCAACCTGACAAGAGACAAGGAGGTCCCCCTTCTGAAGATAGAAGAACCACCCT 1241
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121 GGAACCAGGCCAACCTGACAAGAGACAAGGAGGTCCCCCTTCTGAAGATAGAAGAACCACCCT 180

Qy   1242 CAACAGCGCGGCAGAATAGCTGAGTTTTTCACCGATCTTCTGACGTGGCGTCCACTGGCCC 1301
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181 CAACAGCGCGGCAGGATAGCTGAGTTTTTCACCGATCTTCTGACGTGGCGTCCACTGGCCC 240

Qy   1302 AGGCCACACATAATTCCTGCGTGGCCTCCATTTCCACAAAGACTACTTTCAGCATCCTC 1361
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241 AGGCCACACATAATTCCTGCGTGGCCTCCATTTCCACAAAGACTACTTTCAGCATCCTC 300

Qy   1362 ACTTCTCCACATGGAAAGCTACCACTCTGGATGGCTCCCCAACCAGCTGACACCCTCGG 1421
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   301 ACTTCTCCACATGGAAAGCTACCACTCTGGATGGCTCCCCAACCAGCTGACACCCTCGG 360

Qy   1422 AGCCCCACCTGTGCCTGCTGACGATGTTGGCTACCTCATCAATACCAGCTGCCTGCCCTCC 1481
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   361 AGCCCCACCTGTGCCTGCTGACGATGTTGGCTACCTCATCAATACCAGCTGCCTGCCCTCC 420

Qy   1482 TGCAGCCACTCCGGAGACGTGGACCTGACCTCATCCTCCTGTCATTGGACTACAACCTCCACGGAGCCT 1541
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   421 TGCAGCCACTCCGGAGACGTGGACCTCATCCTCCTGTCATTGGACTACAACCTCCACGGAGCCT 480

Qy   1542 TCCAGCAGTTGCAGCTCCTGGGCCGGTTCTGCCAGGAGCAGGGGATCCCGGTTCCCACCCA 1601
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   481 TCCAGCAGTTGCAGCTCCTGGGCCGGTTCTGCCAGGAGCAGGGGATCCCGGTTCCCACCCA 540

Qy   1602 TCTCGCCCAGCCCCGAAGAGCAGC-TCCAGCCTCGGG-AGTGCCACACCTT--CTCCGAC 1657
          |||||||||||||||||||||||| ||||||||||| |||||||||||| ||||||||
Db   541 TCTCGCCCAGCCCCGAAGAGCAGCATCCAGCCTCGGGAAGTGCCACACCTTCTCCGAC 600

Qy   1658 CCCACCTGCCCCGGAGCCCCTGCGGTGCTGCACTTTTCCTC------- 1698
          ||||||||||||||||||||||||||||||||||||| |||
Db   601 ACCAACTGCCCCGGAGCCCCTGAGTGTGCTGCACTTTTACCTCTGGTCAGGACTCCTTCCG 660

Qy   1699 --------------TGGGGTCCGGCGGACACCCGAGGAGGCGGCAGCTG-GGGAGGT 1740
                        |||||||||||||||||||||||||||||||||| |||||||
Db   661 GGAGTACTCGGCCCCATGGGGTCCGGCGGACACCCGAGGAGGCGGCAGCTGGGGAGGT 720

Qy   1741 GAACCTG---TCTTCATCGGACTCTCCCTACCACTA--CACGAAGTGACCTACAGCCAG 1795
          ||||||| |||||||||||||||||||||||||| |||||||||||||||||||||
Db   721 GAACCTGGACTCTTCATCGGACTCTCCCTACCACTAGCACGAAGTGACCTACAGCAG 780

Qy   1796 GAGGACGTGGACACAG---CTGCTGCACGTGCAGCGGAGCAGC-GTCTGCAACAACCAGGA 1851
          |||||||||||||||| ||||||||||||||||||||||| ||||||||||||||||
Db   781 GAGGACGTGGAACAGAGCTGAACGGCTCATGCACCTGCCACATTACAATGTCTGCAACAACCAGGA 840

Qy   1852 GCAGCTGCT----GGAGCTGTCGGCCAGGCAGCGGAGCGCGGAGC-GGCAGCGCGCAGGGC 1905
          |||||||| ||||||||||||||||||||||||||||||| ||||||||||||||
Db   841 AGACACGCGTGATGGGAGGAACTGAGCCAGCCAGGGAACAGAGGCAGCGAGAGCGCAGGGGC 900

Qy   1906 CCACTGATGGCCGGGGCCCC 1925
          ||||||||||||||||||||
Db   901 ACATAGAATGGCCGAGGCCC 920

RESULT 10
BM906397
LOCUS   BM906397   1149 bp   mRNA   linear   EST 12-MAR-2002
DEFINITION AGENCOURT_6620095 NIH_MGC_125 Homo sapiens cDNA clone IMAGE:5590352
            5', mRNA sequence.
ACCESSION   BM906397
VERSION   BM906397.1 GI:19356776
KEYWORDS   EST.

```
                   sequence that is located between the Not I site and the
                   (dT)18 tail. The sequence tag for this library is
                   CGCGTATACC. This library was created for the program, Gene
                   Discovery in the Visual System, supported by National Eye
                   Institute (NEI).
                   TAG_TISSUE=human fetal eye
                   TAG_LIB=UI-E-EO1
                   TAG_SEQ=CGCGTATACC"

ORIGIN

Query Match        25.9%;  Score 569.8;  DB 13;  Length 653;
Best Local Similarity 94.6%;  Pred. No. 1.7e-103;
Matches  614;  Conservative  0;  Mismatches  2;  Indels  33;  Gaps  1;

Qy  1589 CCGTTCCCACCCATCTCGCCCAGCCCCGAGAGCAGCTCCAGCTCCGGAGTGCCACACC 1648
         ||||||||||||||||||||||||||||||||||||||| ||||||||||||||||||
Db   653 CCGTTCCCACCCATCTCGCCCAGCCCCGAGAGCAGCTCCAGCTCCGGAGTGCCACACC 594

Qy  1649 TTCTCCGACCCCACCTGCCCCGGAGCCCCTGCGGTGCTGCACTTT------------- 1693
         ||||||||||||||||||||||||||||||||||||||||||||
Db   593 TTCTCCGACCCCACCTGCCCCGGAGCCCCTGCGGTGCTGCACTTTCCTCTGGTCAGCGAC 534

Qy  1694 -----------------TCCTTCGGGTTCCGGCGGACACCCGAGGAGGCGGCAGCTGGG 1735
                          |||||||||||||||||||||||||||||||||||||||||||
Db   533 TCCTTCCGGGAGTACTCGGCCCCTGGGTTCCGGCGGACACCCGAGGAGGCGGCAGCTGGG 474

Qy  1736 GAGGTGAACCTGTCTTCATCGGACTCTCCCCACCACTACAGAAGGTGACCTACAGCCAG 1795
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   473 GAGGTGAACCTGTCTTCATCGGACTCTCCCCACCACTACAGAAGGTGACCTACAGCCAG 414

Qy  1796 GAGGACGGTGGACAAGCTGCTGCACCTGACACATTACAATGTCTGCAACCAGGAGCAG 1855
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   413 GAGGACGGTGGACAAGCTGCTGCACCTGACACATTACAATGTCTGCAACCAGGAGCAG 354

Qy  1856 CTGCTGGAGGCTGCTGCGCCAGGCAGTGCAGTGCAGGCGGCAGGCCCCACTGATGG 1915
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   353 CTGCTGGAGGCTGCTGCGCCAGGCAGTGCAGTGCAGGCGGCAGGCCCCACTGATGG 294

Qy  1916 CCGGGGCCCCTGCCACCCTAACTCATTCATTCCTCCTCCTGCTGAGTTGCAGTGGGA 1975
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   293 CCGGGGCCCCTGCCACCCTAACTCATTCATTCCTCCTCCTGCTGAGTTGCAGTGGGA 234

Qy  1976 ACTGTCATCACGCAGTGCTTCAGAGCCTGGGCTGGCACTGTCCCAGGGTCCAGG 2035
         |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   233 ACTGTCATCACGCAGTGCTTCAGAGCCTGGGCTGGCACTGTCCCAGGGTCCAGG 174

Qy  2036 CTGAGGGCTGGGAGCTCCCTGCCCCGGCCTCAGCAGTTTGCAGTGGGGTAAGGAGGCCAAGCC 2095
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   173 CTGAGGGCTGGGAGCTCCCTGCCCCGGCCTCAGCAGTTTGCAGTGGGGTAAGGAGGCCAAGCC 114

Qy  2096 CATTTGTGTAATCACCAAAAACCCCCGGCCGTGCCGTGTTTCCCTTCTGCGCTACCTT 2155
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   113 CATTTGTGTAATCACCAAAAACCCCCGGCCGTGCCGTGTTTCCCTTCTGCGCTACCTT 54

Qy  2156 GAGTAGTTGGAGCACTTGATACATCATCACAGACTCATACAAAAAAAAAAAAAA 2204
         ||||||||||||||||||||||||||||||||||||||||
Db    53 GAGTAGTTGGAGCACTTGATTACATCATCACAGACTCATACAAAAAAAAAAAAAA 5
```

RESULT 12
BQ887656
LOCUS   BQ887656   922 bp   mRNA   linear   EST 16-AUG-2002
DEFINITION AGENCOURT_8764474 NIH_MGC_129 Mus musculus cDNA clone IMAGE:6312998
            5', mRNA sequence.
ACCESSION   BQ887656
VERSION   BQ887656.1 GI:22279670
KEYWORDS   EST.
SOURCE   Mus musculus (house mouse)
  ORGANISM Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1 (bases 1 to 922)
AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.

```
Qy  1939 TCTCATTCATTCCCGGCGTGCTGAGTTGCAGGTGGAACTGTCATCACGCAGTGCTTCAG 1998
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   491 TCTCATTCATTCCCTGGCCTGCTGAGTTGCACGTGGGAACTGTCATCACGCAGTGCTTCAG 550

Qy  1999 AGCCTCGGGGCTCAGGTGGCACTGTCCCAGGGTCCAGGGTGGCTCAGGGCGGCTCCCTTGC 2058
         |||||||||||||||||||||||||||||||||||||  |||||||||||||||||||||
Db   551 AGCCTCGGGCTCAGGTGGCACTGTCCCAGGGTCCAGGCTGGCTCAGGGCTGGGAGCTCCCTTGC 610

Qy  2059 GCCTCAGCAGTTGCAGTGGGGTAAGGAGGCCAAGCCCA-TTTGTGTAATCACCCAAAAC 2117
         ||||||| ||||||||||||||||||||||||||||||  ||||||||||||||  ||||
Db   611 GCCCCAGCAGTTGCCAGGGGGGTAAGGAGGCCCAGCCCATTTTGGGTAATCCCCAAAAAC 670

Qy  2118 CCCCGGCCGTGT--CCTGTTTTCCCTTCTGCGCTACCTTGAGTAGTTGG 2165
         ||||| ||||||  ||||||||||||||||||||| ||||||||||||
Db   671 CCCCGACCCTGTGGCCCTGTTTTCCCCTACAGGGCAACCTTGAATAGTTGG 720
```

RESULT 11
BU742347/c
LOCUS   BU742347   653 bp   mRNA   linear   EST 10-OCT-2002
DEFINITION UI-E-EO1-ajc-i-21-0-UI.s1 UI-E-EO1 Homo sapiens cDNA clone
            UI-E-EO1-ajc-i-21-0-UI 3', mRNA sequence.
ACCESSION   BU742347
VERSION   BU742347.1 GI:23688719
KEYWORDS   EST.
SOURCE   Homo sapiens (human)
  ORGANISM Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 653)
AUTHORS   Bonaldo,M.F., Lennon,G. and Soares,M.B.
TITLE   Normalization and subtraction: two approaches to facilitate gene
            discovery
JOURNAL   Genome Res. 6 (9), 791-806 (1996)
MEDLINE   97044477
PUBMED   8889548
COMMENT   Contact: Soares, MB
            Coordinated Laboratory for Computational Genomics
            University of Iowa
            375 Newton Road , 4156 MEBRF, Iowa City, IA 52242, USA
            Tel: 319 335 8250
            Fax: 319 335 9565
            Email: bento-soares@uiowa.edu
            Tissue Procurement: Dr. Gregg Hageman
            cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
            cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
            DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
            Clone Distribution: Researchers may obtain clones from Research
            Genetics (www.resgen.com).
            Seq primer: M13 FORWARD
            POLYA=Yes.
FEATURES   Location/Qualifiers
     source   1..653
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="UI-E-EO1-ajc-i-21-0-UI"
                     /tissue_type="fetal eye"
                     /dev_stage="fetal"
                     /lab_host="DH10B (Life Technologies) (T1 phage resistant)"
                     /clone_lib="UI-E-EO1"
                     /note="Organ: eye; Vector: pT7T3-Pac (Pharmacia) with a
                     modified polylinker; Site_1: EcoR I; Site_2: Not I;
                     UI-E-EO1 is a normalized cDNA library containing the
                     following tissue(s): fetal eye. The library was
                     constructed according to Bonaldo, Lennon and Soares,
                     Genome Research, 6:791-806, 1996. First strand cDNA
                     synthesis was primed with an oligo-dT primer containing a
                     Not I site. Double stranded cDNA was ligated to an EcoR I
                     adaptor, digested with Not I, and cloned directionally
                     into pT7T3-Pac vector. The oligonucleotide used to prime
                     the synthesis of first-strand cDNA contains a library tag

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Db   602 |||||| ||||||||||| ||| ||||| ||| ||||| ||| |||||| ||| ||||||
         GGTCCCCATCTGAAGATAGCAGAGCCACCGACAATGCTGGCAAGATCGCCGAGCTCTT 661

Qy  1270 CACCGATCTTCTGACGTGGCGTCCACTGGCCCCAGGCCACACATAATTTCCTGCGTGGCCT 1329
         |||| ||||||||| |||||||||||||||||||||||||||| || ||||||| |||||||
Db   662 CACTGACCTCCTGACAAAGCGTCCCTCGCCCACGCCACCGCCACCCACAACTTCACCGAGGCCT 721

Qy  1330 CCATTTCCACAAAGACTACTTTCAGCATCCTCACTTCTCCAC 1371
         ||||||||||||| |||||||
Db   722 CCATTTCCACAAAGGACTATTTCAGAAACTTCAACTTCTC 763
```

RESULT 13

```
LOCUS       AW959903                 666 bp    mRNA    linear   EST 01-JUN-2000
DEFINITION  EST371974 MAGE resequences, MAGF Homo sapiens cDNA, mRNA sequence.
ACCESSION   AW959903
VERSION     AW959903.1  GI:8149587
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 666)
AUTHORS     Hegde,P., Qi,R., Abernathy,K., Dharap,S., Gaspard,R., Gay,C.,
            Holt,I.E., Saeed,A.I., Sharov,V., Lee,N.H., Yeatman,T.J. and
            Quackenbush,J.
TITLE       Assessment of gene expression patterns in a model of colon tumor
            metastasis using a 19,200 element cDNA microarray
JOURNAL     Unpublished (2000)
COMMENT     Contact: John Quackenbush
            The Institute for Genomic Research
            9712 Medical Center Dr., Rockville, MD 20850, USA
            Tel: 301 838 3528
            Fax: 301 838 0208
            Email: johnq@tigr.org
            Plate: 139
            Seq primer: Reverse.
FEATURES             Location/Qualifiers
     source          1..666
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone_lib="MAGE resequences, MAGF"
                     /note="Vector: pBluescriptSKm"
ORIGIN
```

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Query Match           25.3%;   Score 558.2;  DB 10;   Length 666;
Best Local Similarity 92.0%;   Pred. No. 3.6e-101;
Matches   612;   Conservative   0;   Mismatches  20;   Indels  33;   Gaps   1;

Qy  1275 ATCTTCTGACGTGGCGTCCACTGGCCCCAGGCCACACATAATTTCCTGCGTGGCCTCCATT 1334
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1 ATCTTCTGACGTGGCGTCCACTGGCCCCAGGCCACACATAATTTCCTGCGTGGCCTCCATT 60

Qy  1335 TCCACAAAGACTACTTTCAGCATCCTCACTTCTCCACATGGAAAGCTACCACTCTGGATG 1394
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    61 TCCACAAAGACTACTTTCAGCATCCTCACTTCTCCACATGGAAAGCTACCACTCTGGATG 120

Qy  1395 GGCTCCCCAACCAGCTGACACACCCTCGGAGCCCCACCTGTGCCCTGCTGGATGTTGGCTACC 1454
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121 GGCTCCCCAACCAGCTGACACACCCTCGGAGCCCCACCTGTGCCCTGCTGGATGTTGGCTACC 180

Qy  1455 TCATCAATACCAGTGCTGCTGCCCCTCCTGCAGCCCACTGCAGCCGGACTGCGACCTTGGGCCTC 1514
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181 TCATCAATACCAGTGCTGCTGCCCCTCCTGCAGCCCACTGCAGCCGGACTGCGACCTCATCCTGT 240

Qy  1515 CATTGGACTACAACCTCCACCATCTGCCCGGTTCTGCCC 1574
          ||||||||||||||||||||||||||||||||||||||
Db   241 CATTGGACTACAACCTCCACGGAGCCTTCCACCGGTTCTGCCC 300

Qy  1575 AGGAGCAGGGGATCCCGTTCCACCCATCTGCCCAAGAGAGCAGCTCCAGCCTC 1634
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
```

```
FEATURES             Location/Qualifiers
     source          1..922
                     /organism="Mus musculus"
                     /mol_type="mRNA"
                     /db_xref="taxon:10090"
                     /clone="IMAGE:6312998"
                     /lab_host="DH10B (phage-resistant)"
                     /clone_lib="NIH_MGC_129"
                     /note="Organ: olfactory epithelium; Vector: pCMV-SPORT6.1;
                     Site_1: EcoRV; Site_2: NotI; Cloned unidirectionally.
                     Primer: Oligo dT. Average insert size 2.2 kb. Constructed
                     by ResGen, Invitrogen Corp. Note: this is a NIH_MGC
                     Library."
ORIGIN
```

```
Query Match           25.5%;   Score 562;  DB 13;   Length 922;
Best Local Similarity 83.6%;   Pred. No. 6.2e-102;
Matches   637;   Conservative   0;   Mismatches 125;   Indels   0;   Gaps   0;

Qy   610 CACCTGGGCCTTGGCCAACCTTTATGAGGACCCAGAGTGGTCTCCAGAAGGACCTGGCAGG 669
         ||||    ||||||||||  ||||||||||| ||| ||||||||||||||||||||||||
Db     2 CACAGAGACCTGCCAACCTCTATGAGGACCCAGAGTGGTCGCAGAAGGACCTGGCAGG 61

Qy   670 GCCCACTGAGTTGCTGAAGACCCAGGTGACCAAGAACAAGCTGGGTGTGCTGGCCCCCAG 729
         |||||||||| ||||||||||||||| ||||||||||||||||||||||||||||| ||
Db    62 GCCCACTGAGTTGCTGAAGACACAGGTGACAAAGAGCAAGCTGGGTGCGTTGGCCCCTAG 121

Qy   730 CCAGCTGCAGCGTACCGGCAGGAGGCTGGCGCAGAGCGTGCCCCGCTTGGGCGTACCCAAGCTG 789
         ||||  ||||||||||||||||||||||| |||||| |||||||||| ||||||||||||
Db   122 CCAACTTTGGCCGTACCGGCAAGAGCTGGCTGGCTGAGCGTGCTCGGCCTGGCTGGCGCCACCCTG 181

Qy   790 CTTCACCAACCTGTGGGCCCTCATCAACGAGGGCGCTGCTGCATGATGAGCCCCATGATCA 849
         ||||||||||||||||||||||||||||||||| |||||||||||||||||||||||||
Db   182 CTTCACCAACTTGTGGGCCCTCATTAATGAGGCCTTGCTGCACGACAAGCCCCATGAACA 241

Qy   850 CAAGCTCTCAGATCAACGGAGGCCCTGAGTCATGGCCAGAACCCTCGCCCATCTACTCTG 909
         ||||  ||||||||| |||||||||||||| ||||| ||||||||||| |||| |||||
Db   242 CAAACTCTCAGATCAACGAGAGCGCCCTGAGTCGAGGCCAGAACCCTCTGCCTCTCTATTG 301

Qy   910 TGCCCTCAACACCAAAGGCAGAGAGCGCAGAGCCCTGACCACTTTTGAATTTGGGGAGTTGTGCGAGTT 969
         |||||||||| || |||||||| |||||||||||||||| |||| |||||||| ||||| |||||
Db   302 TGCCCTCAACAGAAGCAGGAGCAGGGCGCGGAGTACCTTTGACTTTTGGGGAGTGGTGTGAGTT 361

Qy   970 CTCTTCCCTACGGAGGTCCGGCTTCCCAAGTACGGGGCCTTCATCCCCTCGAGCTCTTTGG 1029
         |||| ||||||||||| |||||| ||||||||||| || |||| |||||||||||||| ||
Db   362 CTCTCCATATGAAGTCGGCTTCCCAAGTATGGAGCGTTCATCCTCCTCCGAGCTCTTTGG 421

Qy  1030 CTCCGAGTTCTTTATGGGGCAGCTGATGAAGAGGCTTCCTGAGTCCGCATCTGCTTCTT 1089
         || ||| ||||||||||||| |||||||||||||||| ||||||| ||||||| |||
Db   422 CTCGGAGTTCTTTATGGGGCGGCTGGTGAAGCAGCTTCCCGAGTCCCGCATCTGCTTCCT 481

Qy  1090 AGAAGGTATCTGGAGCAACCAGATGTATGCGAACATGTGTTTGCGGCAACCAGCTTATACTGGGCCTC 1149
         |||| || ||||||||||||||||| || |||||| || ||||||||||||||| ||||||
Db   482 GGAAGGCATCTGGAGCAATCTGTTTGCGGCAACAGCTGTGCGGCAACCAGCTTGTACTGGTCCTC 541

Qy  1150 AGAGCCCAGCCAGTTCTGGGACCGCGTGGGTCAGGAACCAGCCAACCTGACCAAGAGACA 1209
         |||| ||||||||| ||||||||||| |||||||||||||||||||| |||| ||||||
Db   542 AGAACCCAGCCAGTTGTTCTGGGACCGCGTCTGGGACGGATCAGGCAGCCACCTGACCAAGAAAGAGCA 601

Qy  1210 GGTCCCCTTCTGAAGATAGAAGAAGACCACCCTCACAGCCGGCGAGAATAGCTGAGTTTTT 1269
```

```
Db    301 AGGAGCAGGGGATCCCGTTCCCACCCATCTCGCCCAGCCCCGAGAGCAGTCCAGCCTC 360
              ||||||||||||||||||||||||||||||||||||||||
Qy   1635 GGGAGTGCCACACTTCTCGACCCCACCTGCCCCGGCGCCCTGCGGTGCTGCACTTTT 1694
              ||||||||||||||||||||||||||||||||||||||||
Db    361 GGGAGTGCCACACTTCTCCGACCCACCTGCCCCGGAGCCCCTGCGGTGCTGCACTTTC 420

Qy   1695 C-------------------------------CTCTGGGGTCCGCGGACACCCGAGG 1721
                                           |||||||||||||||||||||||||
Db    421 CTCTGGTCAGCGACTCCTTNCCGGAGTACTCGGCCCCTTGGGTCCGCGGACACCCGAGG 480

Qy   1722 AGGCGGCAGCTGGGGGAGGTGAACCTGTCTTCATCGGACTTCCCCTACCACTACACGAAGG 1781
              ||||||||||||||||||||||||||||||||||||||||||||||||
Db    481 AGGCGGCAGCTGGGGGAGGTGAACCTGTCTTCATCGGACTTCCCTACCACTACACGAAGG 540

Qy   1782 TGACCTACAGCCAGGAGGACGTGGACAAGCTGCTGCACCTGACACATTACAATGTCTGCA 1841
              ||||||||||||||||||||||||||||||||||||||||
Db    541 TGACCTACAGCCAGGAGGACGTGGACAAGCTGCTGCACCTGACACATTACAATGTCTTGC 600

Qy   1842 ACAACCAGGAGGAGCGCGTGCTCGGAGGCTCTGCGGCAGGCAGTGAGCGGCCGGCAGCGCA 1901
              ||||||||||||||||||||||| ||||||||||||||||
Db    601 ACAACCAGAAGGCAANTGCTTGAGCTCTGCNCCCAGCAATGCAACCGAGGCCGCAACGCA 660

Qy   1902 GGCCC 1906
              ||||
Db    661 GGCCC 665
```

RESULT 14
```
CA319426
LOCUS       CA319426                810 bp    mRNA    linear   EST 09-JUL-2003
DEFINITION  UI-M-FW0-cbz-n-15-0-UI.r1 NIH_BMAP_FW0 Mus musculus cDNA clone
            IMAGE:6816688 5', mRNA sequence.
ACCESSION   CA319426
VERSION     CA319426.1  GI:24537550
KEYWORDS    EST.
SOURCE      Mus musculus (house mouse)
ORGANISM    Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 810)
AUTHORS     NIH-MGC http://mgc.nci.nih.gov/.
            National Institutes of Health, Mammalian Gene Collection (MGC)
TITLE       Unpublished (1999)
JOURNAL
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Dr. Jim Lin, University of Iowa
            cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
            cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
            DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
            Clone Distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            This clone was contributed by the Brain Molecular Anatomy Project
            (BMAP)
FEATURES             Location/Qualifiers
     source          1..810
                     /organism="Mus musculus"
                     /mol_type="mRNA"
                     /strain="C57BL/6"
                     /db_xref="taxon:10090"
                     /clone="IMAGE:6816688"
                     /tissue_type="whole brain"
                     /dev_stage="embryo 13.5,14.5,16.5,17.5dpc"
                     /lab_host="DH10B (T1 phage resistant)"
                     /clone_lib="NIH_BMAP_FW0"
                     /note="Organ: Brain; Vector: pYX- Asc; Site_1: EcoR I;
                     Site_2: Not I; The library was constructed according
                     Bonaldo, Lennon and Soares, Genome Research, 6:791-806,
                     1996. Denatured RNA was size fractionated on a 1% agarose
                     gel. First strand cDNA synthesis was primed with oligo-dT
                     primer containing a Not I site. Double strand cDNA was
                     ligated
                     size selected according to mRNA size fraction,
                     Seq primer: pYX-5.
```

with EcoR I adaptor, digested with NotI and then cloned
directionally into pYX-Asc vector. The library tag
sequence located between the Not I site and the polyA tail
is AGCGAGCAG. This library was created for the University
Iowa Brain Anatomy Project (BMAP): 'Gene Discovery in the
Developing Mouse Nervous System', supported by National
Institute of Mental Health (NIMH), Hemin Chin, Ph.D.,
program coordinator."

ORIGIN

```
Query Match     25.2%;  Score 556.2;  DB 14;  Length 810;
Best Local Similarity  82.4%;  Pred. No. 9e-101;
Matches  672;  Conservative  0;  Mismatches 138;  Indels  6;  Gaps  3;
```

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Qy    709 GCTGGGGTGCTGCGCCCCAGCTGCAGCGGTACCGGCGTACCGCGAGCGTGC 768
              |||||||||||||||||  |||||||||||||||||||||||||||||
Db      1 GCTGGGGTGCTGTGGCCCCTAGCCAACTTTGGCCGGTACCGGCAAGAGCGTGCTGGCGGTGC 60

Qy    769 CCGCTTGGGCTACCCAAGCTGCTTCACCAACTGTGGGCCCTCATCAACGAGGCGCTGCT 828
              ||||||||||||||||| ||||||||||| ||||||||||||||||||
Db     61 TCGCCTGGGCCACCACCTGCTTCACCAACTGTGGGCCCTCATTAATGAGGCCTTGCT 120

Qy    829 GCATGATGAGCCCATGATGACAAGCTCTCAGATCAACGGAGGCCCTGAGTCATGGCCA 888
              |||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 GCACGACAAGCCCATGAACACAAACTTCAGATCAACGAGAGGCAGAGCCCTGAGTCGAGGCCA 180

Qy    889 GAACCCTCGCCCATCTACTGTGCCCTCAACACCAGCAGCAAGGACAAGGAGCAGAGCCTG 948
              |||||||||||||||||||||||||||||||||||||||||||||||
Db    181 GAACCCTCGCCCATCTATCTATTGTGCCCTCAACACCAGCAGCAAGGCCAAGGAGCAGAGCCTG 240

Qy    949 ATTTGGGAGGTGTGCGAGTTCTCTCCCTACGAGGTCGGCTTCCCCAAGTACGGGCCCTT 1008
              |||||||||||||||||  ||||||||||||||||||||||||||||
Db    241 CTTTGGGAGGTGGTGTGAGTTCTCTCCATGAGTCGGCTTCCCCAAGTATGGAGCGTT 300

Qy   1009 CATCCCCCTGGGCTCTTTGGCTCCGAGTTCTTTATGGGGCAGCTGATGAAGAGAGGCTTCC 1068
              ||||||||||||||||||||||||||||||||||||||||||||||
Db    301 CATCTCCCTGGGCTCTTTGGCTCCGGAGTTCTTTATGGGGCGGCTGGTGAAGCAGCTTCC 360

Qy   1069 TGAGTCCGGATCTGCTTCTTAGAAGGTATCTCGGAGCAACCTGTATGCAGCCAACCTACAGC 1128
              ||||||||||||||||||||||||||||||||||||||||||||||
Db    361 CGAGTCCCGGATCTGCTTCCTGGAAGGCATCCTGGAGCAATCTGTTTGCGGCCAGCCTCCA 420

Qy   1129 GGACAGCTTATACTGGGCTTCAGAGCCCAGCCAGTTCTGGGACCCGGTCAGGAACCA 1188
              ||||||||||||||||||||||||||||||||||||||||||||||
Db    421 AGACAGCTTCACTGTCTGCTGCTTCTTTCAGAGACCCAGTTCTGGGACCCGTCGGCGCAGGATCA 480

Qy   1189 GGCCAACCTGACAAGGAGGAGCAGGTCCCCCTTCTGAAGATAGAAGAACCACCCTACAACAGC 1248
              ||||||||||||||||||||||||||||||||||||||||||||||
Db    481 GGCCAACCTGACAAGAGACAGGTCCCCATCTGAAGATAGCAGAGCCACCGACAATGGC 540

Qy   1249 CGGCAGAATAGCTGAGTTTTCACCGATCTTCTGACGTGGCGTCCACTGGGCCAGGCCAC 1308
              |||||||||||||||||||||||||||||||| ||||||||||||||
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RESULT 15
BF769253/c

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DEFINITION  QV3-IT0008-111100-413-c05 IT0008 Homo sapiens cDNA, mRNA sequence.
ACCESSION   BF769253
VERSION     BF769253.1  GI:12117153
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
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            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 579)
AUTHORS     Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
            Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
            Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
            Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V.,
            O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
            Simpson,A.J.
TITLE       Shotgun sequencing of the human transcriptome with ORF expressed
            sequence tags
JOURNAL     Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
MEDLINE     20202663
PUBMED      10737800
COMMENT     Contact: Simpson A.J.G.
            Laboratory of Cancer Genetics
            Ludwig Institute for Cancer Research
            Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
            Brazil
            Tel: +55-11-2704922
            Fax: +55-11-2707001
            Email: asimpson@ludwig.org.br
            This sequence was derived from the FAPESP/LICR Human Cancer Genome
            Project. This entry can be seen in the following URL
            (http://www.ludwig.org.br/scripts/gethtml2.pl?t1=QV3&t2=QV3-IT0008-
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            High quality sequence start: 9
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                     /clone_lib="IT0008"
                     /note="Organ: epid tumor; Vector: puc18; Site 1: SmaI;
                     Site 2: SmaI; A mini-library was made by cloning products
                     derived from ORESTES PCR (U.S. Letters Patent application
                     No. 196,716 - Ludwig Institute for Cancer Research)
                     profiles into the pUC 18 vector. Reverse transcription of
                     tissue mRNA and cDNA amplification were performed under
                     low stringency conditions."
ORIGIN
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Query Match        23.3%;  Score 514.4;  DB 10;  Length 579;
Best Local Similarity  96.2%;  Pred. No. 2.1e-92;
Matches 560;  Conservative  0;  Mismatches 16;  Indels  6;  Gaps  3;

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